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(54) Title: BIALLELIC MARKERS

(57) Abstract

The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.

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## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater



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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a  
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays  
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for  
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to  
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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## DETAILED DESCRIPTION OF THE INVENTION

## DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

#### B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,



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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of  
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of  
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30 1988)).

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### 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

### 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

### III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with ~ polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote:  $p(AA) = x^2$
- Homozygote:  $p(BB) = y^2 = (1-x)^2$
- Single Heterozygote:  $p(AB) = p(BA) = xy = x(1-x)$
- Both Heterozygotes:  $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(ID)$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

$$25 \quad p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(ID)$  and  $p(exc)$ .

The cumulative probability of identity ( $\text{cum } p(ID)$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

$$30 \quad \text{cum } p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

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The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5        If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10        B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15        Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20        If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child  
25        attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30        The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the



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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\chi^2$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year-season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the

10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ),

20 ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$  to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30 scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate  
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod  
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.  
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some  
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)  
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or  
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate  
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host  
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include  
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as  
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing  
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,  
5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is  
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene  
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating  
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292  
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate



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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and  
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to  
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*  
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of  
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific  
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.

| 1        | 2   | 3 | 4 | 5   | 6   | 7   |
|----------|-----|---|---|-----|-----|---|
|          |     |   |   |     |     | TGTGAAACTCCACTTGAAGCCAAAGAAACACACACTTAAACACATGCCAGTTGGGAAGGTCT        |
|          |     |   |   |     |     | GAAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT   |
|          |     |   |   |     |     | GTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTTGAGGATAATGT     |
| WI-7070  | 226 | C | T | --- | --- | TACTAGACTTTATGCCATGGTCTTTC/TJAGTTTAAATGCTGTCTCTGTCTG                  |
|          |     |   |   |     |     | AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAAGGAC[G/C]AA  |
|          |     |   |   |     |     | AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT   |
|          |     |   |   |     |     | GATAATACATAAGCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAAATCTGAAT      |
| WI-10744 | 61  | G | C | --- | --- | AAATGAGGTAAAGTTTCAGGCACTCA  |
|          |     |   |   |     |     | GGGCAAAATACCAGCAAAAAGTCAAAATACCAGCATCAAAAGTCAGGTGCAAGGAGGTAGAACAA     |
|          |     |   |   |     |     | TTACAGTAACTATGTCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCCTAGAATA[C/T]JAGTG |
|          |     |   |   |     |     | GGTCCCTAATAGTTATTAGTCTCTTTTCTCCCTCTCTCACTCTCTGAAATTTATTTTATACTTAA     |
| WI-9975  | 126 | C | T | --- | --- | GGGATTAGTTACCACCAAAATGTATGTATCAATTTGATCTTACTGAA                       |
|          |     |   |   |     |     | GCTAGGTTTGTCTGTCTGCTCTCACTAGACTGAGATGACTTGATTACAGTAATCCCTATGT         |
|          |     |   |   |     |     | GATGTAACATAGTCTAGACCTTCCCTCTCCGCAATCCCAAGTCCAGGTTTCAGAAAGTATGCCACAC   |
|          |     |   |   |     |     | TCAACCTTCTCTCCAGTTCATCTGTATTAAATTTCTCCCATATAATTCAAAAGGAGTGGACAGGT     |
| WI-8010  | 247 | G | T | --- | --- | CCCTGGCTGAAAGAAATAAGAGATCCCAAGTGGTGGGG[G/T]CTT                        |
|          |     |   |   |     |     | GCCGGCCTATCTTTTAAATTTTAACTTGATCTTGGTGTCTCCATCCTAGGATTCGCCTTATAAT      |
|          |     |   |   |     |     | CTTTGTCTGTCTGTA[G/C]JATTACCTGATTCTAGCTTTTGATACACAAGGCTGATGGCTCACAATGT |
|          |     |   |   |     |     | AGTAGTGCCAAATCTTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA |
| WI-5222b | 85  | G | C | --- | --- | TCTCGACTCTATAACAACCTCCAACAGAA   |
|          |     |   |   |     |     | GCCGGCCTATCTTTTAAATTTTAACTTGATCTTGGTGTCTCCATCCTA[G/C]JGATTCGCCTTAT    |
|          |     |   |   |     |     | AATCTTTGTCTGTCTGTAGATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT    |
|          |     |   |   |     |     | AGTAGTGCCAAATCTTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA |
| WI-5222  | 52  | G | C | --- | --- | TCTCGACTCTATAACAACCTCCAACAGAA   |
|          |     |   |   |     |     | TATGCACTTCCACAAAAGCGATATAATTTAAAAGTTTTTTCATTAGAAATAAATGATAAAAAATAA    |
|          |     |   |   |     |     | ATATGTTATTATAGGCATTTATTACTAACTATAGTCTCTTGGAAAGAACACCCCAACCAATACTT     |
|          |     |   |   |     |     | ATAAAGTACATGTAATTTATAGTAACATAATTTACTATATACATAATGAAAAAATCATATTCTCACA   |
| WI-8007  | 242 | C | A | --- | --- | GAAAGCTGAACAGACATTCCACAGGATACGACTGTTGGAC[C/A]JAGTGTG                  |
|          |     |   |   |     |     | TCAGTTGCAAAAATGCTGCCATAAACATGCTTTGCTTATCTCTGTCATATGATGTTTTTTGTTAG     |
|          |     |   |   |     |     | TCTATATTCACACATATGAGTGAAATTT[C/T]JGGGGCATGGGAAATACATCTTTATGAGACATTGA  |
|          |     |   |   |     |     | ACTGCTCACCACATCATAGTATCCATTTTAAACAGACCAACAATGTATAAGAAATCCCTTTGTTTTAC  |
| WI-9823  | 97  | C | T | --- | --- | ATGCTTTCCAATCTGATTTTGTATGACTATTGTATGCACAGTTGGATCACC                   |

|          |             |     |  |
|----------|-------------|-----|--|
| WI-9651b | 105 A T --- | --- | TCCTACATTCATGGACAACCTCCATGCCCTTTCACATGCTGATCCCTCCTCTGGAATTCCTTCCT<br>ACTGTCTCATGTACAAATTTCTGCTCGTCTTCA/ATGGGCGAGCTTGCAAGCCTCCCTTTAGAC<br>ACCTACAGGTACAGCCGACCATGCCCTACCTCCATGCGACTGCCAGGGACCTTATAGGCCTCTG<br>TCCTTAAACCTGTAAATGGTATATTAATCCTTGGTGTGAATGCTCTC       |
| WI-9651  | 139 T C --- | --- | TCCTACATTCATGGACAACCTCCATGCCCTTTCACATGCTGATCCCTCCTCTGGAATTCCTTCCT<br>ACTGTCTCATGTACAAATTTCTGCTCGTCTTCAAGGGCGAGCTTGCAAGCCTCCCTTTAGACACCT<br>CT/JACAGGTACAGCCGACCATGCCCTACCTCCATGCGACTGCCAGGGACCTTATAGGCCTCTGT<br>CTTAAACCTGTAAATGGTATATTAATCCTTGGTGTGAATGCTCTC      |
| WI-7676b | 309 A C --- | --- | GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG<br>TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG<br>GCCGGCTCTCTGGTGGCTGTGGTTCAGGGGCGAGGAAGCGTGTGGACTGCAGCTTCTGCTGGTGC<br>TCCCCCGTCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT       |
| WI-7676  | 139 C T --- | --- | GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG<br>TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG<br>GC/JGGCTTCTTGGTGGCTGTGGTTCAGGGGCGAGGAAGCGTGTGGACTGCAGCTTCTGCTG<br>GTGTCCTCCCTCTCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATT         |
| WI-10072 | 105 G A --- | --- | CATTATCTGTCTGGTCTGTTCATTCACCTTCTCTCTCCAAAGAGGATATTTAAGCATCATTT<br>CATCTGGCCCTTTTGGATTTTGAATATTTTGTG/JGTACTCTTATGCACATGATAAATTTGTTA<br>TGTCTGTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAGGGA<br>TCACCCCTTTTGGCTCTACAACTTATAGATATTTAAATATCTTT             |
| WI-9986  | 42 T C ---  | --- | TTGGTGTGAACCTCAGAAATATAGGGAATAAGACAATTTGAAT/A,CJGTACCCCGAGGAACAAGAG<br>CCCTGCACCTTGACTCCAAAGGAGTTCTATTTCTGGCTGTTCCAGACTTTATGTATCTTGAGAA<br>GAGAACTGTTTCCCTCTAAATCAGTTTCATCTGTATCCAGGGTAGTACTCACAAAGACATGTCA<br>ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAATT  |
| WI-7041  | 174 C A --- | --- | GTCTATTGCAGGAGAAACGTCCTTGGCACTCCCACTCTCATCAGGCAAGTGGAGACTGGCCAGA<br>GGGCTGCACATGCAAACTCCAGTCCCTGCCCTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTATTT<br>CAGGGCTTGCATGGCTCTATTCCTCTGCTCTGCTC/CJCCACCTTCTTTGGAGCAAGGAGATGC<br>AGCTGTATTGTGTAAACAGCTCATTTGTACAGTGTCTGTATGTAATAA     |
| WI-7224  | 134 T C --- | --- | ATAAACCTTGTGTATGTATCACCACCTCACTAATTAACACTTATGTGCTATCAGATATCCTCTCT<br>ACCCTCACGTTATTTGAAGAAATCCTAAACATCAAACTTTTATCCATCAAAATGTCAGCATTTT<br>/CJATTTAAAAACAATAACTTTTAAAGAAACATAGGACACATTTTCAAAATTAATAAAATAAAG<br>GCATTTTAAAGGATGGCTGTGATTATCTTTGGGAAGCAGAGTATTCATGCTAG |

|                  |             |     |   |
|------------------|-------------|-----|---|
| WI-10826         | 132 A C --- | --- | TCTATTGCAATTCACAGTAGCCCATGAAGTAGGTATAACAGCCTCTATTTAAACATGAGAAGAT<br>GGAGGCCTTTTCCAAATGGACTAAGTAATGTGCTCAGGTTTCTTAAGCAAGACCTGCAJVC<br>JCCCTGGCTCCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGTCAGCCAGGACCCCATGCGCA<br>GAAAGCCAGCCTCTCCATCCCCAC   |
| TIGR-<br>A004S25 | 145 G A --- | --- | AGATCTGCCATTAGTATTATTCCTTTGAAGATACCTTTGGAGATTCAATTTCTTGAGTGGCACTGCAT<br>GCTCATTAGTGAAACCTTGTTGGGTATAGAAATGGAATGGAGATTTCAACAGCTTTGCTGAAAC<br>TGACTTTGG[G/A]CTCCAGACTTCACTGTCTTAGCATTGAAACCATCACCTGGTTTGCACTTCTC<br>ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC                |
| WI-1021          | 24 A T --   | --- | AAACACACAGAATCATCAAAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG<br>TAAGAAGTAAGTCTGAATAGTAGGATAGTATATCATTTCTGTAAATAGATTACCTCTCAGCAAT<br>TGGTCTGTTTTCATTCTATGGAACCTCTCCGTACTGTAATTTTCATTCTATGGAACCTCCCATACTGT<br>AATTGGACAGTTTGGTTCCAC                                |
| WI-4687          | 121 G T --- | --- | TAGTATGTCACGTCCCATGGTAAGGACTTTGATCACTAGGAATAAGAACACTTTGAATGGTCTTGTC<br>TTTCAATAAAAGAGTGACATGATTGAACATGTGTTTATAGATAAAGGACACTT[G/T]GCAGGAGTGT<br>TTAGGATGAAGAGAGAGAAAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAAAATAG<br>GAGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGTAT |
| WI-4719b         | 107 T G --- | --- | TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTGGGTGAGCGGATT<br>ATGCTGACGCCATGGGTTCATAGTGACTTGAGAGTTGAGAGGCTACACAGAAATCT<br>CTGTGAGGGGCATGTAATTGATTTCATTCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC<br>TGCTCAAAATTCCTTGTCAACTTATCCTTAAGACATTTTTCACAGGA                        |
| WI-4719          | 70 G A ---  | --- | TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTGGGTGAGCGGATT<br>AT[G/A]CTGACGCCATGGGTTCATAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT<br>CTGTGAGGGGCATGTAATTGATTTCATTCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC<br>TGCTCAAAATTCCTTGTCAACTTATCCTTAAGACATTTTTCACAGGA                |
| WI-9484b         | 216 G C --- | --- | TCAACACGCTTTTATGGCCTTCTGGCTCCCTCGTCCAGCAAGATTCCTACCTCTTACCCCTGTAGG<br>AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCCTCTGCACACTGCCAAGT<br>TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGCCAGACAGGGAGGAATCAAGGGCATGTATGGCTC<br>AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGACCCAGGGTTCCAAACCTT      |
| WI-9484          | 178 G A --- | --- | TCAACACGCTTTTATGGCCTTCTGGCTCCCTCGTCCAGCAAGATTCCTACCTCTTACCCCTGTAGG<br>AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCCTCTGCACACTGCCAAGT<br>TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGCCAGACAGG[G/A]AGGAATCAAGGGCATGTATG<br>GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCCAGGGTTCCAAACCTT     |



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| WI-7330  | 207 | C T --- | --- | AGGATGGAAGGAGACACGGGGCAGGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTGTCT<br>TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAATGTGGCATATAGGTTT<br>GTGACACAAGAAAGTCATACCTTTGGTGGCTAAGTTTACTAAGGAAAAAATAACTGAAAAAGATTAAAAAG<br>TGAGAGTC/TTGAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTACAG |
| WI-9443  | 211 | G A --- | --- | TTAAAAACAGTTCAGGTTGGTGAAGCAGAAAGGGATGTATTACAATTTAAATGAATCAGTCACATT<br>GCACAATTAATCCTCTTGGCATCATACAACTGGGTTTAAATGGCAAATGATGACATCATAGCATGA<br>CCAACTCATGGAAGGCAGTCTAGAGTCCATCAGCTCACACCTGAGGGGAAAGGCACTGCAOCCA<br>CTGACGAGAC/G/A/CAGAGACCTTGGACTACAGATGACACCAATGCCACCTT     |
| WI-7166  | 59  | C T --- | --- | TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA/C/TTGGAT<br>CATCAACAAGATTTCTTTGTGCAAAATATTTGACTATTCTGTATCTTTTCATCCTTGACTAAATTCGTG<br>ATTTCAAGCAGCATCTCTGGTTTAAACTTTGCTGTGAACAAATGTGAAAAAGAGTCTTCCAAT<br>TAATGCTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCGAG        |
| WI-7259b | 189 | T C --- | --- | GCCTTCCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGAGGGGAGCAATTTTAGCC<br>CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGCGCT<br>GGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGCCACAGT/C/TTGGGGGAGCAG<br>AGCCAGCAGTGGACAGGTGTTTCAGGGGGCCCAACTTCCCCTGGAGCTC            |
| WI-7259  | 188 | G T --- | --- | GCCTTCCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGAGGGGAGCAATTTTAGCC<br>CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGCGCT<br>GGCAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGCCACAGT/C/TTGGGGGAGCAG<br>GAGCCAGCAGTGGACAGGTGTTTCAGGGGGCCCAACTTCCCCTGGAGC             |
| WI-7322  | 275 | A G --- | --- | GTACTTTAGGCCTGTGGAGGGTGGGCAATTTAGTGGTGACCCCTTGACCCAGGGTTTCTAACAGATGAC<br>CCTGTGAATCATAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATATG<br>GCCATAAAGTGCCTAAGCACTCAGGCCTCCCACTCATCAACCCCTTGACCCAGAGAAAGCACTC<br>TGGTCTCTATCCCTTGTACATAGAGAGTTTGTATGGGGCCCTCTGGCTG    |
| WI-7685  | 46  | T C --- | --- | TCAGTTCTAGTCTCTGGGGCCACACAGAACTCTTTTGGGCTC/CTTTTCTCCCTCTGGATCA<br>AAGTAGGCAGGACCATGGGACAGGCTCTGGAGCTGAGCTCTCACTGACTCTCCGAAAAATCCT<br>CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCATGGCTTCTCTCCCTCTGCGGACTC<br>CTGGGTGAGCTGTGCTCAGTCCCCCAACAGATGCTTTCTGTCTC                     |
| WI-563   | 87  | G A --- | --- | TGTGACCAATTTGTTATTTTAGAGGGTTTAAACATGGCCTGACTATCACCTGATGGTCGCCAGAAATTC<br>CTGGGGGAGGGCCTCCCTTG/A/CCCTGATCATGTCTACCTAACTGCTACTCTAACAACTACTCTCC<br>TGTGGTATGGGATCCTAAGCCAAAAAGCTGAATGAACATGTTCTAGCACTACAGAAATCCATACT<br>GCCCTCAGTAAAGGCAAAATTTAAATCTCTTTGGATAACCCAGGGCAGAT   |

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| WI-931c   | 191 | C A --- | --- | GACCAGGGCACCAGAAAGCCACGGAAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT<br>TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTCTTATCTGTGTGTCAAAATGATCCTCT<br>GTTGCTGCAGTGTCACTTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCC[C/A]CGAGCCTGG<br>TACAGAAAAGGCATGGGAAAGATGTGTGAGA                               |
| WI-931b   | 81  | A G --- | --- | GACCAGGGCACCAGAAAGCCACGGAAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT<br>TCTCTCCCTCCCTA/GTCCCTCACCACACCTTCCAGTGTCTTATCTGTGTGTCAAAATGATCCT<br>TCTGTGTGCTGCAGTGTCACTTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG<br>TACAGAAAAGGCATGGGAAAGATGTGTGAGA                              |
| WI-931    | 31  | A G --- | --- | GACCAGGGCACCAGAAAGCCACGGAAAGCCAC/GJGCCACTAGCCCTGAACCTTGACACCCCTGGA<br>GTTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTATCTGTGTGTCAAAATGATCCT<br>TCTGTTGCTGCAGTGTCACTTACTGTTGTATGGATTATAATTATTGTCCAAAAAGCCCGAGCCTGG<br>TACAGAAAAGGCATGGGAAAGATGTGTGAGA                               |
| WI-10870b | 91  | C T --- | --- | GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA<br>GACATCCACCTTAGCAAAGTGGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCCCC<br>TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTGAGC<br>CTGAGCCACTCTTAAACCATGAACCATCACCAITTTAAATAACGTTGCCCCCCC |
| WI-10870  | 103 | G A --- | --- | GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA<br>GACATCCACCTTAGCAAAGTGGGCACCTACTTAGA/GA/CAGTGGAGTACCCCTGAGTACGACCCCC<br>TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTGAGC<br>CTGAGCCACTCTTAAACCATGAACCATCACCAITTTAAATAACGTTGCCCCCCC   |
| WI-7719b  | 281 | T C --- | --- | AGTTTATTTCTCCAGATGACCAGCAGTAGACAAATGGATACTAGCAGAGTCTTAGGTAAAAGTCTT<br>GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAAACCCCTAGC<br>TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG<br>ATTTCTGGACATTGCCCATGTATAATCTCACTGATGATTTCAAGCTAAAGCAA      |
| WI-7719   | 163 | A G --- | --- | AGTTTATTTCTCCAGATGACCAGCAGTAGACAAATGGATACTAGCAGAGTCTTAGGTAAAAGTCTT<br>GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAAACCCCTAGC<br>TTCTTAGTGAAGACAATGTACAGTTATCC/GA/GTTAGATCAAGACTACACGGTCTATGAGCAATAAT<br>GTGATTTCTGGACATTGCCCATGTATAATCTCACTGATGATTTCAAGCTAAA      |
| WI-10396  | 72  | C A --- | --- | GCCTTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA<br>GAGT[C/A]GTGACTTTTATGCCCAGTTTCCCTCTCAGATTTTATGACGGTGTGTTTTCTTTTGTTA<br>TGCCATTTGAGGGAATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTTACGG<br>TTAACAGCCACCATTTGTAAACACTTTGT                           |

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| WI-10673 | 94 C G ---  | --- | TCCCTTTATGCAOCCCAAGAGATATTTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC<br>CACCCCCGTGGCACTCATGGAGGGGCGJTGACAGTTGGAACATATGCAAGTGTGCTCCGGCCACACA<br>TCCTGCTGGGCCCTACCCTGCCCAATTCAATCTGCCAATAAATCCTGTCTTATTGTTTCATCCTG<br>GAGAAITGAAGGGAGGTCAAGTTGTTGTCAATGATTGTGTGAGAGAACCT    |
| WI-7842  | 57 T C ---  | --- | CACAGCCATGCCCTTGAGGAGCCGCCACCAGAGTGTGAATCCCCTATCCCATTCTGT/CJGTATGAG<br>TCCCATTTGCCTTGCAATTAGCAATCTGTCTCCCCCAAAAAAGAAATGTGTATGAAGCTTTCTTTCCCT<br>ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTCAGTGTCTCAGAAT<br>TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTGAGTCCCTTATA |
| WI-7721  | 145 A C --- | --- | CTGCTCATCAGCCACTGGAGTCCACACTTGAATTTGGGAGCTACCACGGGTCTGCCATGCTCTGG<br>AGGAGCAAGGGGGCCACATCCOACCCAGCTGTACCCAGCCGGGCGAGTGCAGCCCTTCTCTOOC<br>TGCTCTGCAJCTGACTCTCTTTGAGGTCCCTGTATGTCTACCTCTGACTTCTGTGTCCCTCTG<br>TGCTGCTCTCATCCATTCTCTTACTGGGGCTGGGGCTCTAGCCCCA                |
| WI-4767b | 173 C A --- | --- | TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCCCT<br>CAGGTCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGGTATGTTT<br>CTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACA/CJA/AAATCACTAAGGAATTCACCTAAGA<br>CTOCTCTAACCCAGAGATTTTAACTT                          |
| WI-4767  | 50 A G ---  | --- | TTTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGA/CJA/TTTCATAAAGAGTT<br>CCTCAGGTCTGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGGTATG<br>TTTCTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCACCTAAGAC<br>TCCTCTAACCCAGAGATTTTAACTT                          |
| WI-7718f | 222 C T --- | --- | ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA<br>TTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGTG<br>ACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTGAAACAGAAAAATAAGTCAAA<br>AGGAACAAAAATTACAAAGAA/CJTCATGCAGGAAGGAAAACTATGTATTAAAT   |
| WI-7718e | 60 T C ---  | --- | ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT/CJGCAA<br>GGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG<br>ATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTGAAACAGAAAAATAAGTC<br>AAAAGGAACAAAAATTACAAAGAACCTATGCAGGAAGGAAAACTATGTATTAAAT |
| WI-7718d | 31 G A ---  | --- | ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA<br>GGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG<br>ATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTGAAACAGAAAAATAAGTC<br>AAAAGGAACAAAAATTACAAAGAACCTATGCAGGAAGGAAAACTATGTATTAAAT    |

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| WI-7718c | 91 C G ---  |   |  | ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA<br>TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG<br>ATGACCTTTCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTTGAAACAGAAAAATAAGTC<br>AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT     |
| WI-7718b | 248 A G --- |   |  | ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA<br>TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAGTG<br>ACTTTCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTTGAAACAGAAAAATAAGTCAAA<br>AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[AG/G]AT     |
| WI-7718a | 42 A T ---  | C |  | ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGC[C/A/C, T]GTTACTCCCTACACTGATGC<br>AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGAT<br>AGATGACCTTTCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTTGAAACAGAAAAATAAG<br>TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTA |
| WI-7227d | 99 G C ---  |   |  | AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC<br>CGTGGACCAATTTCATCTTTCAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC<br>TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA<br>GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCCAGCGACTAATG    |
| WI-7227c | 291 G A --- |   |  | AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC<br>CGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT<br>GGTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACAGTG<br>TTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCCAGCGACTAATGCAAT     |
| WI-7227b | 93 G T ---  |   |  | AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC<br>CGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC<br>TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA<br>GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCCAGCGACTAATG        |
| WI-7227a | 24 A G ---  |   |  | AGGGAATTGTTGCTCCTGGAGG[A/G]AGCCCAAGGCATCATTAACAAGCCAGTAGGTACCTGGC<br>TTCCGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC<br>TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA<br>GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCCAGCGACTAATG  |
| WI-7310b | 234 A C --- |   |  | CCACAATGCTCTCCACGATGTCAGGACTCTGCTGTCTGCTGGAGGTGGGAGACAAGGAACCTCGG<br>AAGAGGAAGCAAGAAAGCCGCTACTGTCTATGTTGTATGCTCTCATCGAACAACTGATGCGAAAACT<br>TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACTGAGCCAAACACACTGTAAT<br>ATCCACAGACTCCCTCCCTGCCCCCATCCCA[A/C]ATGATCTTGAGATTC    |

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| WI-7310a | 64 T A ---  |  |  | CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTGTCTGTCTGGAGGTGGGAGACAAAGGAACCT/A<br>JCCGAAGAGGAAGCAAGAACCCGTACTGTCTATGTGTGATCCTTCATCGAACAACTGATGCGAA<br>AACTTGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAAGTGAAGCCAAACACACTGT<br>AAATATCCACAGACTCCTCCCTGCCCTGCCCATCCCAATGATCTTGAGATTTC |
| WI-7878b | 162 A G --- |  |  | CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCCTGCTGGTTGATAATAATCA<br>GATCATGCCCAAGACGGCCCTCCTGATAATCGCTTGGGCATGATTGCAATGGAGGCAAAATGCGTCC<br>CTGAGGAGAAATCTGGGAGGAGCTGAGGTGATGAAGGTGATGTTGGGAGGGAGACACAGTGT<br>CTGTGGGAGGCCAGGAAGCTGCTACCCAAAGATTGTTGTCAGGAAACTA         |
| WI-7878a | 51 C G ---  |  |  | CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCCTGCTGGTTGATAATAATCA<br>TCAGATCATGCCCAAGACGGCCCTCCTGATAATCGCTTGGGCATGATTGCAATGGAGGCAAAATGCG<br>GTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGATGTTGGGAGGGAGCACAGTG<br>TCTGTGGGAGGCCAGGAAGCTGCTACCCAAAGATTGTTGTCAGGAAACTA     |
| WI-7381c | 213 C T --- |  |  | CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTTCTTTCTAACC<br>AGCCTGCAAGTTTCTCATGACGCTCGCAGGAGCAGGCTGCAGGTTCTGCTGCTATGGTGAGATC<br>AGATGTGGCCAAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA<br>AAAGGCTCTGCTGAGCAGATAATCCTTGGCAGGGCTCAGCAGG                |
| WI-7381b | 54 C G ---  |  |  | CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTTCTTTCTTCT<br>ACCAGCCTGCAAGTTTCTCATGACGCTCGCAGGAGCAGGCTGCAGGTTCTGCTGCTATGGTGAG<br>ATCAGATGTGGCCAAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG<br>ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG           |
| WI-7381a | 53 C G ---  |  |  | CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTTCTTTCTTCT<br>ACCAGCCTGCAAGTTTCTCATGACGCTCGCAGGAGCAGGCTGCAGGTTCTGCTGCTATGGTGAG<br>ATCAGATGTGGCCAAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG<br>ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG           |
| WI-1017b | 93 G A ---  |  |  | AAATTGCTCTATTGGACCTCATATTAATAAGAGCAATGAGAGCGGAGGAAATGAACCTCTCTC<br>AGGTACTGACTGTGGACCCAGACAAAG[G/A]GATGTAGATTGTACATTCAATCCTGAACAAACCTG<br>CCAGGCAAGTCTTCTCCCATTTACAAATAAGGAGACAAATAATAGGAGATTAAATAACTCATCAC<br>TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC                          |
| WI-1017a | 92 G A ---  |  |  | AAATTGCTCTATTGGACCTCATATTAATAAGAGCAATGAGAGCGGAGGAAATGAACCTCTCTC<br>AGGTACTGACTGTGGACCCAGACAAAG[G/A]GGATGTAGATTGTACATTCAATCCTGAACAAACCTG<br>CCAGGCAAGTCTTCTCCCATTTACAAATAAGGAGACAAATAATAGGAGATTAAATAACTCATCAC<br>TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC                         |

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| WI-1795b  | 130 T C --- | --- | GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGCTGGGTTCTCCAGACTCCTACGATTA<br>AATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGCCTTGCGAGAAAGAAAAGT[C/C<br>GTCTACCATTTTACCACAAATTTTCGTAGTACAATTTAAGTATCTCTTGTTATCTCTCCCTTAGGAGTCTAA<br>AGTGAGCTGGGGAAGGCAGGATTT                     |
| WI-1795a  | 47 T C ---  | --- | GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGCTGGGTT[C/CTTCCAGACTCCTACGA<br>TTAAATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGCCTTGCGAGAAAGAAAAGTC<br>GTCTACCATTTTACCACAAATTTTCGTAGTACAATTTAAGTATCTCTTGTTATCTCTCCCTTAGGAGTCTAA<br>AGTGAGCTGGGGAAGGCAGGATTT                    |
| WI-10616d | 136 GA ---  | --- | CACACAAATTTGCAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT<br>CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTCTGGTCTCTCATCACAATTGCCA<br>C[G/A]TAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCC<br>ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTTAACTCCTTTTTTGT |
| WI-10616c | 136 GA ---  | --- | CACACAAATTTGCAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT<br>CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTCTGGTCTCTCATCACAATTGCCA<br>C[G/A]TAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCC<br>ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTTAACTCCTTTTTTGT |
| WI-10616b | 141 CT ---  | --- | CACACAAATTTGCAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT<br>CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTCTGGTCTCTCATCACAATTGCCA<br>CGTAGC[C/T]CTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCC<br>ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTTAACTCCTTTTTTGT |
| WI-10616a | 116 GC ---  | --- | CACACAAATTTGCAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT<br>CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTG[C/T]CTCTCATCACAATTG<br>CCAGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCAAGTCCCTCTGAGACTCC<br>ATGGATCATCTCTGTTCTGTATCAGGCAGTGAATTTAACTCCTTTTTTGT     |
| WI-1126c  | 52 GA ---   | --- | CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGGCAAACTCCAGTATCACTG[A]TACTAATAA<br>AAACCCGTGAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAA<br>AATTTTATTTCTCAAGATATAAAAAATAAATAATTTAATTCAGTTTCTCAAAGGAATATGAAATTT<br>TGTTAAATGCAAAATCCAGCTGTAACTTTTTTGGACTTGCTTTTTATTCTT      |
| WI-1126b  | 230 TC ---  | --- | CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGGCAAACTCCAGTATCACTGATACTAATAAAAA<br>CCCTGTAAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAAATTT<br>TTATTTCTCAAGATATAAAAAATAAATAATTTAATTCAGTTTCTCAAAGGAATATGAAATTTGTT<br>AAAAATGCAAAATCCAGCTGTAACTTTTTTGGACTTGCTTTTTATTCTT      |

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| WI-1126a  | 97 T C ---  |  |  | CTCTTATTTCTGCGCACTGCTTTCTTTGGGGCAAACTCCAGTATCAGTACATAATAAAAA<br>CCCTGTAAGTGTGCTTGCATTTTCAAGATT/CJCAATATATATCCAGATTGTTTTCCAGCAAGAAA<br>ATTTTATTTCTCAAGATATAAAAAATAATATTAATTTTCAGTTTCTCAAAAGGAATATGAAATTT<br>GTTAAATGCAATCCAGCTGTAACCTTTTGGAGCTTGCTTTTATTTCTT              |
| WI-11183c | 124 C T --- |  |  | TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACCTTGAAAAATTTAGAGTAC<br>ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCTTGTC/TAATAACA<br>TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGAAGTAGAGTTTAAATATTGGT<br>ATGTGGTGCTAGAGTTAGTAATGGAA                                  |
| WI-11183b | 192 T C --- |  |  | TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACCTTGAAAAATTTAGAGTAC<br>ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCTTGTCACATAACATTT<br>ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGAAGTAGAGTTTAAAT/CJATTGGT<br>ATGTGGTGCTAGAGTTAGTAATGGAA                                |
| WI-11183a | 118 C T --- |  |  | TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACCTTGAAAAATTTAGAGTAC<br>ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCTTGTCACATAACA<br>TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGAAGTAGAGTTTAAATATTGGT<br>ATGTGGTGCTAGAGTTAGTAATGGAA                                   |
| WI-10770b | 174 G A --- |  |  | GCTTGGTTTGGCTTATGCTCAGTCTGAGTTCTCCCTTTCTGCTGGCCCTTTTGTATTCA<br>CCCATACCTCTATGCTCGCTCAGACCATTTCTCTATCTGGAGCGCTCTCTGTTACTTTCTCCTG<br>TTCACCAACCTCTTTTATCTCAGGACACTCA/GA/TTCACATGCCACTCTCGTGACACTGTCTCT<br>TTCACATCTTTCTGTGCCCCCTTTCCC                                      |
| WI-10770a | 49 G T ---  |  |  | GCTTGGTTTGGCTTATGCTCAGTCTGAGTTCTCCCTTTCTG/TCCTGGCCCTTTTGTATT<br>TCACCCATACCTCTATGCTCGCTCAGACCATTTCTCTATCTGGAGCGCTCTCTGTTACTTTCTC<br>CTGTTTACCAACCTCTTTTATCTTTCAGGACACTCAGTTTCACATGCCACTCTCGTGACACTGTCTCT<br>TTCACATCTTTCTGTGCCCCCTTTCCC                                  |
| WI-9667b  | 82 C T ---  |  |  | GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTCATGACACTTTTCAATCTCTGCCCTGTATCATGG<br>TTATCACTGGACA/C/TAAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA<br>ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT<br>GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT |
| WI-9667a  | 68 G C ---  |  |  | GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTCATGACACTTTTCAATCTCTGCCCTGTATCATG<br>G/C/TTATCACTGGACACAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA<br>ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT<br>GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT  |

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| WI-10400d | 189 A G --- |  |  | ACATTTTATTAGCAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG<br>GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTAATTT<br>TCITTCCTTACCTTTACTCTCCACCCCAAAATAACGTAAGTACCTATGTC[G]TGCCATGTAG<br>TTTTTGGTTCATTTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG  |
| WI-10400c | 166 A C --- |  |  | ACATTTTATTAGCAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG<br>GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTAATTT<br>TCITTCCTTACCTTTACTCTCCACCCCAAAATAACGTAAGTACCTATGTCATGCCATGTAG<br>TTTTTGGTTCATTTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG    |
| WI-10400b | 165 A G --- |  |  | ACATTTTATTAGCAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG<br>GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTAATTT<br>TCITTCCTTACCTTTACTCTCCACCCCAAAATAACGTAAGTACCTATGTCATGCCATGTAG<br>TTTTTGGTTCATTTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG    |
| WI-10400a | 46 T C ---  |  |  | ACATTTTATTAGCAACAAATCAGCAAAATAATAATAGAAAGTAATTCATTTTCAGACATCT<br>GCTGGTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTA<br>ATTTTCCTTCCCTTACCTTTACTCTCCACCCCAAAATAACGTAAGTACCTATGTCATGCCATGT<br>AGTTTITGGTTCATTTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG    |
| WI-10809b | 78 C T ---  |  |  | AAAGGGCTACAACTAAGGCCAAACCATGAACGGTATAAGGAGGGTAATGCAAGGGGAGACCC<br>CACCTCTACCA[C]/JT TAGAAAGGGCATTCAAGCACATTCAATGAGGCTTCATATACTGGTTAG<br>CAACAAATGGAATGTATTAGCCCAAGGCGAGGTATGGACCAAAAGTGCCAGTGATGAGGCCACA<br>GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA  |
| WI-10809a | 33 C T ---  |  |  | AAAGGGCTACAACTAAGGCCAAACCATGAAC/JTGGTATAAGGAGGGTAAATGCAAGGGGAGA<br>CCCCACCTCTACCACTTAGAAAGGGCATTCAAGCACATTCAATGAGGCTTCATATACTGGTTAGC<br>AAACAAATGGAATGTATTAGCCCAAGGCGAGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG<br>TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA  |
| WI-7038c  | 266 T C --- |  |  | CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC<br>CAATGAAATAGTATGAGATGCTGGGCTGTCTCTCCCTTCAGGAATGCTGGGCCCCAGCCTGGCCAGAC<br>AAGAAGACTGTCAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT<br>CATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC |
| WI-7038b  | 140 A C --- |  |  | CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC<br>CAATGAAATAGTATGAGATGCTGGGCTGTCTCTCCCTTCAGGAATGCTGGGCCCCAGCCTGGCCAGAC<br>AAGA[C]GACTGTCAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT<br>GATCATTTTATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGA     |



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| WI-7038a | 31  | G A | --- | --- | CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTTCCCTGCCACATCCAGCTTGTG<br>TCCCAATGAAATACTGAGATGCTGGGCTGTCTCCCTCCAGGAATGCTGGGCCOCCAGCCTGGCCA<br>GACAAGAAGACTGTCAGGAAGGTCGGAGTCTGTAACACAGCATACAGTTTGGCTTTTTCACATT<br>GATCATTTTATATGAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGA    |
| WI-3429b | 64  | G T | --- | --- | ATAGGCTTCTGTCTGCCACAGTGGAAOCCAGCAOCCAGGTGGCCAGGGTCCACACA[G/T]<br>CCCTCAGCCCTTCAGCTTTGCATGTGTCATCGGTGACTCAGCAGAGATTTTCCACCTCATGTGA<br>CAAAATACAGATTCAGATCTCCTCTCTCTGATTTGGATCTAGCAAGACAGAGACGGTCTCTAGAA<br>TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC           |
| WI-3429a | 62  | C T | --- | --- | ATAGGCTTCTGTCTGCCACAGTGGAAOCCAGCAOCCAGGTGGCCAGGGTCCACACA[C/T]AG<br>CCCTCAGCCCTTCAGCTTTGCATGTGTCATCGGTGACTCAGCAGAGATTTTCCACCTCATGTGA<br>CAAAATACAGATTCAGATCTCCTCTCTCTGATTTGGATCTAGCAAGACAGAGACGGTCTCTAGAA<br>TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC         |
| WI-6786c | 151 | G A | --- | --- | ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT<br>GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGGAAAGGATAAAGAGTGAGTGACGGTGACCT<br>GTAGCCCCATCTCT[G/A]TGGGATAAGGTGCCATTTGTTCTTGGAGGGTGAATGCCACATTC<br>TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATGCTCAGTTTCATCATTT        |
| WI-6786b | 111 | A T | --- | --- | ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT<br>GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGGAAAGGATAAAGAGTGAGTGACGGTGGA<br>CCTGTAGCCCCATCTCTGTGGGATAAGGTGCCATTTGTTCTTGGAGGGTGAATGCCACATTC<br>TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATGCTCAGTTTCATCATTT           |
| WI-6786a | 106 | A T | --- | --- | ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT<br>GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGGAAAGGATAAAGAGTGAGTGACGGTGA<br>CCTGTAGCCCCATCTCTGTGGGATAAGGTGCCATTTGTTCTTGGAGGGTGAATGCCACATTC<br>TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATGCTCAGTTTCATCATTT            |
| WI-6711b | 226 | G T | --- | --- | GGCTATTTGTAAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT<br>ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTGAAT<br>TTCAATACCTCCATTATAAATTCAATACATCATTCGAGAGAAAAGACAAACGGTGCCAACTGGGTT<br>TGGTTGGTGGCTGCACACCCACA[G/T]TGGCAACTAAGTGAATCTCTAAA |
| WI-6711a | 36  | T C | --- | --- | GGCTATTTGTAAATGCTTGGTATTGACTCCAAAAT/CJTGAATAAGTATTGGGGAAGAATCCCTC<br>ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTCT<br>GAATTCATATACCTCCATTATAAATTCAATACATCATTCGAGAGAAAAGACAAACGGTGCCAACTG<br>GGTTGGTGGCTGCACACCCACAGTGGCAACTAAGTGAATCTCTAAA     |

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| WI-10613b | 172 | A C | --- | --- | ATGTATGCCAAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAATTTTGAGCCATA<br>TGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTGATTT<br>TTTGTCAACTTTTGACAAGGCCAGGCAATTTATTTG/C/GCCCTAGGAGGGTTACTATAATTTAGA<br>AAGGCTCTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG   |
| WI-10613a | 44  | G A | --- | --- | ATTGTATGCCAAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAATTTTGAGCC<br>ATATGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTG<br>ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTATTTGAGCCCTAGGAGGGTTACTATAATTTAG<br>AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG     |
| WI-7587c  | 133 | A T | --- | --- | GCTCTAGTGGGAAACCTCAGGTAGTCTCCCGAAGATCTGTGCTTCCAAACAAGTGACTACCCCTTGAAGC<br>ACATCCCCTTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA(A/<br>TJGGAAATGAACCACTCCCTGCCCATTCCTTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCT<br>TTCCACATGCCCCCATATGCTGAGCCAAACTGCACCTGGGGGCTGCCCTC |
| WI-7587b  | 81  | G A | --- | --- | GCTCTAGTGGGAAACCTCAGGTAGTCTCCCGAAGATCTGTGCTTCCAAACAAGTGACTACCCCTTGAAGC<br>ACATCCCCTTCTG/G/ATCTGAAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA<br>AGGAATGAACCACTCCCTGCCCATTCCTTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCTT<br>TCCACATGCCCCCATATGCTGAGCCAAACTGCACCTGGGGGCTGCCCTC   |
| WI-7587a  | 28  | C T | --- | --- | GCTCTAGTGGGAAACCTCAGGTAGTCTC/C/JGAAATCTGTGCTTTCCAAACAAGTGACTACCCCTTGA<br>AGCACATCCCCTTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA<br>AGGAATGAACCACTCCCTGCCCATTCCTTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCTT<br>TCCACATGCCCCCATATGCTGAGCCAAACTGCACCTGGGGGCTGCCCTC   |
| WI-10681b | 103 | T A | --- | --- | ATGACTCAGGTGACAAAAGAACGATGTCCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAAACC<br>ACAGAAAAGCTAAAGACATCCCTTTTAAAAAGCC(T/A)AAAGACAGCCATTTTAACTCAATTCG<br>TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA<br>CCATTGCTAACACTATTGCTTTGGAGAGGAGGAGTGACGCTCTGTTAAAG    |
| WI-10681a | 41  | A T | --- | --- | ATGACTCAGGTGACAAAAGAACGATGTCCTAGACCCCATTTG/A/TCTTACGCAAACTCAATCAGCCAA<br>ACCACAGAAAAGCTAAAGACATCCCTTTTAAAAAGCC(TAAAGACAGCCATTTTAACTCAATTCG<br>TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA<br>CCATTGCTAACACTATTGCTTTGGAGAGGAGGAGTGACGCTCTGTTAAAG    |
| WI-7222c  | 126 | G T | --- | --- | GCCTCTCCTCAACTGTCCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT<br>AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTTGGGGATGGG(G/J)AATAA<br>AGGAGGGGGAATCCCTTGAACAAGAAAGTGGGATAGTTATTTCCACCTGCCCTTGAAGCTT<br>TAAGACAGTGATTTTGTGTAAGGTTGTAATTTCAAAAGACTCGAATTCATTTT    |

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| WI-7222b  | 255 | G A --- | --- |  | GCCTCTCTCAACTGTCTCTGGAOCCAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT<br>AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGATGGGAATAAAGG<br>AGGGGGAATTCCTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA<br>GACAGTGATTTTGTGTAAGGTTGATTTCAAAGACTCGAATTCATTTCTCA        |
| WI-7222a  | 126 | G T --- | --- |  | GCCTCTCTCAACTGTCTCTGGAOCCAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT<br>AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGATGGG[G/TAATAA<br>AGGAGGGGGAATTCCTTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT<br>TAAGACAGTGATTTTGTGTAAGGTTGATTTCAAAGACTCGAATTCATTTT       |
| WI-8054d  | 41  | C A --- | --- |  | AAAGATGACACTTAGAACTGATCACTTGGCCCTTCTCTTTC/AJTATCTCTCCAGTTCAAAATG<br>CTTGATCTTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCA<br>CAATCTCTTTGTAGTTTAGCCTTTTCCGGAATAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT<br>TCCTGTCATAACGCCGCTTTCCTGGGCGTACAGAGAAATCCTTGGCCCTT   |
| WI-8054c  | 237 | G T --- | --- |  | AAAGATGACACTTAGAACTGATCACTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT<br>GCATCTTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA<br>TCTCTTTGTAGTTTAGCCTTTTCCGGAATAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCTTCC<br>TGTATAACGCCGCTTTCCTGGGCGTACAGAGAAATCCTTGGCCCTT       |
| WI-8054b  | 148 | T C --- | --- |  | AAAGATGACACTTAGAACTGATCACTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT<br>GCATCTTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA<br>TCTCTTTGTAGTTTCTTTAGCCTTTTCCGGAATAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT<br>TCCTGTCATAACGCCGCTTTCCTGGGCGTACAGAGAAATCCTTGGCCCTT  |
| WI-8054a  | 131 | C G --- | --- |  | AAAGATGACACTTAGAACTGATCACTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT<br>GCATCTTTTAATAGCCAGCATTTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGC/GJA<br>CAATCTTCTTTGTAGTTTAGCCTTTTCCGGAATAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT<br>TCCTGTCATAACGCCGCTTTCCTGGGCGTACAGAGAAATCCTTGGCCCTT |
| WI-10854b | 152 | G T --- | --- |  | TCCACAAAAAATCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAAGTGGATAGTTTAATAA<br>ATGTTTATATTTTACTTTAAGCGAAGTTGAAACACGAAAGACGATAGTTAACGCTGTTAAGTTTAT<br>ACGGTGTGCGAGGCAACA[G/TGGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATCTTTGTG<br>TTTTAGACACAGGGTCTGCTGTGTG                               |
| WI-10854a | 102 | C T --- | --- |  | TCCACAAAAAATCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAAGTGGATAGTTTAATAA<br>ATGTTTATATTTTACTTTAAGCGAAGTTGAAACACGAAAGTGAACA[C/T]GAAGACGATAGTTAACGCTGTTAAGTT<br>TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATCTTTGTG<br>TTTTAGACACAGGGTCTGCTGTGTG                   |

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| WI-9826b | 127 G A ---      | ---                                   | ---                                   | AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCCTATTTTGTG<br>TGCCTGATGGCTGTTGGTGTTTGCACGCAGTTAGCCATTGTGACAGAGGCTGTATG[A]GCCTT<br>CAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAA<br>GGCAGAGAAGATCAGAAGTGTGAA                                   |
| WI-9826  | 125 A T ---      | ---                                   | ---                                   | AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCCTATTTTGTG<br>TGCCTGATGGCTGTTGGTGTTTGCACGCAGTTAGCCATTGTGACAGAGGCTGT[A]TJGGCCTTC<br>AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAG<br>GCAGAGAAGATCAGAAGTGTGAA                                   |
| WI-15986 | 60 T G GTGGGTTTT | TGACATTATAT<br>AAACGTAAAA<br>GAAAATGT | TTGTTTTGTGT<br>AGGAAACCAG             | CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTGTGTGGGTTTTTTTTT[G]TTAC<br>ATTTCTTTTACGTTTTATATAATGTCAGCAITTTCAA   |
| WI-8655  | 29 A G AG        | AACTGCAAAAT<br>AGGAAACCAG             | CCACCTGGGGC<br>TCCC                   | TTCAAGTAACTGCAAAATAGGAAACCAGAG[A]GJGGGAGCCCCAGGTGGGACAAATCATGGCTACCCC<br>TCCCCAACAGAACAGGGGGAGGAGGTGGCCCTACACCCTTTAT   |
| WI-8170b | 259 G A ---      | ---                                   | ---                                   | GCACCTCTCTCTGAGCAACAGGTACACATTTTCTCTAACATTGATCTATAACACACACAGAACCG<br>TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGAAGGTTAG<br>CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAAGTGCAATCCTATCAATCAGAA<br>ATAAAGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA   |
| WI-8170a | 204 T A ---      | ---                                   | ---                                   | GCACCTCTCTCTGAGCAACAGGTACACATTTTCTCTAACATTGATCTATAACACACACAGAACCG<br>TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGAAGGTTAG<br>CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAAGTGCAATCCTATCAATCAGAA<br>A[T]A/AAAGGTAAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC |
| WI-8172  | 136 C G GACA     | CCTTTATTAAA<br>ATTGTTTTCTT<br>GACA    | GAAGAGAAAT<br>GTAATACCTGT<br>AAAGGTAC | CAGGATTCCTTAAGTCATCTTCCAATACTCCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA<br>ATCTAACCATTAACAAAGCTTTAAATCCTTCGGTAACTCCCTTTATTAAATTTGTTTCTTGACAT<br>A/C/GIAGTACCTTTACAGGTATTACATTTCTCTCACCGTTTACA   |
| WI-8183  | 56 G A TGC       | TGAAATAAAA<br>ACAAATTTCTGT            | TGTGTTGAAAT<br>CAAACCTGC              | AGCAGGGTTTGAAATTGATCCCTTATTTTACATGAAATAAAACAAATTTCTGTTGC[G/A]GCAGGTT<br>TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT<br>ATTTAAACTGCAAGCACCATGC   |
| WI-14149 | 83 C T ---       | ---                                   | ---                                   | GCCTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAAACCCCAAGCATGGGATTTTCCCGGAAAT<br>ATTAGCGTTAAAGGAG[C/T]TGAGTTGAGTCAAAACACGGG  |
| WI-8712  | 44 G A G         | CACAGGGAAG<br>AGGTAGTGA               | CAGGAAGCCTG<br>ACCATCTC               | TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG[G/A]GAGATGTCAGGCTTCCTG<br>TTCCCTAACAGCAGAGCCCCAGCAACCTAGAAAGCGCCTACCTAGCCTCTTAAT   |

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| WI-8827  | 22 C T  | TCCTGGGAG<br>TCTACTAGG         | GGATTAGGAT<br>TTTAGTGTTCAC | GGTGTCCCTGGGAGACTATGG[C]/TAGTGAACACTAAATCCTAATCGCCATGCATTGGAATTATT<br>CCGACTATTACTTCTTCTTAGTCCCTTCTTATCCACCAGTCTTCT  |
| WI-8833  | 51 A T  | TCTTCATGCC<br>ATTCTCTG         | CCTCACACATT<br>ATAGGGCA    | CTCCGGCCTTTAAAGCTCTCTGTAGACTGTCTCTTCCATGCCATTCTCTG[A]/TTGCCCTTATAATGT<br>GTGAGGGATTACAATAGTCCCTATTCAAACCTGCCTTGTCTATAAAAGGTCAAGCTATGT  |
| WI-8377  | 63 A G  | ---                            | ---                        | ATTTTAGCCATGTTGGTAAAGTTCAITTTTTCAGTACATGGGTAAACCCAGGCCCTTTCCC[A]/GJT<br>TATATCCAGGTATGCTACAAGTTCTTTTAACTCTTATCAGAAGTTATATTACTGTTTCTTAGAGAG<br>GCTACCAGGCTAAATTCACCTTAGTTGGTTGTCTAATGTCTCATATTATCCIGAAGCTCGTG   |
| WI-8850  | 21 A G  | GGGACTTAAC<br>CTTTGGCCT        | CAACAGGCA<br>GGCAGG        | GAGGGACTTAACCTTTGGCCT[A]/GJCCTGCCCTGGCTGTTGGCTCTGGCTGTGCTGTTTGGTTCTT<br>TCTCTTCTACTGGTCTTCTTTGTCTTTGCCAGCCACTATGCTGCTGT  |
| WI-8853  | 79 C T  | CCGGGCATTG<br>AGGATA           | AGTCTTCTGA<br>GCTTCCAT     | ACTTTCTTGAGCTGAGCAACCTCATCTCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG<br>CATTGAGGATA[C]/TATGGAAGGCTCAGGAAGACTTTCATTCTCAA   |
| WI-8865b | 52 A G  | ---                            | ---                        | AGGGTGAAGTGGAAATCAGGACAGACTGAGGAAGACAGCATGGTGGAAACA[A]/GJACAACATGCT<br>TCGGACTTACCAAAGGGAGAGTCGAGCTTTCATATAAA  |
| WI-8865a | 42 T C  | CACAGACTGA<br>GGAAGACAGT<br>CA | GGTAAGTCCGA<br>AGCATGTTG   | AGGGTGAAGTGGAAATCAGGACAGACTGAGGAAGACAGTCAT[C]/GGTCGAACAACAACATGCT<br>TCGGACTTACCAAAGGGAGAGTCGAGCTTTCATATAAA  |
| WI-8895  | 32 A C  | ---                            | ---                        | GTGCCACAAACCTGGACACCAACCAACAGAA[A]/CJCTCCCGTCTTTGAAATTTCCATTAAAGAGCA<br>CAATGGGGTAATTATACCAGGATGCTCCAATCGCTCTTTC   |
| WI-8456  | 93 G C  | ---                            | ---                        | CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATTTGTGAAATATAATAAACTCTTTTCC<br>AAGGCTCCCATGCTTGGATGTCACA[G]/JTATGTCAAGTTAATAAACAATTTCTAAGTGTCACTC<br>TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTTACACGGCAGACCCACAAGTTGTGTAGCAC<br>TGGCATAGACGAGGGCTTCTCAAACCTCCCGTCTGCTCAGTCAACCCAC |
| WI-8496b | 157 A G | ---                            | ---                        | TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCAGTGCATATTCTATGGAAA<br>ATTCTATCTCAAGTAAGTACAGCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAGTCA<br>AAGACACAATGCTGCCAATGCA[G]/JTATGATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT<br>GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC               |
| WI-8496  | 41 G A  | ---                            | ---                        | TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCAGTGCATATTCTATGG<br>AAAAATTCATATCTCAAGTAAGTACAGCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAG<br>GTCAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC<br>TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC                |
| WI-14153 | 28 A G  | GTGAGGGAAG<br>GCCAGC           | AACGGCAGGA<br>GGGA         | CTGCAGGTCTATGTGAGGAAGGCCAGC[G]/JTCCCTCTGCTGCCGTTGTACCCACATCCACAGAGCA<br>GCCCTAGTCCAGGTGACGCCACTGCCACCCACGGCACACGGGAACAGGACCCATGCTGC  |

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| WI-12108 | 40  | C | T | A   | T   | TGAAAAGGG<br>TTAAACTCAA    | TTGACCTGGTA<br>TAATGAAAGT<br>ATTT      | TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC[CT]GAAATACTTTTCATTATACCAGGT<br>CAAGAAAAATGCCACAGCCAGAAAAATTTATTTAA  |
| WI-5989  | 29  | G | A | C   | A   | CCACAAAGGT<br>CACAGGCA     | GGGTATAACAG<br>AACCGTATGTA<br>OG       | CAGGCAACGTCACAAAGGTACAGGCA[GA]CGTACATACGGTCTGTATACCCCATATATTAC<br>CCCTTCATGTCCTAAAGAAGACATTTCTCTAGAGATTTTCATTTAGTGATCTTTAAAAAAAAT<br>CTTGTTAACTTGCCTCCATCTTTCTTGGGTGAGGACACC |
| WI-12201 | 61  | C | T | O   | C   | CCACTGATCA<br>OCTGCATG     | CCGACCACATA<br>OCTGGC                  | ATAGCTTTTAGCCTTTTCTCGAGTGTTATGTCCCAAGCCCACTGATCACCTGCATG[CT]GCCA<br>GGTATGGTGGGGTGTGATGACGTGGGTTTGCAGCCCTCCACTGCTCGATAAAAGGC   |
| WI-12018 | 31  | A | T | T   | C   | GGCAGCCAGC<br>TCTGACTT     | GGAGAGATGAC<br>AGAAACAGAG<br>AG        | TTTTATCTGTCAGGCAGCCAGCTCTGACTT[AT]CTCTCTGTTCTGTCATCTCTCCCCACATACCA<br>ACTTCTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAAATTAGAC<br>AGTGAAGCATGTTGCAG               |
| WI-14162 | 57  | A | G | C   | C   | TGGCTCGCTG<br>CCTC         | AGGGATCAA<br>GAGAAAGGC                 | TTTTCGTTTGTAAATGATCCGAATGCTTGAGAAGAAACCCCTGGCCTCGCTGCCTC[AG]GCCTTTT<br>CTCTTTGATCCCTGAGTTGCTGAGATTAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG<br>AGCGG                            |
| WI-15407 | 92  | A | G | T   | T   | CATGCCCTTA<br>AGGATTAAGT   | TCCTTTCTCTTT<br>TGGTAGTGTGG            | AGCATGTAAGGAGCAGTTTTATTGATTGGTATATTCAGGTTCTAACCCAGCTGAAAAATTCAAATA<br>CATGCCCTTTAAGGATTAAGTTAA[AG]CCACACTACCAAAAAAGAAAAAGATTATATGATCACAT<br>ATAAGCAATGGAAATCAGCA             |
| WI-12319 | 109 | T | C | A   | A   | GTTGAGTATTT<br>GTTCTGCTCAT | GGGAAGGTCGTG<br>GTACATATTGG            | TCTGATGTCATTTATTGGCACAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTTA<br>TACTTTGTGCATTTAGTTGAGTATTTGTTCTGCTCATAATTT[CT]CCAAATATGTACCAGACCTTCCC                                |
| WI-12326 | 25  | G | A | C   | A   | GACAGACTC<br>AAAGCAATT     | AGGTTTGA AAA<br>TATGTATTAA<br>TACTTTGT | CTGACAGACTTCAAAAAGCAATTAC[GA]CTTCCAGAATACAAAGTACTTTAATACATATTTTCAAAG<br>CTGTTTGCAATTTCAACAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT                                       |
| WI-12361 | 63  | C | T | --- | --- | ---                        | ---                                    | TTAAATCCACACTGAAGATCTGGAGTATGGGGGGGATATAGGAATTCAGCATATGTATTAT[CT]<br>TGAACATAATTTACAAAAGTGAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC                                       |
| WI-11305 | 87  | C | T | A   | T   | CAGACACAGC<br>ATCACACCA    | GACCCTCCCGT<br>GGGC                    | ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAGGGAAGGACAAAGTACCTTTGTATAGAATAT<br>ACAGACACAGCATCACACCA[CT]AGGGCCACACGGGAGGGTGGGGAGACGACACTTTTCCCTGGG<br>AAAGG                           |
| WI-11321 | 67  | A | G | T   | T   | GGGAGGAAAA<br>TCCAATAAT    | CATTGGGGAAT<br>AGCTAAACCTT             | ATTTTATATGAAGGTTTTCTGGTAAATCTTTTAAGCAGGGGAGAAAAATCCAAATAAATTTTTTAA[<br>A/G]AAGGTTTAGCTATTTCCCAATGCTATTTAATACAATTGAGGTTAGGACGTTAAGTCTTATCAGA<br>CTGTGACTGGAGCCCGG             |
| WI-11324 | 40  | C | G | T   | G   | GGATAAATCA<br>TGTGCCCCA    | ATCAAGCTTTG<br>GGGCTCT                 | AGCATACTGCATCTCTTTATGGATAAATCATGTGCCCCA[CT]GAGAGCCCCAAAGCTTGATGACAT<br>TCTGTAAAGTTACAAAAATGTATCTGAAGAAGTTATCTGTCTTGTCC   |

|           |     |                         |                           |                            |   |
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| WI-11352a | 69  | T C G                   | AGCAGCAGC<br>ATAGTGGAAA   | GACCTCTCGTA<br>GGACACTTAGC | TGACACATGGTTCTGTTTCCAGAAGGAGAGAGAGTATCATATAGCAGCAGCAGCATAGTGGAA<br>AGT/C/GCTAAGTGTCCTACGAGAGGTCAGATCATATCCATAGAAAACAGCTCTCTTTACTTGCA<br>CACCTA                |
| WI-11371  | 84  | C T G                   | CAGCTGGAG<br>ATTCTGATTCA  | GCCCCGCTGA<br>GCAC         | TTAGCCCATGCTGTCAATTTGCAATCACCTGTGAACCTATGAAACTATACCTGCCAGGCTCAGCTT<br>GGAGATTCTGATTGAGT/C/GTGTCTAGGCGGGCTGACATCCATGTTTGGGAAGAGTTGCGCGGGT<br>GATTCGATCGGTATAT  |
| WI-11385  | 75  | T C G                   | ACAGAAGACT<br>TTCATATTCCT | GATTCATTCT<br>AGTCATGGTCA  | CTTAAAGCATTATAGTTTGGCCTGATGGTGACACAGAGACTTTCATATTTCTTTTAAAGTC<br>TCTTCAGT/C/JAGGAAAAAGCTACAGATTTAAAAATATGACCATGACTAGAAATAGAATCAGC                             |
| WI-11388  | 88  | C A A G T T C           | ACACGTAAC<br>AAGTTC       | CAAGTTAAAT<br>T            | TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAATTAAGAATGAATGTTT<br>AAATTACACGTAACTAAGTTC/C/ATATAATTTAACCTGGATACAGGCATTGTTATGCTAAT                            |
| WI-11392  | 55  | T G A T A A T A C       | GGTATGTGT<br>CTTGAACCTTA  | GTACATTCAG<br>TGTTTTGTAAA  | TTCTATCATTCATTAAATGGGAGTTATGTCTTGAACCTTAATAAATAC/T/G]CTTTTACA<br>AAACAGTGAATGACTTTCTTGTGAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT<br>CATACTCCTTCCCCAGA       |
| WI-11396  | 52  | A T T                   | TTTGTGTTTG<br>AAATGGTGTT  | AGCTTATTTT<br>ATATTCACCCA  | AAAGAATAAGATGGCATTGTTCAAGTTAATTTTGTGAAATGGTGTTTT/A/T]GATGGGTGAATA<br>TGAAAAAAGCTTAACCTCATCCACTCTAAAGGTAGTTGGTGAITTTTGAACCGTTGTCAAT                            |
| WI-11441  | 100 | C A C A G C             | TCCCCACCAAC<br>CAGC       | TGCCAGGGCT<br>TATTTG       | CTGTGAGCTTTCCCAACTAAACCGTGAGTCCAGTATGTCTGGCAGCAGCTGTCTTGTCTTGGTG<br>TATTCCTATTACTGAATCCCCACCACCAAGC/C/A]CAAAATAAGGCCCTGGCACAAAGTAAGCTCTCC<br>ATTTTGTAGAATGAAT |
| WI-11466  | 26  | C T T T T A T T T G C A | TGAGAAGCCA<br>TTTATTTTGCA | GTTTATTGTTA<br>TAAAAATGAC  | ACTTGAGAAGCCATTATTTTGCAG/C/T]CTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTTT<br>TATATAAGTTGAGGTCAATTTTATAACAATAAACTTTCTATTATCTATTATCTCTCACATACATTT<br>CATGTATCCTG       |
| WI-13364  | 35  | A G ...                 | ...                       | ---                        | TTTTCTTTTGTGCTCTTTTATTTAGTAGAAGC/A/G]GGAACAGTTGTCAATACTACCTTCTGTTGG<br>TCCTCTGTTAGACAACATACCTTTCTTTGAATGTAAAAATGTCA   |
| WI-11276  | 41  | A G A G C A G A C       | GGCAGCCAGG<br>AGCAGAC     | TGTAAGTGAAG<br>GCGGCTG     | AGGCAACACTGCTTTATTAGGCGGGCAGCCAGGAGCAGAC/A/G]CACCGGCTCCTCAGTACACATT<br>CCCCACCCCTGCTCGGTGCTCCCACTCAGGGCTGGGCATGGAGGGGCGAGCTAGGTCTGGAA                         |
| WI-12210  | 76  | A G A                   | CACTATTGC<br>CACTATTGC    | TGCTAGTTTGC<br>ATATGTTTTCC | ATTGGAACAACCTTAATAATTTGCATCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACA<br>CTATTGCAT/A/G]GGAACAACATATGCAAACTAGCATATTGCTCTAGA  |
| WI-14186b | 88  | A G ...                 | ...                       | ---                        | AATGGTCTGGTTTATTGAGAAGCTGTGGTCAATTTGATGGAAGACACATACGGGTACAAAAATTACA<br>GGTGGTTTAGTTCAATACATG/A/G]TACAAATCATTAGAGTCTTTACAAGTCAATTAGAGTCTTTGGAT<br>TTT          |

|           |     |       |                           |                                      |   |
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| WI-14186a | 52  | C T A | GGTCATTGAT<br>GGAAGACAC   | AACATAACCA<br>CCTGTAATTT<br>GTACC    | AATGGTCTGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATA[C/T]GGTACAAAATT<br>ACAGGTGGTTTAGTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT<br>TTT                 |
| WI-12234  | 66  | A G   | GAGAACACTT<br>GTGGGGCTT   | GGACCTATCAG<br>TCCATGTTTGA           | ATTTTTTTTGGCTATAGGTGAGTGGTTCTAAACCTTGAGCTTGCAAGAGAACACTTTGTGGGGCTT[A/<br>G]TTCAACATGGACTGATAGGTCCACCCAGATTCTTAAGTGGTGGTGGTG                                       |
| WI-12345  | 37  | C A   | GTGGCAGGAA<br>AAAGAGGAA   | TTGAGAGGGG<br>TTCAGG                 | GGAAACAGACCTGATCCACGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT<br>TTCCTGACCAGCTGGGCTTGGCACCTTTGTGAGATTGCAAAA   |
| WI-13416  | 71  | C A   | AAATTTTGG<br>AAGTTTTTCAG  | AGTGTATTAG<br>TTCAATGAATA<br>ATTTCAA | GAAAAGGCTGTAATTTTATTTCAAATTTTGGAAAGTTTTCAGAAAAAATAAAATGACAAGAACA<br>CATA[C/A]AAATATTGAAATTTTCACTGAACATAAACACTTAGCAGAGGAAGGACTTTTGAT                               |
| WI-12310  | 46  | A A   | TTATCCCAAG<br>TATAATTTTA  | TGTTTAAATAT<br>GTTTGGTCT<br>AAA      | TTTGAAGATGCTGAAATTTATCCCAAGTATAATTTTAAAAAGCT[G/A]TTTAGACCCCAACATA<br>TTTAAACATCTCTTACACATACAGAAATTCAGTTTACAAATATCCAGAAAGGCAATTTTCTTAAGCAG<br>T                    |
| WI-12086  | 72  | C T   | CCGGGAAAC<br>TTGGATT      | GGAGTCTCGG<br>GTCTGG                 | GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAACAAAACGTTTCCGGGAAAACTTG<br>GATTT[C/T]CCAGACCCGAGAGACTCTCCAAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA<br>ACAGGAACATGCCTTAGCT |
| WI-11549  | 102 | T G   | GGCATAAAGT<br>TCATAATATTC | GGAAAGTCTGT<br>ACAAATCCCC            | ATGCTTTCACAGGTTGATTTTGTTAAGAGTTTGCTATCTAAATTTTCATATTTTATGGCATAAAGT<br>TCATAATATCTTTTATGATCTTTTAAATATCTG[T/G]GGGGATTGTACAGACTTTCCTC                                |
| WI-11585  | 79  | T C   | TGGGTTTGCA<br>AAACAAAA    | CCATGCTTCAC<br>TGATCTTCC             | TTAGAGGAAAGAAATAAACACCGGTAAATGGGAAATCAGTTTCAGAGTAGGAAGGAGCTGGGTT<br>TGCAAAAACAAAAT[C/G]GGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAAGAGCAGGGGTAGAGT<br>TT                   |
| WI-11604  | 68  | G C   | ---                       | ---                                  | TTAGTTGGTTTCTGAAACCTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT<br>G/C]AGAAGTACGGACTTTTCCATGAAATAAATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTTTC<br>TTTGTTACTCTGCAGT |
| WI-11614c | 108 | C A   | ---                       | ---                                  | CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT<br>GTTCCACCCCTGGACTTGCCAACTTCACTGTGAAACTGCA[C/A]ATATTAAAGTATTCAGCTAC<br>GGACTTCGT              |
| WI-11614a | 60  | A G   | CCAGAAGACT<br>CAGCTGCTTG  | AGGTGGGAAC<br>ATGCC                  | CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG<br>CATGTTCCACCCCTGGACTTGCCAACTTTCAGTGTGAAACTGCAACATATTAAAGTATTCAGCTAC<br>GGACTTCGT            |
| WI-11626b | 83  | T C   | ---                       | ---                                  | TTGATTTTACTAAGGCTCTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG<br>ATATTTTAAAAATAAA[T/C]TACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTGCTAC<br>AAGAACAATTTGGCAATGA |



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| WI-11626a | 39  | G A G                   | TCCACTGGAA<br>CATGAAGGTA   | GTGGTATGGCT<br>AATTTCTTATT<br>ATTAAGT  | TTGATTTTACTAAGTCTCCACTGGAACATGAAGGTAG[G/A]GATAAGGTGTACAGGATAATATACT<br>CAGATATTTTTAAATAAATTAATTAATAAAGAAATAGCCATACCACATTGTTCCATTTGGCTAC<br>AAGAACAATTTGGCAATGA         |
| WI-11627  | 23  | T C                     | CCITTCCTCC<br>ATTGTCCTC    | CATTTGCAAC<br>CATCTCAAG                | ACCCCTTCCTCCATTGTCCTC[G/C]CTTGAGATGGGTGCAAAATGGGAAGTAAAGCAAAAAGGG<br>AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTCCGATGCAAGTCCATCCATG                                   |
| WI-11636  | 61  | A G T C C T             | GGACTTAAAA<br>AGATCTGCTTA  | AGAAACTTGGT<br>AAATATTTTAT<br>GTAACACT | TCAGAAATGTTGCAAGCAAAATACTATTTGTAAGGTGGACTTAAAGATCTGCTTATCCTTA/GJTA<br>TATCCACATAACTCTAGTGTACATAAAATATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC<br>TTTGACTCCTTTTTTGGTA        |
| WI-11537  | 119 | C G T                   | ATTGCTCATCT<br>TACTCTGACCA | GACCCAGCAA<br>AAAGAATGAT<br>T          | GTACCAATTTCTATGGTGGCAAAATAGCAAACTGTGAGTAAACGAGGCGAGCTGAATAAATTTACAG<br>TATACAATATTAGAGAAATATTATGTTGCAATTGCTCATCTTACTCTGACCAT[G/J]ATAATCATTTCTT<br>TTTGCTGGGTCCAGGACC   |
| WI-11654  | 37  | G C C T G               | GCCAAAAGAC<br>TATTCAGCAA   | GGCTCTCCAG<br>GACAGTTT                 | AGTAGAACATCAGTGCCAAAAGACTATTACAGCAACTG[G/C]AAACTGTCTGGGAGAGCCACTCCAG<br>AGCTATTTCTAAGACTTTTCTGTGGTGTTCATACTCTACTCTCAGAGTTCACACTCATATTTTCATATTTT<br>ATTTTGGGTGTTGGT     |
| WI-11656  | 28  | G A A A                 | ATTGATTTTAG<br>AAGGAACTGC  | CAAGGCTTTGT<br>CCTCAAGTAA              | ACCTGATTTGATTTTAGAAGGAACGCA[G/A]GCTTACTTGTAGGACAAAGCCTTGCCTGCAGTTGTTT<br>AAAATGCTCTGAACAATCAGATTCCAGCCTGGAT  |
| WI-11680  | 55  | T C ...                 |                            | ...                                    | ACAGATCTTTTCCAGCAACATTTCTGAAATGAAGCTTTGATTCTCCCCCTTTT[G/C]TTGCATAAA<br>GGCTGGGAAGGTGTTTGGCCAGACCGTACATCTTTT  |
| WI-11696  | 47  | T C A G G G A C A G     | TTATCACAGC<br>TAGGGGACAG   | GGCATTAGAGA<br>AGCCAACTT               | GTCCAAGAACAAAGATACTTTGACATCTTTATCACAGCAGGGGACAG[G/C]AAGGTTGGCTTCTCTA<br>ATGCCACCATCTTGTTTTCAGAACTTTCCACTTCGCC  |
| WI-11702  | 69  | C T C A G C A G         | GAATAATACT<br>GAAATAACCA   | AGAACAACTT<br>AAGCAAAATTAT<br>ACTGAAA  | TTACATGTGGTCAATGGTGACATACTTTCAATAATTAATAATCGAATAATACTGAAATAACCCACAGC<br>AG[C/T]TTTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAAATTTTGTTCCTGCAGA                              |
| WI-11706  | 60  | C T T C T C T C T T     | TGGCTGGAATT<br>TTCTCTCTT   | ATCACCAAAG<br>AACAAATCCA               | TGCTGATTCATCGCTTACCATCTGGCTGGAATTTTCTCTTCTGTACAATTTATTG[C/T]GGCTG<br>GAATTTGTTCTTTGGTGATTTGTCCCTTGTGCT   |
| WI-11709  | 105 | T A T T C A G T T T G C | AGAAGCTTGC<br>TTTCAGTTTGC  | TCATTTCTTCT<br>AATTTACGGG<br>A         | AATATCATCACTCATATCAGGCATGTTTATAAAAAATGAGAGATTATGTCCTTTTTTGGCATACTTCATC<br>TTCTTCAGGACACAGAGAGAAAGCTTGTCTCAGTTTGC[T/A]GTCCCGTAAAAATTAGAAAGAAATGAAT<br>GGCCAGATGGATGAAAA |
| WI-11710  | 103 | C A C A G T C T T C A   | GCACCTAGCCT<br>CAGTCTTCA   | GTGTGGAGGAG<br>GGAGGAG                 | TTATTACCACTAACCTGTCCCGAGCTTCCAGCACACAGCCAGCCACACTCTAGACACGCTTCAG<br>TCCAGTCCATCTGGCACCTAGCCTCAGCTTCAC[C/A]CTCTCTCTCTCTCCACACTCTCTC                                     |

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| WI-11715b | 123 C T                  | AGCTT | AGGCTGGCTGC                        | TCCCATCCTG<br>TGGCT        | AGAATGGAGCTGTTGGGGAGGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG<br>TGTAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTCTTAGCCAC<br>AGGATGGGACTGGGAAGA |
| WI-11715a | 49 A C A A A             | A     | GCACACAATG<br>TAAACAGAC            | CATTACACAC<br>AGTTGTAATGC  | AGAATGGAGCTGTTGGGGAGGGACATGCACACAATGTAAACAGACAAA/CJTGCATTACAACCTG<br>TGGTGAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTACGCCAC<br>AGGATGGGACTGGGAAGA   |
| WI-11727  | 43 G C T C A A C A       |       | AACAATCCTT<br>AAAACAATA            | OCTGTGGTTG<br>TGTTGCAG     | CTGGATTTCCCTATACCTAACAATCCTTAAACAACATATCAACA/CJCTGCAACACAAACCACAGGC<br>AAAATGAAAAACAGATGCCAGACAGACGCCACCACATGGCACAC  |
| WI-11728  | 16 C G ---               |       |                                    | ---                        | TTTTATTATCAAAC/CJCAATTCATTTCCAAATGTAAAGTTATCATCAGCTCCCCATCCACTTT<br>CTCCATCTTCTATCTTTCCACCCCTACACTTCTCTCCCTACAACCCGGGTTCCAAA                                   |
| WI-11758  | 61 A G T C G C T G       |       | ATCTGTGGTTT<br>T C G C C T G       | TGATTGGCCCT<br>GTGGTCTA    | TTTTCTCTTTTATTAGTCGCTATACCTAAGGAGAACTGTGGTTTCGCCTG/CJGTAG<br>ACCACAGGGCCAATCACACAGCTTCTGTAGAGAACATGGAGTGCCAAAGATCACCATCA                                       |
| WI-11295  | 37 A G A A T A T A A     |       | GCCTCACA A<br>G T A T T T C T A A  | AAAAGTGCTCA<br>TCTGTGAATC  | CCGGCTCACAAGTATTTCTAAATATAATTTGCT/CJGTAGAGTTCACAGATGAGCATTTC<br>CATTAGGTGATATGCAACAATCACTATTTGGCTCAGCAGGAACAGACTTTT  |
| WI-11773  | 93 T C ---               |       |                                    | ---                        | AGCACATGATTTCTGCCTGGAGTTTCTGTAGCTCAGCAACAGCAGAGTCAGAGATTAAAGATT<br>ATTATTGCCTCCTTTTTTTCCCTT/CJGTGATTGTTAATAGGGAGTCAAGGCCAAGTTATC                               |
| WI-11282  | 42 C G G C A A G G G A A |       | GGCTCAGAGA<br>G C A A G G G A A    | AAAACTCAGA<br>CTGTAAATTTT  | CATGACAACTCTTTATTATTAATGGGCTCAGAGAGCAAGGAA/CJGCACACAAAAATTTACAGTCTGA<br>GTTTTGCGGCGCAGAGACCCCTCTCCACCTTTTTCATGCTGTGTACACACACACTGTCCAAAGCCTC<br>AGA             |
| WI-11790  | 28 A G A A C C T C T G   |       | CCCAACTTACG<br>A A A C C T C T G   | CGGTAGGCGAG<br>GCTAAGC     | TAATCACCCCACTTACCAACCTCTGT/CJGCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC<br>TTACATTAACTACAATGGGCAAAATCATCTAACACAAAGC  |
| WI-11879  | 61 C A A G T A T A C A   |       | TCATCTAATCT<br>GTGAGGTATTT         | GATAGTTGAAC<br>CTCTTCACTTT | TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTAGTATACAG/CJAGT<br>GATTTTCTCTCTTTCTTTTATAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA                                |
| WI-12469b | 91 C T A A G T T A A A   |       | GTTTTTAATGT<br>GGTATTAGAA          | CAATTTTCAGA<br>TTGCTATAGC  | TTTACTAATTTCCATTCTCCCTTTTATAGTTTTTAAATGTGGTATTAGAAAAAGTTTAAATTACAT<br>ATGTGGCTTATATCTATTCTA/CJTTTGACAGCAGAGTCTTCAAAGTTTGTATAGACAATCTGA<br>AAATGGGTTCTGAAC      |
| WI-11906  | 52 A G A T C T G A A     |       | TGTTATAACAT<br>C A A A G A A A G A | TTAATTTCTGC<br>AGTCCCTCA   | ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAAATCTGAAT/CJGTGAGGGAACCTG<br>CAGAAATTAACCTTCAGTCTAATCTCAGAATGCCAGAGTAAGATGAACCCCTTTACAG                             |

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| WI-11909  | 78 A G  | TTTGTTGGG<br>TGGTCAAG            | CCTCCTCTGAG<br>ATTTTCTGAAT<br>AG       | GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCCCTAAATGGCTATTTGTGTTG<br>GGTGGTCAAGTGA/GTCTATTTCAGAAAATCTCAGAGGAGGACAAATGATAGTGCACCTGCAGCCAGCTCG<br>GACTGGCTTGCAGAGTC                                     |
| WI-11806  | 60 T G  | CATGAAGAGT<br>GGGCAATTCA         | TCCTGTAAAGC<br>CAATTTTATAT<br>ACTAATAA | AAAAATACCATTAGCATCAATGCCCAAGTTTGGCAGGCATGAAGAGTGGCAGTTCA/T/GJGTT<br>TTATTAGTATATAAAATGGCTTTACAGGAAGCATTATGG   |
| WI-11946  | 31 C A  | ---                              | ---                                    | CCCTAGTGAATACAAACCTTTGTCTGGAGAC/C/JCCAGCTAGTCTAAGAAAACCTTCTAGGCTGAG<br>CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCTCTGGGAAGGGAA  |
| WI-11965  | 65 T G  | TGAAGATCAG<br>ATCTCTGGTT<br>GATT | CAGCTGTGGTG<br>AATGTTGAT               | ACAAAAATTCACAAGTACAACACTGCTTATTTCTTGCTTGAAGATCAGATCTCTGGTTTATTTAA/T/<br>GJATCAACATTCACACAGCTGAAGGAAATTAACCTGAACCT   |
| WI-11027  | 90 T A  | TGCCCTACTAC<br>GCCTTTAAAA<br>A   | TGAGGAAATGT<br>GTTACAGTATT<br>TTTATT   | ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAAACAAATCATTTCATAGATTTTCTGGGAAATAT<br>TGCCCTACTACGCTTTTAAAAAT/JAATAAAAAATCTGTAAACACATTTCTCTCATTTCTCTACGA<br>ATACCTCTTTTGTATGTGCAAAATCTATGGCATACACAGAGGCACCTCTCTCAATGCCCTG |
| WI-11049  | 95 C T  | ---                              | ---                                    | TTCTGCTGAAGATCACAAAACAAATTTCAACCTCTGTGTTCAAAATAATTTAAGGATCTTGACCTTT<br>GTGTTTATTTCTGTTTCAACTAAGGA/C/JTAGACTTCAGAAAGGCATAGCTTCCCTTGTAAAGGTTTTT<br>AAACATCTTTTTCATTGTGAGGAAGAACATTTCAAAAGCCCAA              |
| WI-15488  | 69 C T  | AAAAGGACAG<br>CCAGATATCA<br>AC   | TTTCCATCTTA<br>TTTCATTTCTG<br>TAAC     | CAACATTTATCAACATGGTAGGGAAAAGTTCTCACTCTGCACTATAAAAAGGACAGCCAGATATCA<br>AC/C/JGTTACAGAAATGAAATAAGATGGAAAATTTTAACAAAATTG   |
| WI-13654  | 49 A G  | AACAGTTAAT<br>GAAACACATC<br>CGT  | GGCTGGTGAAA<br>TGATGTCAT               | TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAAACACATCCGT/A/GJGTATGACATCATTT<br>CACCAGCCAGCTACTTCATGTGGCAGAAAAGTAACTTTTCCCATTTTACAGACAAAACCCAGT  |
| WI-11070b | 135 C T | ---                              | ---                                    | ATGAGACCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT<br>TCAAGTAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTT/JGTTGTCAGAGAGGTACTCCAA<br>C/C/JGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCCAACAGAAAGGAA       |
| WI-11070a | 110 G T | CAGAAAATCA<br>GCCAGCTATCT        | TTGGAGTACCT<br>CTCTGCACC               | ATGAGACCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT<br>TCAAGTAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTT/JGTTGTCAGAGAGGTACTCCAA<br>GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCCAACAGAAAGGAA       |
| WI-12020  | 121 T C | ---                              | ---                                    | AATCTTTATATTTCCAGCTGTTGAGACAGTATTTTGGGGCTGATTTACCTCTAGCGCGGAAACC<br>AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAATTTGAATACATGACCATT/CJCTCTTTTAGC<br>ACGTTCTTTGTTCTCCTC   |

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| WI-11076b | 142 G A ---         | ---                                |  | CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATGGCTTATCTTCTGGAGGCCTCAGGAA<br>ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGATGTACATACCCAGAGCAGGAGAGAG<br>AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT<br>G   |
| WI-11076a | 106 T C AGCA        | TOCTGCTCTGG<br>GTATGTGAC           |  | CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATGGCTTATCTTCTGGAGGCCTCAGGAA<br>ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCA[T/C]GTACATACCCAGAGCAGGAGAGA<br>GAGAAAGAGAGGAAGTCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT<br>G   |
| WI-14263  | 49 T C GGCATATTC A  | GGTTATTCAAA<br>AATTAGTATGG<br>GACA |  | ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAAT[C/J]TGTCCTCACTAATT<br>TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGTTTCTTTTGGCTACAAGTAACA<br>AATTATTGCTGAATTAGGAAGGAGCA[T/C]TGAAATGGGAAGGGGAGGTTAGAGAAGACAGAG<br>ATTTAAAGAAGCAAGTACCATTTTCCAAGTATAAACTCGTA                            |
| WI-14267  | 28 T C ---          | ---                                |  | GATTTGTTTATTCAATTCGCTTTTCAATTTTGCCTTTTAAATAGAACA[G/A]CTTTGATTTTAGTA<br>TATGACATCATCATGAAATTTTCTCTTACTTTGATTTAGGCTCCACCTCAGTAGTTTGACAA<br>AGTGAATGAGTTCA   |
| WI-15288  | 108 C G TTCCCTCTCTC | AAAAGCTTCTT<br>TCCCTTGA            |  | ACCTCTTCTGATGACACTTGACCTGTAAAGGGTCTAGAGAGAAAGAGTAGTACTCTACTTTGC<br>TACAATTCAGGATGCGGATGAGAGGATCCCTCTCT[C/G]TCCAAAGGAAAGACTTTTGGC<br>AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG<br>GCCTTCTTGTTAATTCTGGAGCA[G/C]ATTCAAGCAGCAAAATATTACTGAACACTTGCTATGTGCTG<br>G |
| WI-13951b | 88 G C ---          | ---                                |  | AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCAGATCAGAGGAAGAG<br>ATGGCTTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAAAATATTACTGAACACTTGCTATGTGCTG<br>G   |
| WI-13951a | 39 C T CAAA         | TTCTCTGATC<br>TGGGGTCT             |  | GAGACCAAAAAGGCTCTTGCCCAT[G/A]ATTCCCGTCTCTCCCTCTGACTGACCCCAAGTGTCTT<br>ACAATGAACATCCCTCAGCCCCATGGCATGGTGATCCCTCTCTTGGGATCTGTGAATATAACCA<br>ACTGTCTTGTCATTTGGC  |
| WI-13264  | 25 G A TTGCCAT      | GGAGGGAGAG<br>ACGGGAATA            |  | TTATTTGTCAATTAGCAAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAAATTTGTCTTTTCATGCA<br>TTTGTGGAGCAAGTACTAATCTGTTCACTGTCAITTTCCCTCACAAGGAGTTGAGCCCTTAGATGAC  |
| WI-13960  | 39 A C TGATAGA      | CATGAAAGGA<br>CAAATTTGCAT<br>C     |  | AACTCTTTATTGTTTAGCTAGCCCCAGTACTTTATGCATCTTATAACCAAGAGCCTTCAG[C/T]JAG<br>AGCAAGTCTGAGCCAGAGGTTTATCACACTTTGTCTCAGGGTCCACCGAACCAGGCTTGGCT  |
| WI-15843  | 62 C T CAG          | CTCTGGCTCAG<br>ACTTGTCT            |  |   |

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| WI-13983  | 52 | G A         | TCTCTCCCACT<br>CCTTAAACCT  | CAATACCTCTCT<br>TAGCCCACTGG | TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCTCTTAAACCTT[G/A]CCACTGGGCTAA<br>GAGAGTATTGTACAGAAATATGCACCTCACTGACTTAACAGAAATTAGAACATCCAGGCACCTCACTGAGA                 |
| WI-13850  | 51 | A G TT      | AATCTCAGGG<br>TCACAGCTTTA  | TGTTCCCTGAC<br>AATGTTTGTA   | CATGAATCTCAGGGTCACAGCTTTATTTTATAGATTTTAAACACAGCCAT[G/G]TTACAAAACATTGT<br>CAGGGAACATTACAAGAAATAAATAGATGGACTTGCAGGTGTAAAAAGATTACACTTCA                               |
| WI-15295  | 27 | G C A       | TGTCAGTTTGA<br>ATGTATTCTTG | TGAATAGTTGG<br>CAAAGGAAAA   | AGATGTCAGTTTGAATGTATTCTCTGAT[G/C]TTTTCCTTTGCCAACTATTCAATTATGACCATCTTTTC<br>CTCGTCAAGTGACCTGCCATCATCACAAGAAAAAGGCCCGGAAAAATATGAGTGAGACTCA                           |
| WI-14284  | 55 | C T ...     | ...                        | ...                         | ATTTCAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCCTTTAGTGCAAAAAACA[C/T]TATGCCAT<br>GCGGGAAATAAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA  |
| WI-14288  | 85 | G C CCCAGAT | CCGCTGCTATT<br>CCCAGAT     | GGTCTCTTCC<br>ACCAAATCTT    | ATGACCAGACCAGAACGCCCTGTCTATATGAAGACAAACAGGTGGCCATACTTGGGTGGAGGGATA<br>CCGCTGCTATTCCCAGAT[G/C]AAGATTTGGTGAAGGAGACCATGACAGATGACAAACGG                                |
| WI-13522  | 33 | C T ACAAC   | TGATGTAGTTA<br>CCCCACTAAT  | CATAATATTG<br>AAGTCAGTGGT   | TTTATTTGATGTAGTTACCCCACTAATAACAAC[C/T]GAGAACCCACTGACTTCAAATATTATGAGAG<br>AAAATTACTCCAGGGAAATTTTGCAGAGAAGATAATA   |
| WI-13529  | 42 | T C TTACCA  | CACAAACATT<br>TATTGAACAG   | TCTATACACTT<br>CTCACTCTCTT  | AAATATGATTCCTATCCACAACATTTATTGAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAAGTGT<br>ATAGAGGTGATTAAGAGTGGTCCCTGTCTCGAGGGTTTATAGTCTAACAGGGGAAACACCTCTC<br>A                      |
| WI-13859  | 84 | G A ...     | ...                        | ...                         | TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC<br>TTTGAAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTCAGGAAAGGGACTCTCTAGAACTTTGAGCA<br>ACA            |
| WI-13536  | 29 | T C ...     | ...                        | ...                         | TGAAAGGATACAGAAAAAACTCAGCGAAGT[C/G]GAAAAAGGTGGATAGCGTGAGTAGAGGAGAAAT<br>TAAGCACCAGCTCCAGTTGTCTCTCCAGTCCCATTTACATGGAGTACACTTAATTTTCTCAGCA                           |
| WI-13373  | 52 | G A ...     | ...                        | ...                         | TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTGCGCTC<br>CTAGATTACAAAAAGTCAAAACCAATTTCTTTGACGCCGGCCCTTGAATCTGACATTCAAGTCAC<br>CGTAATAGAAACCAGAGCT   |
| WI-13477b | 61 | A G ...     | ...                        | ...                         | TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTGTTTTTTCATTAGCTTGTCTTCAAA[G/G]GAC<br>AGAGAAATAAGATAAATACCTTAAAGAAATTAATAAGAAAAATTAAAGGAACATGTACCAAGGTGG<br>TTTTAGACTCTCCTCAGTT |
| WI-13477a | 32 | A G AAGG    | TTAATACCTCT<br>TGTTGGATAA  | GAAGACAAGC<br>TAATGAAAAA    | TTGGTTTTTAATACCTCTTGTGGATAAAAGG[G/G]CATTGTTTTTTCATTAGCTTGTCTTCAAAAGAC<br>AGAGAAATAAGATAAATACCTTAAAGAAATTAATAAGAAAAATTAAAGGAACATGTACCAAGGTGG<br>TTTTAGACTCTCCTCAGTT |

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| WI-14297  | 86 A T G          | AATGTTGGGT<br>ACTTTTCCAA   | TGTGCACATTC<br>AGAAACATTTT          | CTGACTTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTCAGTTATAAAAAAT<br>GTTGGGTACTTTTCCAAAG[A/T]AAATGTTTCTGAATGTGCACACTAGAATATATGCAGAATCCTTT<br>AACAGTGGACT           |
| WI-12229  | 89 T G AAA        | CATGTGCACA<br>AAAAGAGTAA   | ACATGTGAATT<br>GTCCCAAAAA           | TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAAGAAATCAACA<br>TGTGCACAAAAAGAGTAAAAAT[G/ACC]AAAAAATTAAGATTTTTTTGGGACAAATTCACATGTTT<br>AAAAAT              |
| WI-13582  | 43 C A            | TGCAATCTAG<br>AGACTGGGA    | TCTGGCGAGTT<br>AGATTCCA             | AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAAATCTAACTGCGCAGAG<br>AAATCAAGACCGATGGTGAAATCTGGGCGAGCTTCAAAAATTTCTGCCTCTTAAACACATTTTCAC<br>CCAATTTTTCATTATGGC    |
| WI-13857  | 28 A G ---        | ---                        | ---                                 | TCTGAGTTGATAAAATGCTTTTCTGAAC[G/J]TACATTTTAGGTATCTGGCACAAATTAACCAATGT<br>CTGCCAATTTTGTAGCTTTTCATACAGTACAGATTTTCATTGATGTCGCTCCACATCTG                                |
| WI-15809  | 77 T G TGTAAATGCC | TGGTTTCTGT<br>TGTAAATGCC   | TAAGGTAGCTA<br>ATTCAATGTTT<br>GTAAA | GTTTAAAGTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT<br>GTAAATGCC[T/G]TTTACAAACATTGAATAGTACCTTAAGTATTGAAGAGCTTCCATT                                  |
| WI-15892  | 123 A T ---       | ---                        | ---                                 | TTAATCAGTCTGTGTCGAAGAAGAAACAGGACTTGATCAAGCTTCCAGCCCTCACCACCTATCAGCA<br>TAGCAATTTTAAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAGAGAAGGAA[A/T]JGGAATCA<br>ACTCCACAGATCAACATGT |
| WI-15801b | 81 T G AA         | CATACTCCACT<br>CTAGCTGCAGT | AGAAGAGTGG<br>ATGGGATGC             | TCCTTTATCCAAAGATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACTTA<br>GCTGCAGTAATACT[G/G]CATCCCATCCACTCTCTCTCTCTTTTGTGACTGAAACTCTTCAAAAGAACT<br>GCTGAATGTCCTCTCTC  |
| WI-15801a | 24 G A AATGGGAAGC | TTTATTCCAAAG<br>AATGGGAAGC | TCATTCAAGCC<br>AATGAAAATG           | TCCTTTATCCAAAGATGGGAAGC[G/A]CATTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACT<br>CTAGCTGCAGTAATACTGCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAAAGAACT<br>GCTGAATGTCCTCTCTC   |
| WI-13763  | 59 T C GCAGTGAT   | GGCTGGACACT<br>GCAGTGAT    | CCACACCTGC<br>OCT                   | GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGATT/CJAGGG<br>GCAGGTGTGGGCGAGGTGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA                               |
| WI-13578  | 48 T A AACC       | TCAATAAAGA<br>GCAGAAAGAA   | CAGTGTGTAAG<br>AACATCTTTT<br>GTC    | TTTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACC[T/A]AGACAAAAAGATGTT<br>CTTACACACTGAGCTTACACAGTCACCCAAACATTTGATATTTTGCCTTTTCCCGAGGGCAAAAAGA<br>GAGCTCTCCCAAGAACTC      |
| WI-13789  | 62 G A AGGGAG     | TTGGATGGCTG<br>AGGGAG      | CAGTGCCTTC<br>CTCTGTTT              | TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAATGGATGGCTGAGGGAG[G/A]<br>GAACAGAGGAAGCGCACTGGGCTGGGACTGAATATGGACAGTGGATGGTGGTCTCTACTCTCTT<br>GAGGTCCCT                 |
| WI-13594  | 66 G A AGC        | TTTTTAACACA<br>GATCACAAA   | CCTTGGCGCA<br>GTACTTTT              | AATAACAAGTTTAAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACAGATCACAAAAAGC[<br>G/AT]GCACAAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC                           |

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| WI-15625  | 40 C T ---        | ---                                     | GTTCCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[C/T]GTGCCATACTAATTTTGAATAA<br>CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA  |
| WI-13367  | 84 C G A          | TCCCAACCCCA<br>OCC                      | GTCTACCTTTCTGTCTAGGCTGTAAATTTTTCAGTTTAAAGTTTCTTATGTGATTTGTGGCCACACT<br>GAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT<br>GAAATCCAGTTATTCTCT        |
| WI-13600  | 26 G T AAGCATCCAT | CATATTGAAAA<br>TTGTTACTAGA<br>TGATGG    | CTCACCTTTAATGAGCCAGCATCCAT[G/T]CCATCATCTAGTAACAAATTTTCAATATGCACATTATAT<br>TATACTGGAAAAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT<br>TGATTCCCTTCTCTACCC |
| WI-13602  | 89 G T GACAACACA  | GCATACCTCAT<br>GACAAATATTTA<br>ATATTAAT | GATAGGAAAAAGAAATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC<br>CTTCCATTCTGGAGACAACACA[G/T]AAATCTATTATAATTAATATTTGTCATGAGGTATGCACCT<br>GCCC                       |
| WI-13650  | 76 A T TTTAAAC    | CAGGCTAGGAT<br>ATGAAGAGTA<br>GTTTT      | GCATTAACATTTAAAAATTTCTGAGGATATTGATGAGAACTATGATGAAGATTACAAATATTTTCAC<br>TTTTAAAC[A/T]TAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAAAGTTACCGG                                   |
| WI-14319  | 83 C T A          | CATAATCATCT<br>ATATTGTTGCA<br>TG        | TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAAATAGCAATT<br>CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGACAGTACAGAATT                               |
| WI-13528  | 80 A G AAAA       | CATGATACCAC<br>AGTTTTCTCTG<br>AA        | ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTTGCATTTTCCATAAAA<br>AAAGAAGACATTT[A/G]TTACAGAGAAAACCTGGTATCATGCAGGAAAAAGCAGAAAAAAATTT                             |
| WI-13909c | 93 A T ---        | ---                                     | ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT<br>CTCTTCAAACTCGAATATCTTTTCT[A/T]GAGATGCTCTAGCTAGTACCCACTGCAACATCTCTCAA                            |
| WI-13909b | 80 G A C          | GCAGTGGGTAC<br>TAGCTAGACAT<br>CTC       | ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT<br>CTCTTCAAACTG[A/A]AATATCTTTTTCAGAGATGCTCTAGCTAGTACCCACTGCAACATCTCTCAA                            |
| WI-14323b | 86 C A ---        | ---                                     | TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAAATTAATAAAGGGACAGAAAAATTAAG<br>AATCAAAACATCAATCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA                            |
| WI-14323a | 78 T C ACATCA     | GCCTTTTCAAG<br>GTTCCCAT                 | TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAAATTAATAAAGGGACAGAAAAATTAAG<br>AATCAAAACATCA[T/C]CTCTGGACCATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA                           |
| WI-15389b | 104 G A AAA       | GATGAGGTGAT<br>TCCACACACTT              | AAAAATTGACAAATCAACTAGCTTGTCTTTTGTCTGTTTGGAAAGACTACCATTAATTCAAAATTTATATGT<br>AATACACTCATCCAGATAATGAACATCTCGAAA[A/G/A]AAGTGGGAATCACCTCATCTGTGC                           |

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| WI-15389a | 33 G A T C                | AATCAACTAG<br>CTTGCTTTTIG  | TTTGAATAATG<br>GTAGTCTTCCA<br>AA      | AAAAATGACAAATCAACTAGCTTGCTTTTGTGTC[G/A]JTGGGAAGACTACCATTTATTCAAAATTTATTT<br>ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAGAAAGTGTGGAAATCACCTCATCTGTGTGC                     |
| WI-15747  | 88 T C A G T G T T        | TGCTTCATTTT<br>AAACTAAATTT | CATAATTCACC<br>AAAAGTTTCATA<br>TAATTT | TGTAATCTGCTTACAGTCTTTGCGAAAGACAGACATATGTTTTGCATAAAGATATAAAATGCTTCAT<br>TTTAAACTAATTTAGTGTTT[C/J]TTTAAATATATGAACCTTTTGGTGAATATGAACCTGTACCAAAC                         |
| WI-13752b | 117 C T ---               |                            | ---                                   | AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT<br>CTCTGCGATGAGTTCCTCTCTCTGTTAAGTGCTGGATATAC[T/C]JGGCTTGCAACCGGACACCTTTTACG<br>GAGGGATTCCGGACAAC |
| WI-13752a | 106 T C A G T G T G A     | CCCTCTCGTTA<br>CAGTACATGA  | CCCTCCGTAAA<br>AGGTGTCC               | AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT<br>CTCTGCGATGAGTTCCTCTCTCTGTTAAGTGCTGGATATAC[T/C]JGGCTTGCAACCGGACACCTTTTACG<br>GAGGGATTCCGGACAAC |
| WI-14339  | 102 T G T T A C           | CCCAATCAAA<br>CAGTACATGA   | TCCAGATTTCT<br>GGAAACCG               | AATCATTAAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAATTTCACTGGGATGGAAG<br>CAGATGAACCCACCCCAATCAACAGTACATGATTAC[T/G]GGGTTCCAGAAATCTGGATAC                                |
| WI-13744  | 115 C T A A A A C T G A A | TGGTGCTGAAC<br>TAAACTGAA   | AATCAGGAAA<br>GATAAGCACA<br>GC        | TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACGTAAATGGAACCTCATGCAGCTTTAGAT<br>TTCCTTTGCCAGCTAGGAGCTTGTGTATGGTGTGAACAAAACCTGAAC[T/G]GCTGTGCTTATCTTTC<br>CTGATTCT             |
| WI-14061  | 68 C T ---                |                            | ---                                   | CCTTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACTTAT<br>[C/T]JAACCATTTTCATCCACCATTGTGTAATAATCTCATCTTCTGGGCTGGATACTCAAAAACAGAT                           |
| WI-15719  | 69 A C C A T T C A G C    | ACCCTTTCATC<br>CATTGAGC    | TGATACTGGC<br>AAGAGTTTTAA<br>ATT      | TTACAGTTGGATTAACTACCACACTACCACTGAATATACTGAATTAACCTTCAACCCCTTTCATCCATTGAG<br>C[A/C]AATTTAAAACCTCTGCCAAGTATCATGAACTTACGAAGAGGAGATAAGAGATCTGATC                         |
| WI-13810  | 106 T C A A C T T         | CTCTAAATCG<br>ATACATCCAA   | GAACTGATGCT<br>TGCTGCTAAT             | TAATCCATCAATCTAAAATCACACATACATAGATCAACACAGAAGTACCACAGTATGCTTTATTTTGCA<br>GGTATTAATTGGTCTCTAAATGATACATCCAAAACCTT[C/J]AGTTAGCAGCAAGCATCAGTTCTTC                        |
| WI-15736a | 27 G T C A C A            | ATTTTATTCAC<br>ATTAACCTTG  | GTCTTTTGATA<br>TGTTGGCTTAGT<br>TTT    | GGATTTTATTCACATTAACTTGCCACA[G/T]TAGCAAAAAAATCAAAACATAAAACATAAGCCACA<br>TATCAAGAACAATATACATAGAGATTGAAATTTCTCAATAGCATTGGAAGGTTATTCATAAATA                              |
| WI-13785d | 72 G A ---                |                            | ---                                   | TCAAACTGCACACTATAAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGACACACAAATGAAC<br>AAGTGC[G/A]TAGTGACACATAGCTGTCAACACACAGT  |
| WI-13785c | 56 A C ---                |                            | ---                                   | TCAAACTGCACACTATAAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGAC[A/C]CAAAATG<br>AACAAGTGGTAGTGACACATAGCTGTCAACACACAGT  |



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| WI-13785b | 40 C G ---         | ---                        | ---                             | TCAAACTGCACACTATAAAAGTGTCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACACAAATG<br>AACAAAGTGGGTAGTGACACATAGCTGTCAACACACAGTG   |
| WI-13785a | 27 T C TGCTT       | AAACTGCAC<br>ACTATAAAG     | TGTTGTGACAG<br>CTATGTGTGAC<br>T | TCAAACTGCACACTATAAAAGTGTCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACACAAATG<br>AACAAAGTGGGTAGTGACACATAGCTGTCAACACACAGTG  |
| WI-13793  | 88 C G ATAGG       | GGATTTTACAT<br>TCAGCCTAGAT | GGGCAGGAGGA<br>TTTGTACT         | AGAAACCAAGTATATCATAGGCAAAATAAAATAGTTTTTACCCCATTTGATACAACATAAGGGATTT<br>TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCATAAATCTATGACTTG                                   |
| WI-13794  | 52 A G TTCTTTCTC   | TTCTCACCCT<br>TTCTTTCTC    | AGAATGGGCTC<br>TTAACCTTGT       | TAGTCTCCTACAATTCCTTCAATCCATTTTCTCTCCTCACCCCTTTCTTCTC[C/J]TACAAGGTTAAGA<br>GCCCATTTCTTCAACAAACAAACAAACATAGAGCAAT  |
| WI-15729  | 35 A G GTGTAGACTGC | CTTTGAACCAT<br>GTGTAGACTGC | CTCAGCTTCTT<br>TCTAAAGTGCC      | TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C/J]GGCACCTTTAGAAAGAAGCTGAGACTGAA<br>AAGTCTGTCTGACTTCCAAGGAAGGTAAAGTCCCTGTTTGCAGCCCCGGGCTGCTCATTTGTA                              |
| WI-13424  | 66 G A C           | TGAGGTTTTTC<br>ACCTATTCTT  | TTTTCTCCCC<br>AGGGTCTA          | GTCCTTTGCACAAAGTCTCCCAACTGGTTTGGAGTTTCCCTCTCTGAGGTTTTTACCCCTATTCTTC[C/J]A<br>JTAGACCTGGGGAGAAACACACATGTGTAAAGTGGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT<br>GCTGGCTAAGCGGCTTC |
| WI-14065  | 29 T C AATT        | TCTTATAAAA<br>GGTCAGAGGC   | CAAGCTGAATC<br>TGGGATCTC        | AACTGTCTTATAAAGGTGAGAGGCAATTT[C/J]GAGATCCAGATTGAGCTTGTCTCATAAAAAGAT<br>TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTTAACTCTGAACATTTTGAAGCACGAA                                    |
| WI-13446  | 22 G C TCACTCATCA  | GCCATGTTCTT<br>TCACTCATCA  | AAGGGAATCA<br>AAATCAGAAG<br>G   | TGCCATGTTCTTCACTCATCA[C/J]CCTCTCTGATTTTGAATCCCTTCTGCTCTGTATTTTTTCTTC<br>TTCCCTTTTAGGGCCTAGTCTGTTTAGAAATCTGGTTTTTGAGAGTAGTGAGCCCTTTACTTTTTT<br>CTGACTGCCTAAT            |
| WI-13725  | 56 A C TGGGTGOC    | TGAGCACATA<br>TGGGTGOC     | CCTGCTGTCTC<br>GGGC             | TCACACAAGGCATTTGGAATGTCACTTACACATGGTGAGCACATATGGGTGCC[C/J]GCCCGAG<br>ACAGCAGGATAAGTTTTCACAAAACCTTGACCAGGCAGGTAGAAAGCAAGGCATGGTTCAAGGATG                                |
| WI-15702d | 107 T C ---        | ---                        | ---                             | CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAAGGGGGTAAAGGGGTGAGG<br>AAAGCATGTGAGAGAAACTGTAAACCTGTAAACCAATACTAA[C/J]GGGTTCTTTGAACAAATAGTTT<br>TGA                     |
| WI-15702c | 101 T C ---        | ---                        | ---                             | CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAAGGGGGTAAAGGGGTGAGG<br>AAAGCATGTGAGAGAAACTGTAAACCTGTAAACCAATACTAA[C/J]GGGTTCTTTGAACAAATAGTTT<br>TGA                     |
| WI-15702b | 90 C T ---         | ---                        | ---                             | CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAAGGGGGTAAAGGGGTGAGG<br>AAAGCATGTGAGAGAAACTGTAAAC[C/J]TGTAAACCAATACTAAATAGGGTTCTTTGAACAAATAGTTT<br>TGA                   |

|           |                     |  |   |   |
|-----------|---------------------|--|---|---|
| WI-15702a | 48 G C A A A G      | A C A A A A T A A<br>A G G C T T T C A A   | C C T C A C C C C T T<br>T A C C C C                      | C A A A T G T T T A T G A A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G G T A A A G G G G T G<br>A G G A A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A A C A A T A C T A A T A A G G G T C T T T G A A C A A A T A G T T T<br>T G A                                   |
| WI-13831b | 113 T C             |  | ---   | T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A<br>A C T T C C A C T G A T C C T C C G G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A C A G T C A A G<br>T A T A A A C A T G G C T C A                             |
| WI-13831a | 56 G C              |  | ---   | T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A<br>C A T A C T T C C A C T G A T C C T C C G G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A C A G T C A A G<br>T A T A A A C A T G G C T C A                       |
| WI-13806  | 62 G A              |  | ---   | T G A T T G A C T T A G A A A G G A A G T C A T G T T G A A A T C A G A G A G A G C C A A A A C T A G G C C T C A G G T [G/A] C<br>C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A<br>C A T   |
| WI-14372  | 86 A G              |  | ---   | C A C A T T T C A G C A A A C A A A T C G A G G T G C A A A C A G G T T A T T T C A C A T T A T A T A T A A C T G G A T T T<br>T T T G C A A A T A A A T A G G G A [A/G] T T C T C T T A A A T A C C A T C T C T C A C T T C A T G G C C A G T  |
| WI-14373  | 95 A G              |  | ---   | A G G C T G T T T T T G A G G C C T G A G G C C C C A A C A C A T G A C A A C G T A A G A C T G T A A C C A T G G T C A T G T G A G T T<br>A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C C A C C T C C C A A C G C C T T T<br>A C T T T C A C A G C C T C T G C A |
| WI-14078  | 61 C T G C A A G A  | A A A G A A G T A A<br>A T T A G G A A G A | T G T G T G C A T G T<br>C T C T T A C T G C              | A G A A A C C G A G A A C T C A A A G A A C C A C A C A T G G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G<br>C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G G A A G G A C T T T A G A T G G T C A C G  |
| WI-14083  | 47 C T A C A C T    | A G A C T T G A G A<br>G C T T A A A A C A | G C C T A C T G G A C<br>C T C T A A A C T A C<br>T G A   | T T G C T A C A T A C A C A T T A C T C C A G A C T T G A G A G C T T A A A C A A C A C T [C/T] A T T T G T T A T T T C A C A G<br>C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A  |
| WI-14085  | 31 A G A A A A A    | C A T T T A T T T C<br>A T G T G T A A G A | C A G T C A T G T T C<br>A C G T G C T A G T T            | T G C A T T T A T T T C A T G T G T A A G A A G A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C<br>A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T T A A G T G A A A<br>T A A C A G A A C A G G A G G C C T T       |
| WI-12169  | 121 G C T T G C T T | A A T A A A A C T T<br>C C T A T T T C T T | G G G T T C T G A G G<br>T G A A A G A A A A<br>A         | G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T C A T T C T A A A<br>T T T T C A C C T T A T T G C T A G T T A A A A T A A A A C T C C T A T T T C T T T T G C T T [G/C] T T T T T C T T T C A<br>C C T C A G A A C C C C C T T A                       |
| WI-15705  | 50 A G A T C        | G G A G G G A G A T<br>T T T A G A C T G A | A G C T G T A G T C G<br>T C A A A T A C T C T<br>A G A A | T T G T T T T A T T T G G G G A A A T G A A G G A G G A G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G T A T T T<br>G A C G A C T A C A G C T C C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A C A G A A A T C C T C A<br>T C T G C G G T T G C C A G A C A G                   |

|           |            |                                  |                                       |   |
|-----------|------------|----------------------------------|---------------------------------------|---|
| WI-14379  | 102 C T    | TCTATTAACA<br>GGGTATGTCA<br>CAAC | ATCATCTGTTT<br>TGAGGTTGACA<br>---     | TTTATGCTGTTGTTTCTACTGGTGGTCTCGCTCACTAATATCAATCCTAGTAGATTTTCTTT<br>TACTTGTGCTATTAAACAGGTTATGTACACC[C/T]TGTCACCTCAAAACAGATGATACT<br>TAAATAAAAACAAAGCAGAAA[C/A]CCCACTTTAAACAAGAGGACACTGCAGAGGCTTATGTACA<br>ACACGTGTCGCCGAGGCTGGCGCAGGACTGCGACTCACTCCAAAATTTCTTTGGAGCAGAG |
| WI-14102  | 22 C A     | CGCAGAGCTG<br>CTGTATTTAAA<br>A   | GCAGAGATCCA<br>GACGCTGT               | ACCGCAGAGCTGCTGTTTAAAAA/GJACAAGCGTCTGGATCTCTGCAGGGGCTGGGACCAGCTGC<br>AGTGGGGCTCCGGCACTGCTCTCTCCAGGACTCTCCACCACCCC   |
| WI-15937  | 24 A G A   | AAACTGAAAC<br>GTATTTCTCTCC       | GGCCTTTAAGT<br>TTCTACGGTG             | TGAACTGAAACGTATTTCTCTCCA/JACACCGTAGAACTTTAAAGCGCGCAAAAGACTCACACCC<br>ACCACCTAGCGGCGCAAAAAGGAAGTTTCAGGTGATACAAGATGTCTCTGCCATCACACCTGAAGGAT<br>GGTT   |
| WI-15944  | 24 A C A   |                                  |                                       | ATGTTTTATGATCAATTCACAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATCAT<br>ATTTAAGTCCCGGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT<br>CACCAAAAGCTCAGTCACTAC   |
| WI-14124  | 92 A G     |                                  | ---                                   | GACAAAGGCGAGTTTCTGTAGTCCAGCAGGGCCAGAGGTTATCAGAACGGTGGTTTGACCT<br>GCATAGATTTTTCAGCAGCTA[C/T]GTGGCCATGCCATTCCTGTAGTGAAATTAATGAACA   |
| WI-14125  | 88 C T     | GGTTGACCTG<br>CATAGATTTT         | GGAATGGCATG<br>GOCAC                  | GTTTATTTCTCACAGTTCTGGAGGTTAGAACTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT<br>GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGTCTTCACAT[G/A]GCCCCAAAGAGAC<br>AGAACAAAGCTCTCTGGT  |
| WI-14136  | 120 G A    | ATGTCTTCACA                      | TCITTTGGGC                            | TTGTTGTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT<br>GCAATTAATATTGTTTCTTATGATTTGTTTCAATG  |
| WI-14138  | 23 C T     | TGTTGGCACCA<br>GAAAGCT           | CAGTATGTACA<br>GTGACATAACA<br>TAGAACA | GGCAGGTTTATTCATAATTTTCAAACTTGGAAGCAACCAAGATGTCCTTCAGTAGTAGTATATCA<br>GACAATC[G/A]AATATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG<br>AACCTTAAATGGATATTACT   |
| WI-13551  | 74 G A     | GACAATC                          | TAATATT                               | TTTTTAAAGAGTGCTCTTCACATCATTTATTTGATTGTCACACAAAACCTTTTAACTC[C/T]GTCAA<br>AAACAACAAGAACAGATGAATAAGGAAGGCCAGTGCTTTTGGATAGAAGCCCTTCTTCAGAATCA<br>CCTCC  |
| WI-15953b | 59 C T     | ---                              | ---                                   | TTTTTAAAGAGTGCTCTTCACATCATTTATTTGATTGTCACACAAAACCTTTTAACTCCGTCAA<br>AAACAACAAGAACAGATGAATAAGGAAGGCCAGTGCTTTTGGATAGAAGCCCTTCTTCAGAATCA<br>CCTCC  |
| WI-15953a | 26 T G A T | TTTTAAGAGTG<br>TCCTTCACATC       | TCATCTGTTCT<br>TGTTGTTTTG<br>A        | TTTTTAAAGAGTGCTCTTCACATCATTTATTTGATTGTCACACAAAACCTTTTAACTCCGTCAA<br>AAACAACAAGAACAGATGAATAAGGAAGGCCAGTGCTTTTGGATAGAAGCCCTTCTTCAGAATCA<br>CCTCC  |

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| WI-14631  | 82  | G A ---       | ---         |             | TGAATCAATGGACAGTTTGGCTCTGTTTGTAGTAAACCCCTCACAAGCACTCTGATAGTCGGCTTTCTGTCTTTTAACTG/AJTGCCCTGGTCCCTCTGCCAAACTTTTAGGATTGGCCCTCTCAGGGCCTTGTCTCTGA   |
| WI-6053   | 24  | A G ---       | ---         |             | ATCACCCCGTGTCTAAGAACAAC/AJGTCTTCATGTCCAACCTCATATCCCCGGGACTTTGTCAACTGCAGTACACTTCTGCAATTGAACCTGGCTTCTCTGGAGGAAAGCCCTCTAGAGGCCAGGTAAGGGGGTGCAGCAGTGAAGGGGTATATCTGGCTGGCCAGTTGGAACCCACGGAG |
| WI-15964  | 99  | T A CTGGAGGTA | GACTTCTCCAC | OCCTCTGC    | CAGAAACCTCTTCTGTGTATTAAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGTCCCTGGAGGTAT/AJGCAAGAGGGTGGAGAAAGTCTTGGCAAG   |
| WI-12075  | 103 | G A GGCAC     | AGCAGCTGGG  | CCCTCTCTTC  | CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAAAATACCCATCAGAGCAGTGACAAGAGCAGCTGGGGGCACGGGGGAGGC/G/AJGAAGGAAGAGAAAGAGGGGGAGGAGCCT  |
| WI-12179  | 96  | G A TGGAGGTCA | GGAGGTACGG  | TGTAATGAC   | TAATTTAAACACGCCCTTCCACATAGTGGCTGAGGCATCTGCACATTTCTCTAGAAGGACATGATAGTGATGGAGGTACGGTGGAGGTCA/GA/GCATCTACAGGGTCAATCGAGGGAGAACAG   |
| WI-14651  | 49  | C G ATTGT     | CAAGAATCAT  | GGAGATATTGA | CACAAATAGTGAAATATCTGAGCAAGAATCATCTCTATTTAAATTTGTC/GJAAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA   |
| WI-14666  | 105 | T A ---       | ---         | ---         | AATGTGGACTTCAACAAGGGTTTAAACATAATCTAATAACAACCTCTACAACACATCTCCAGAGCATATAACAAGAATTTACAGGCAGCTAATGTATTAAAT/AJAAACCATGAAAGAAAAAATTTG  |
| WI-13473  | 31  | C T ---       | ---         | ---         | ATCTAGATGTCAGCAATGGGTGAGACTGTC/JTGTCTGGTAGATGCAGTGTGTGTATGTTTCTACCTATTACAAAAATTAACAGAAATATGGCTTGTGCAAAATGTTTATATCACAGTC  |
| WI-13967  | 103 | A C AAATAAAAA | AAAAGACTAC  | TTGTGTTTCA  | AATTTAATAGCAGCTGTGTGTGATTTTAAAGAACAGATAAAATATGTCATTACAGCAGTCATTTAAAAATAAAGACTACAGATACAAGGAAATAAAAA/A/CACCTTTAGGAGATGAAAAACACAAA  |
| WI-14408  | 60  | T A G         | GCAGACACAC  | TTAATTGTGTA | TTAATATTTACGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTGT/AJAAAGTAACAAATGAGTTTACACAATTAATAATAATTAACACATACCTTATGGGATTTGTTGAATGA  |
| WI-13683  | 47  | C G ---       | ---         | ---         | TTTTGTGTTAAGAACAGCATTTTGAAAAATAAAACCTATCTGCCCATG/CJGTTTACAGCCCTTTTAAATTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC   |
| WI-13910b | 63  | C T CGTCT     | CACCATGGCA  | CATTGAGATAA | TTAGAAAACCTGATAAAGCAACACAACTTTTGGGAAAGCACCATGGCAGCTCCTTTGTGCTA/CJTGTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA   |
| WI-14635  | 22  | G A ---       | ---         | ---         | ACATGGCAGATACAGAGCTGTG/AJGTCTTGAAGACCACCACCTGACCAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGTTTCTGACCGTCTGGAGCGTTGAAGGGTGACCAGCACATTTGCACATGCAAAA                                  |

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| WI-16002  | 59 T  | GATAACATAA<br>AATGATCATG<br>CAGAAATTC | GCCATCTCCTC<br>TTTGACTTTT          | CCAACATTTTAAACCTATGACTGGTGCTATTGATAACATAAAATGATCATGAGAAATTCATTCGTTA<br>AAAGTCAAGAGGAGATGGCTAATGCATGCTGGCT  |
| WI-15361b | 101 A | CCCACTGAAC<br>TCAAGTCATC<br>G A       | AAACTAAAC<br>CTTTGTGCTA<br>AAA     | GTGGAATTTTAAAGCCATCAAAATTCCTTCACACTCAATACTGTTGAACAACAAGATAACACAT<br>CTTCTGTGCTCATCCCACTTGAAGTCAAGTCATCAAGTTTTAGGCACAAAGGTTTTAGTTTTCTCGG<br>GAAATCAAGTTTTAACCA  |
| WI-14759  | 73 T  | GGGTTTGACTT<br>GTGGGG                 | TCCACACTGC<br>OCC                  | TGAGTTACAACAATGAGCAACAAGTTAGAAAAATGGTTTTATTCAAACCTCCTAGCGTTTGACTT<br>GTGGGGTCGCTGACTCAATGGGGGCGAGTGTGGACGGGGGATTGCAACCCAGAGTTTCATACTG<br>CAA   |
| WI-12535  | 50 A  | CTAGGAGGGTT<br>GAGGTGTAGA<br>TAT      | GCTCCACGAGA<br>AGAGAGGAA           | TCCCTAACATTTATTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATATATCTTCTCTCTCTC<br>GTGGAGCCTTACTGAAGACAGGATCGCGTTCTTGTTTTATCAGCTGAGAAGGGCAGTCTCGCCATC<br>TTAAAGACCTGCCCTCC   |
| WI-13805a | 112 G | AAAGGCACAC<br>GGGAA                   | CTCAGCCTGOC<br>TTGACC              | TTCCATTATTGCTTGGCTTTACCAATTTTTATAGCTATTGGGAGGCAGGAAAGGAAATTTTGGC<br>CCCAGAAACCATGAGATTTGGTGCAGAAAAGGCACACGGGAAAGGAGTCAAGGCAGGCTGAG<br>AGTCACATTTCCAGACCTC  |
| WI-12340  | 18 T  | ---                                   | ---                                | ACACAATAATTCCTATTCGAGTGATTAAACCTATTTGTTGTTTAGAACCAACAAAACTAC<br>AAGAAAAATTTCAAACCTTTTTTTCAGGCTGA   |
| WI-14808  | 52 T  | ACCCACCACA<br>CTACCCCTGT              | GAGGCATCACA<br>ATGTTAAGATT<br>TT   | CTTTGAAACACTTTAAGCAACAGTTAAAAAGTACCCACACTACCCTGTTTAAATACTTTAAC<br>ATTGTGATGCCCTCTGCATCAATTTTAGAAAAACAAGAAAAACACAACTGAAGGCCCATGTA<br>AGTTAAAAAAAATCGAGTCAGCATTTATTATTAJAAAAACTGGACACGCTTCTATATTGCAAGCTCAT<br>TCAAATGCATTTATTTTGTATCCCAAGCCCTGAACATGAAAAAATATTACTAAAGGAATGTTG<br>ATTACCAGCTACGACTTTC |
| WI-12542c | 71 G  | ---                                   | ---                                | CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGGCTCTAGATC<br>ATGCTTJAGGTGATTGATACAAATACGATCCATAA   |
| WI-12542b | 70 GT | ---                                   | ---                                | CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGGCTCTAGATC<br>ATGCTTJAGGTGATTGATACAAATACGATCCATAA   |
| WI-12542a | 45 C  | GCTATTAGGC<br>AAACTGAACA<br>TTTAAA    | TCTAGAGCCT<br>CACATGGAT            | CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGGCTCTAG<br>ATCATGGTAGGTGATTGATACAAATACGATCCATAA   |
| WI-12173  | 57 C  | GGATACAGCA<br>GTAAAGAATA<br>TCAAAA    | CCACCTCTAGA<br>ATGTATGCTCT<br>ATAA | CACCTAAATCATCTAGAAACTGGGGATACAGCAGTAAAGAAATACAAAAATCCTGCCTCTTATA<br>GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA  |

|           |            |                           |                                  |  |   |
|-----------|------------|---------------------------|----------------------------------|--|---|
| WI-14836  | 28 T C --- |                           | ---                              |  | TCITGGAGGGATAGAGGACAGAGTGTTC/CJGTTGATTTTCGTTTCGGTTTCAGITTTGGTTGCATT<br>GGTTTTGTTTTGCTAATTTTGGCCCACTATAAAAAGCAGTGCACCCAGAGGCAG   |
| WI-14856  | 60 A T A A | TGGTGACAG<br>GAAAATACTT   | TTTGTTCCTA<br>CTTTTACAAA<br>CTTT |  | ACATTTCTTATGATGCAACAATAATATGATGGATGGTGACACGGAATACTTAATAT/TTTAA<br>AGTTTGTAAAGTAGCAACAAAATTTGAGTATATACATAAGTGATAGAGGATGTATATGAAAAA<br>GGCTATAAAAGCTCCAAA               |
| WI-14863  | 61 G A --- |                           | ---                              |  | ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAAGGGCAAAATATTTTGTCTG/G/AJAG<br>TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACATATTATTGATTGGCCACT<br>ACCTGGC              |
| WI-14867  | 46 T C A   | GACATTCCAA<br>GGCTCTCTAAG | TGGGGCTGCAG<br>ACACTC            |  | TTTTAATTAACGTAAAAAGGCGAGACATTCCAAAGGCTCTCTAACA/T/CJGAGTGTCTGCAGCCCCA<br>TTGGCTTTGAGATGTGAATGTGTTAACCCAGGTGGA  |
| WI-14733  | 98 G A A   | CCAAATTGAC<br>AGATATTCTGC | GATGAGGTCAG<br>GCCATTATT         |  | ACGGAGTCGTCTCTGATGATTTCTTTGTCAAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAAAT<br>AGAAAAATCCAAATTTGACAGATATTCTGCA/G/AJATAAATGGCCTGACCTCATCAAAAAACATCA<br>ATGTCATGAAAAACACAAAA   |
| WI-14898b | 79 A C --- |                           | ---                              |  | TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCTATAAGGTGCCACTAAGGAAA<br>ACTTCTCCAT/CJAAAGCTGCCTGCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCATCT<br>GCCTGTGTTCTGCTT       |
| WI-14898a | 50 A C C A | CATGTACAGG<br>AAGAGTTGTCT | AAGTTTTCCCT<br>AGTGGCACT         |  | TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCTAT/CJAGGTGCCACTAAGG<br>AAAACTTTCTCCATAAAGCTGCCTGCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCATC<br>TGCCGTGTTCTGCTT        |
| WI-14907  | 48 G A     | GGCACACATT<br>GGACTCTGAC  | TCTGCTGCAAG<br>GGGAAT            |  | TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/G/AJATTCCCTTGCAGCAG<br>ACATTTGTGAAGCTGCTGGTGGCACACACCCATCAATCAGTGACTCTGCTGACACTGCAGAGGGGCCACATG<br>CAGCATGCTCACGTGTG |
| WI-14911  | 52 G A C   | CCAATACATT<br>CAGTTCTGTT  | CAAAACCAGGA<br>AAAGGACCTT        |  | CTAGAATCTGGGAAGTCCAAAGCTCAGTGCACCAATACATTTCAGTTCTGTC/G/AJAGGTCTTTTC<br>CTGGTTTGCAGACAGATACCTTGCTGTATCTCCTCAGATGGCAGAGAAAGAGAGAGTAATCT                                 |
| WI-14913  | 88 C A --- |                           | ---                              |  | CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGCCAAATTC<br>TAGTGATAGTAGAGGACTCA/CJ/CCTGCACGTGCACCTTTCTATATACAGATCAACCAATCCAAAAAC<br>CTACACCTCCAAACCCT     |
| WI-14914  | 66 G C A   | CTGGACACAG<br>TTTTCTCTAGC | CAAGCCAGGA<br>CAATAAATTC         |  | ATTTCTTGTATTGGCTGTCGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTTCTCTAGCA/G/<br>CJGAATTTATTGCTCGGGCTTGATGGCTTTTCACAGC   |
| WI-14926  | 49 T C --- |                           | ---                              |  | GTTTATTTTCAAAATGACACATCCACAGATTGAAATGGGCACCTTAGCGAA/T/CJACTTGTGGACCACA<br>AGACTGTCTGAGAACATGTTCAAGACAGTTTTTCAAAATAAAAAATTTTCTTAATCAGGTCCA                             |

|           |          |                                    |                                      |   |
|-----------|----------|------------------------------------|--------------------------------------|---|
| WI-16083  | 89 C T   | ATGTTTAAACA<br>CAACATATC<br>AAGGAT | TGGAAGAAGATT<br>CCAGGCC              | GCATCTTTATACCAGAAACTCATTTATGTCCTTAATCATTTGTTTAAATATATATAAGCATGTT<br>TAACACAAACATATCAAGGATC/TGGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAACCATC<br>CATTAAAGCAG           |
| WI-14930  | 55 C T   | GGAGGAGTCC<br>CTCATGGAT            | CACAACCAACC<br>AATACCGC              | CAGTCTGTGTTCTGGAACAGCTCTCTTTCCACAGGAGGAGTCCCTCATGGATC/TJGCGGTATTG<br>GTTGGTTGTGGTATTGGGGAGCACGAGGGAGAGCAA   |
| WI-14946  | 47 T C   | ---                                | ---                                  | TCAATCTGAAGGTGTCAAAGTGGTCTATTGGCCCCAGACATAACAT/TCTCTAAATCATCTCTA<br>GATCAGGGAGTCTATAAGGACCATTAAAGGCTCATTACACACAGTACTTTATGGAAGGATT                               |
| WI-15987b | 80 A G   | ---                                | ---                                  | ACATTAAACAGCACAAATTAAGGGGTCCCAACGAGGTGGTAGTGCCCTCCACTATGTGAGGACAC<br>TAAGAAGATGGTC/A/GTCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC                              |
| WI-15987a | 32 C T   | CACAATTAAA<br>GGGGTCCAA            | GGAAGGCACTA<br>CCAACCTC              | ACATTAAACAGCACAAATTAAGGGGTCCCAAC/A/TJGAGGTGGTAGTGCCCTCCACTATGTGAGGA<br>CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC                             |
| WI-14948  | 56 T C G | AGGGAACCTG<br>CTAAGTTGTCA<br>G     | GATGATCTTAC<br>ATCAGTTGTTG<br>GA     | GAATAAAGTCTTATTGCCGTTCTTCAGGGAACAGGGAACCTGCTAACTTGTGAGT/CJTCCAACA<br>ACTGATGTAAGATCATCTCTGACCATAGCGAACCTGTAAAGGCTTGCTTCCCTCCAGCTGA                              |
| WI-16100  | 52 A G   | CAAAAGCTA<br>TTTTCTACAC<br>TTGA    | ACAGGAATGTC<br>AGAAAACAGT<br>ATATTAC | TTGTTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC/A/GJGTAATATACTG<br>TTTTCTGACATCTCTGTTATCAACTCTCTGAAAAATC   |
| WI-14958  | 83 A G   | AATAATTTAT<br>CTCTTCTTTT<br>CAAGGG | AATGCATTCAT<br>TTGGGTTTTT            | GTGATTGATCTGTAATATTGGGATTATTATTTCAACTCTAAAAATCCAAGATGAAAAATTTATCT<br>CTTTCTTTTCAAGGG/A/GJAAAAACCCCAATGAATGCATTTTCAAGTTCTCCAGGCCCTTTGAACTGC<br>AGCAGAAAAATTCAGGA |
| WI-14976  | 35 C T   | GTTGATTTGCT<br>TCGTTCAAAG          | TCAAACATAAT<br>CTTCCATTCTA<br>AGC    | TATTTTTTAATTGGTTGATTTGCTTCGTTCAAAGC/TJGCTTAGAATGGAAGATTAGTTTGAGGAG<br>GGGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAAAGATGCCCATCTCACACCTGGAG<br>ACGTCCATGAGCACTCG     |
| WI-14981  | 31 G T   | TCAGTGGTGT<br>TATTGGATTT           | CACCTCTGACA<br>TAATACTTAGC<br>ATAAA  | TAATTGATTCAGTGGTGTATTGGATTTT/G/JTTTATGCTAAGTATTATGTCAGAGGTGGAGAAT<br>AAAGAGGAAAAAGAAAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA<br>GAGCTCACAAA        |
| WI-14992  | 80 C T   | TGCATTAAT<br>GAAGCTGCAG            | GCTATGTGCTC<br>AGCTTTCTC             | TGATTACATTTTTTAAATATCATGCTACCAGCCCATCTAAGCCAAATTTCAAACACCACCTCTGCATTA<br>AATGAAGCTGCAGC/TJAGGAAAGCTGAGCACATAGCACCCAACTGATCGGAAAGAAACGTA                         |
| WI-15002  | 72 T A   | ---                                | ---                                  | AAATCTCTTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAAATGCCCTCTTGA<br>TTTCCCT/AJTTTCAGTTTAGGCTCAAATGGGCTCTCCTCAAGGCTGGACCTCAAAGGCCAGTT                       |
| WI-15000  | 90 G A   | GACAGAAAA<br>GACTCAGACT<br>GTCTAA  | GTTTCTAGTTC<br>TGCACAAACTT<br>CA     | TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG<br>AAAAAGACTCAGACTGTCTAAGTA/GJTAGGATTTGTGCAGAACTAGAAACAAAAATCCACCT                           |

|          |     |                   |                            |                             |   |
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| WI-12323 | 68  | G A               | CACAATACCTT<br>CATGTACCTAT | CACTGGACATA<br>TTCCCTACCTG  | ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACCTTATGTACCTATGAAATAA<br>G/AJACAGGTAGGGAATATGTCAGTGCAAAACAGAGGACTCACACCTGTGCTAGACAGCACC                                |
| WI-14683 | 91  | A T A A C A       | AAGGGACGAT<br>TTAGTATCTAA  | GGCATGTCCCA<br>GTGTTTT      | CATAAGTTGCATTTATTCACGTCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA<br>GGGACGATTTAGTATCTAAACA[A/T]CAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT<br>TGGAGTTCGTAAGAATCTAC    |
| WI-13470 | 100 | C A T             | CTGCCCTTTAT<br>ATTGGAATTC  | GGGAGACCATG<br>GGTCTCT      | ATTTGTTGTTTATTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT<br>CAAAATTCCTGCTTTATATTGGAATTTCTA[C/A]AGAGACCCATGGTCTCCCCAAGTGAGGAAGCC<br>AGGCACTAGCCCTC       |
| WI-14712 | 38  | T A C A           | TGAATGCTCC<br>AAGTACAAAT   | TGAAAGTATGT<br>TGATATGGTA   | TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA[T/A]CTACAATACCATATACAACATACT<br>TTCAATCACAACTCAAAATATAAAATAACCTACAAAATCACATTGC   |
| WI-13712 | 40  | A C T C T A T T G | TTTACTTTGTT<br>GTCAATTTTAT | CCATAAGGTCT<br>CACACTTTTCT  | TGGGATACCCCTTTTACTTTGTTGTCATTTTATTCTATTG[A/C]ATTATAAGAAAAAGTGTGAGACCTT<br>ATGGCTTCTGCTTATGGGCAATATGCAATAATAATTGTGTGTTGTTAAAAATTTATGCAT                            |
| WI-16163 | 35  | C T A             | TCTGGTGATGC<br>AATTGAAATA  | GCTGCCAATTA<br>CATTAACCTTAC | TCTAAGATTTTACTCTGGTGATGCAATTTGAAATAA[C/]/ATTGTAAGTTAATGTAATTGGCAGCATT<br>GCCAAAGTTTAAGAGGACTATTTCTTTAAACAAGACAGTGTCTGACATTTATTTCAGGT                              |
| WI-13453 | 88  | T A T C           | AATGCACAAA<br>ATCTTGCTCT   | TCAGATTTTAA<br>CATCTCTTCT   | TTTTTTTATTGCAATTTGAGTGCTTTATTATATTGGGAATTGCAGTGATTTAACATTTGTACAAAT<br>GCACAAATCTTGCTCTCTCT[]/A/TGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT<br>AATGAACCTCATTGTCCAT |
| WI-16167 | 58  | T C G A T T T T   | CGCACTCTAA<br>ATTAGAGATA   | TGCTCGTGGTG<br>AATAAGATG    | CGGATATAATTATGTACCGCACCTCTAAATTAGAGATAGATTTTTTCTGATATACATTT[C]CATCTT<br>ATTACACGAGCACACCCACACGACAGTAGAACAGTCCACACCTGATAAAATTGCACAAGATG                            |
| WI-14482 | 17  | G A ---           | ---                        | ---                         | GCAGAACCAATTAA[A/G/A]AATCTGCAAGTTTCCCCAAGAACTCTGGAACCATAGTGCCTAAT<br>GCCCTTTAAATCGATACTAAAGGAGAGAGATAAAAGGAGTGTCTGATGTGACAGTCACTGGT                               |
| WI-15069 | 81  | T C ---           | ---                        | ---                         | TGTAGTTCTCAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTATCCCAGTATCATGTAC<br>GCACTAAAAAAAT[C/GTGTGCTTGTGCTGTGAGTGAACCATGCTTAAGATAAA  |
| WI-16156 | 97  | A C               | TGAAGATTAA<br>CCAGAGTCGC   | AATGTGTGCA<br>TTTTGAAGAGA   | ATCTGGTATTGTGTATCCCAACAGTATACAGAATACTCTATAAAACCAACCCACCCCTTCAATA<br>TTACACTAATGAAGATTAAACCCAGAGTCGC[A/C]TCTCTTCAAAATGCACACAATTAAAGACG                             |
| WI-15012 | 59  | G T A T G T       | GCAGCAAGAT<br>TACATCAGTA   | CTCCAAATAGC<br>CTAGAGTATAG  | CATGGCAGCAAGATTACATCAGTAATGTAATAATAATACAGCTTTTTTTCATTGAAGCTTT[G/T]TACCT<br>TACTACTCTAGGCTATTGGAGTGTCCCCAC   |



|           |    |                |                           |                                      |  |  |
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| WI-15100  | 74 | G A ---        |                           |                                      |  | TCATTACAGCCAGAAAAATACCCAAATTATTTCCAAATAAGCAAAAAATTGGAACAGACTGGA<br>GTGAGAAAC[G/A]GGTTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGTTCTGGGGT<br>GCATTTCTAGTGGACTTTAT   |
| WI-14492  | 92 | A T AATTACT    | CCTTATTTC<br>CCAAATATAA   | GTCACCATGTT<br>ATATTTCTTT<br>TAAGAC  |  | TGGTACAGAAATGTTAATTACAGCAGGGCAGTGATTCCAGTTAAATAAAAAACCTTTATTTT<br>CCCAATATAAAATTACTAAATAA[A/T]GTCITTAAGAGAAAAATATAACATGGTGACAGCTTT                               |
| WI-12002c | 89 | T C ---        |                           |                                      |  | TCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACCCAAAAACCACATGGAGACAGAAG<br>ACGAGACACAACCTCTCCCCAC[T/C]GCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGTGAGAC<br>AG                      |
| WI-12002b | 68 | G A ---        |                           |                                      |  | TCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACCCAAAAACCACATGGAGACAGAAG<br>AC[G/A]GAGACACAACCTCTCCCCACTGCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGTGAGAC<br>AG                     |
| WI-12002a | 30 | C G GGACACAA   | TCGGAATCCA<br>GGGAGCCCTA  | TGGTTTTGGG<br>TGTTTTCTT              |  | TCTTAATTTTATCGGAATCCAGGACACAACA[G/A]AGAAAAACACCCAAAAACCACATGGAGACAG<br>AAGACGAGACACAACCTCTCCCCACTGCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGTGAGAC<br>AG                   |
| WI-15116  | 96 | C T GTTGACGTAA | GGGAGCCCTA<br>GTTGACGTAA  | CCTGAATATGC<br>AATTATTTATT<br>ATGACA |  | TTTTCATTTTATTTCCAGAAAAAGAAATCACATTTTCAGTAACAACCTACATATAGAAATTAACCTTG<br>TTCTGGAATGGGAGCCCTAGTTGCAGTA[A/C]TGTCATAATAATAATTGCATATTCAGGATTTTG<br>TGAAATAGGTGATTGGGA |
| WI-12578  | 37 | C T AATGGGAA   | GGCTAAAGG<br>AATGGGAA     | TCAAGCGACCA<br>CCAACAC               |  | GCAAAAGCAAAGCTATGGAGGCCCTAAAGGAATGGGA[C/T]GTGTTGGTGGCTGACTTGGT<br>GCTTGTCATGGAGCAGAAAGTCTTCTGCTGTCATGCAGGGGGTCACATATTTAACTGCACATAAT<br>TTGGGCAAACTGTCAATC        |
| WI-15153  | 40 | A G GCATTGCA   | CCCTTATGTTG<br>GCATTGCA   | AACCTCAGATA<br>AGTGCAGTGC<br>T       |  | ATTCACGTTGGCCAAAGATCTCCCTTATGTTGGCATTGCA[G/A]GAGACACTGCACCTTATCTGAGGTTA<br>GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATACCATTTCCTAA                          |
| WI-15215  | 84 | G C TCAAATGGG  | TGGCTTTAGAA<br>TCAAATGGG  | CCAACAGGGGA<br>AAAAGTCA              |  | CCTTGGCTCTGAACTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC<br>TTAGAATCAAATGGG[G/C]TGACITTTCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGGCA                               |
| WI-15225  | 80 | C T C          | CTTGAGGACCT<br>AGAAAGCAAA | TTTGATTGGCA<br>TAATCACTCC            |  | AGGAAAGAGTGTGAAGCAAAGGCGATCATTGGATGGAATGATTATGTGTCCAGGACCTTGAGGAC<br>CTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAAATTCGAAGTTGGAGATATGCTAAAA                            |
| WI-15152  | 51 | G A ---        |                           |                                      |  | AATTTGCTAGTGCAAAATGGACCCAGAAATTTGGAAGGGCTATGTAACTACACA[G/A]TATGCACACCAC<br>AGCCATGTCACTGTACAGATCCTCTTGTGCATTACGCTTTCTTAAAAACACATCAAAAGGCTGCA                     |
| WI-15123  | 55 | C T TAGGATG    | TGTTAGTGACA<br>GACAGATAAA | TTGCTTAAGGG<br>CAAACAGAC             |  | TGACTGTATACCAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT<br>GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAACACGAGATAAAACACAAT                         |

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| WI-15182 | 49  | C A | GCACAACCAG<br>GGCAAAATA       | GCATGGGTAA<br>TCCAGCA              | GAGACTGCCCTGTGACACAACACTAGCTAGCTGCACAACCCAGGGCAAAATAC/AJTGCTGGATTAAACCC<br>ATGCTAATGGGTTACCTTTATTAGTAATCATGGGTCCCTCATAGCATGGTCCAGATCCG                         |
| WI-15198 | 38  | T C | GGGOCCTGGC<br>ACTATG          | ACTTATCCGTC<br>AGGCAGAGTAG         | GTGGACCTCTACAAGTACCATGGCCCTTGGCACTATGTC/CJCTACTCTGCTGACGGATAAGATTGGC<br>ATATGGTTCAGATTGCTTGCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT                           |
| WI-12601 | 42  | T C | TGAT                          | GTGTAGTCTT<br>ACATGCTTACG<br>TAGAC | TCAAGTGGTAAATAGCCATTATTGAGTATTTCTGCTTTGATTC/CJGCTACGTAAAGCATGTAAAGACT<br>ACAACATTACGACCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAAAACATTTTGTCAITTCAGAT<br>T            |
| WI-14510 | 104 | A T | TGCAAAATA<br>TGCATAACAA<br>AA | TTGAAAATGGT<br>TAAACTGGCA          | ATGTTGAGAGTAATAATGCCCTACATATTTAGTGTAAAGTACACCCACAGATATTTTGGGAGAAAGAG<br>TTGTTTGCCTTTTGTGGCAAAATATGCATAACAAAATATTTGCCAGTTTAAACCATTTTCAAGAGT                     |
| WI-15239 | 57  | T C | CAATTGCAAT<br>AAACACCATC<br>A | GGACCTTATCT<br>GTGGACTCAGG         | CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTGCAATAAACACCATCATTT/CJCTGAG<br>TCCACAGATAAGGTCCCGGAGAAAGGGCTTCCCTCTCTTCTCGCTGGTTGACGTTCCACGGAGT                        |
| WI-12634 | 52  | T C | AGT                           | AAACATAGCT<br>AATAGC               | ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATTATTC/GCTATTAGCTA<br>TGTTTACAAATTTGTCTGAAGGGGTCTAGATGTGTACACCCACAGAAAGTGGTATTCTCTGA                         |
| WI-15249 | 34  | T C | AAAGTTCTAA<br>AA              | GGAAAGCCAG<br>AGATTTTAAAC<br>AA    | TTTGCTGAAGGGCTTGACACAAGTTCTAACTTT/CJTTGTTAAAAATCTCTGGCTTTCTGGCTGG<br>TGAGGAGGCACAGGCTGGGCTTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCTCCACTCCCCAG<br>CCACATCTTGGCTCT     |
| WI-12159 | 28  | C T | GCAAAATGC                     | CCCTCTCCTCA<br>GTGCACCTT           | CTGTCCGGGAAGACACCGTGCAATGC/CJAAAGTGCAGTGAAGAGAGGGGAGGGTCTGTGACTC<br>CCAAACCCCTCGAATATTTATGATCTAAGAGTCCAGACGCAGTTTCATCCACGGAGATCTGC                             |
| WI-12648 | 41  | A G | TAAGGATGC                     | TTGCTACTAAA<br>AGTGGACATCC<br>T    | TCCOCAGATTGTATGGAATGCCCTAGTGGCATTAAAGGATGC/A/GTGGAGATGCCACTTTTAGTAGC<br>AACCGATGTTAATTCACCTACTCCATGTTAGGTGCTTTACTTTGGATTATCTCAGTTTAAAAACACACA                  |
| WI-12684 | 64  | G T | ACAGCTGTGC                    | GGAAACAACAA<br>AGCCTAAATGG         | ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC/CJ/<br>TCCATTAGGCTTTGTTGTTCCATTATAGAGAGCACAGGAGGAAATTTAGCATAATCTT                              |
| WI-15260 | 75  | G A | GA                            | TCTCTCCAGG<br>AGCTTGC              | TTTATAAGCTGAATGAAGAGGTCGACACAGCGGACACTGTCTATAAGTGGAAACAAAGGATGAAGCT<br>AATCATGGA/GA/GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGAAATTA<br>TCTG               |
| WI-15325 | 39  | T C | GAGGC                         | CCTTCCACCAT<br>GATTGTGA            | AAGTTTAAATGGACTCACAGTCCATGTGGCTGGAGGCTTC/JTCACAATCATGTGTGGAGGCAAAA<br>GGCACATCTTACATGGTGGCAGTCAAGAGAAATGAGAGC  |
| WI-13936 | 123 | C T | C                             | TGAAACTCCCA<br>CATGGAGTT           | TATTTGAGTATTTTCATCCATGGGCTTCTCACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC<br>CCATAGGTTTCAGAACCTATGACCTGTATCTTCAGTTGGCATTCATAGCCTATC/CJAACTCCATGT<br>GGGAGTTTCATAATAA |

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| WI-14528 | 62 T G  | TTTAACTTTT<br>TCTGGATGGTA<br>TAAAT   | CTCGATTAGCA<br>CTTATTATAAA<br>AATTAAAA | TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAAAT/GJTT<br>GAATTATAAAATTTTAAATTTTATAATAAGTCTAATCGAGACATCACTGGGTATAATTGA   |
| WI-15347 | 74 C T  | GACTTCAAAG<br>GAAAAGAACA<br>AATTT    | TCACCTCCCCA<br>AGTCTTTG                | TATTTCTTTGCGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA<br>ACAAATTT/C/TCAAAGACTTTGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA<br>CG  |
| WI-14546 | 95 C A  | CCAATTTCTAG<br>TGATAGTAGA<br>GGACTCA | AAGGTGCACGT<br>GCAGG                   | GTATTTTCTGATGCTTTGACATCTGGGGCACTTGTCTCTAGAGAGACTACTTCTCTGGGACCAGC<br>CAATTTCTAGTAGTAGAGGACTCA/C/AJCTGCGACGTGCACCTTTTCATATACAGATCA  |
| WI-15353 | 37 G A  | ---                                  | ---                                    | TTTATTGGCTGTCTCTGTAATACAATGTGGTGAACAC/G/AJCTTAAATTCAGGACATCTTCCACCTTG<br>TTTTGGCTTCCAGTTGTACTGCAAGACCAGTGTGAGGCACATAGGCTGATTAATCAGTGG  |
| WI-14580 | 100 G A | CATTTCCATCT<br>GCTTTGCA              | CCGACCAAGAT<br>CCCTDC                  | AGAAATTTTCTCTTTTAAACAGGACAAAGTAACAGATTACATCAAACTTCAGAACTTCTCAAAATAC<br>CTAGTTATTATACACATTCCTCTGTCTTGCA/G/AJGGAGGGATCTTGGTCGGCTTAACA  |
| WI-8540  | 73 T C  | GGCTGCAATT<br>GGCTTA                 | GGCTTCTTTT<br>TCAGGCAC                 | CCAGCTGGAGGTGGAATAAATGCGGCAACACACAGAAAAACACACAGCTACACAGGCCTGCATT<br>TGGCTTAT/CJGTGCTGAAAAAGAGGGCGGACCTCTTGATAAAGAATGTCT  |
| WI-8039b | 97 T C  | ---                                  | ---                                    | AAGTAGAACACAATAGATGGCTCAAAAATATCAGAAATGCACACTACGCACATCAGCAGTAAATACTG<br>TTTGGTAAACTTGTTCAGTTAAATATGAT/CJGTGTCGGTGCATGTGATGATTAATATCTCTCT<br>TACCACAGTCACCTTAAAGAACCAAGCTTAGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA<br>GACCAGACACTCTGGTTGAGATGATGATTTTAAATGCCGACGCCACACCCACA |
| WI-8039a | 87 T C  | ---                                  | ---                                    | AAGTAGAACACAATAGATGGCTCAAAAATATCAGAAATGCACACTACGCACATCAGCAGTAAATACTG<br>TTTGGTAAACTTGTTCAGTT/CJAAATATGATGTGTCGGTGCATGTGATTAATATCTCTCT<br>TACCACAGTCACCTTAAAGAACCAAGCTTAGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA<br>GACCAGACACTCTGGTTGAGATGATGATTTTAAATGCCGACGCCACACCCACA    |
| WI-8044  | 107 C A | ---                                  | ---                                    | CACAACATTCAGAAAGTTTCTGCAATGTGCTCTCTGATGTCTAAAAAGATTTGAGCTTTGACTAT<br>ACGATTTCCACACTGAACGCATTATAGGTTTCTCC/C/AJAGTATGATGATCTCTGATGATTAATA<br>AGCCCGAATCTGGCTAAAGGCTTCCACATTCAGACATTCAGAGTTTCTCCAGTGTGGAC<br>TCTCTGGTTGTCACAAGATGGAATCTGGCTGAATGCTTCCACACT                |
| WI-8550  | 32 G A  | GGGAACATCA<br>ATGCAACAAG             | TTTGGGCTTG<br>AGTTTACAAAT<br>T         | CTTACTACATGGGGAACATCAATGCAACAAGTGA/G/AJAAATTTGTAAACTCAAGCCACAACTTAGTTA<br>ATAATCATGGTTAAGGGACATTGCCAAAGAGCAACTGATGCCTCAGTGAA   |
| WI-8057  | 87 T A  | ---                                  | ---                                    | TATTAGATAAAACCCCTTTGTTCCCGATTCCAGGATGTTTAAATTTGCTTCTCTTAAACTCTGTGACTTTT<br>CCTGGTTCAAAAGGACAGT/AJGATGGACAGCAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT<br>GTGTCAAGGCACCTGTGGCCTCACAACTGCCCTGTGAGGGATGTGCTTCCAGGCCCTAAAG<br>ACACTAGGGCTTTTCAATGGACGGGGTGTGAAGCAGCCAGATGGTAAGG    |

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| WI-6192  | 91  | A G G A T             | G A C T G C T A A G<br>G A T T T A A T T T G<br>T T A A A A | T G A A G T G T T A G<br>A T G G C T A A G T A<br>T T A A A A | A A G A G G A A C A A A T T A G C T C A G T C C A A C A T G A T T G G C A G T T G G C A T A T T C T A G T A A G C A A G T G T T C T<br>G A C T G C T A A G G A T T A A T T T G G A T A G A T T T A A T A C T T A G C C A C T A A C A C T T C A A G C A T A A C  |
| WI-6194  | 105 | T A G A A A           | C A C A T G G C A A<br>T G A T A A T A A A                  | T C T A T C C T C A G<br>A G T G T A G T C T G<br>C A         | A A G T A G T G T C C T C A C A A A T A C A T T C T C A A C T C A A A C A T C A T G C T T G A A A T A T C A C T G A A C T T<br>G T C A C A A A G A A G T C A C A T G G C A A T G A T A A T A A G A A A T T A J A T G C A G A C T A C A C T C T G A G G A T A G<br>A G C T C A A A G A G T A A A A C A A T G G A A T T T G G A A A A A T A G G A G T A A A   |
| WI-6213  | 164 | C T ...               | ...   | ...   | C A T A T G C T G C T T A T T C T G T A A G G A T A C A C T G A A A C G T T A G A T G A T A A T A G C T A A T G A C A G A A T G T<br>A G A A T G A G G C A T C A G C T T C T A A C C A C T C C T A C A A G A A T G T T A G T A T G T A T T G C A T T A C A T G T T T<br>A C T T T G A T A T T G T C T A T T A C T A T G T C T A T A T A A T A A T A G A T A C A G A T A G T A A G T A G T G A T C C<br>T G C A T T C A G G T A A G C G T A G T G G A A T C C A G A T T C C T C T T G A G G A A A A  |
| WI-6217  | 131 | C T ...               | ...   | ...   | C G G G T T A A G A A A T A C C T T T A A A T T T A G T A A A T A A A G C T C A A G G A G T G G G C T G T C A T C T G T G G T G<br>T C A G T C C T T C T G G C C C C T G G C T G T C A G T G T C G C T C C A G G C C T T G A C A A G C A G C T C A T T C A A G C T<br>G G C C C A C C A T G G C C C T A G G G T C G T C A A C A A G T C C A G C A G C A A T C A T G G C G T T C T G T A T A T C T G A T C C<br>A C  |
| WI-6238  | 175 | G A ...               | ...   | ...   | A T A G T C T T A T T T G T C A A C G A A G G C T A C A C G G G A T C A C T T C T G G T T T G T T T A T G C T T T T T T T T T C<br>T A G A A G G T A T C A C A T C T G C A T T A T T A C A G C C T T G T G G T A T T A C A G A T T A C A G T C A A G A T A C A G T G T T A<br>G A A C A C A A A A G T T T G A G A A A A A A C T T C T C A A A A T T G A J G T T C C A G A C T T C A G G A A A A T G A T T<br>T C C A C A T G G T A A G C C A G A G T C C A G T G T T G G T C A T C C A G A A G C A G C T T G  |
| WI-6272  | 86  | C T T A A             | G C A T T T A T T C A<br>G G G A A A A C T T                | C T G T T T T G G A<br>G A A G A C A A A G<br>A A             | C T T G A T T A A T C A G G G C T T G G G T C A T A G G G G A T T A G T C A C T G T C A C A G T C A T A A T A A T G C A T T T A<br>T T C A G G G A A A C T T T A A T C T C T C T C T T T G T C T C C A A A A C A G C T G C T G G A A C A C C T C A A A T T A A<br>G G G A T G T T C A T C T A A A C A C C T T T A C I G A A A C T T G A T T C C T T G G C C A G A G A A G G T C T T T A C T G T A G<br>C A G A G G A C T T A A T G C A A T G C C T A T T C G G G C A A T A A A T G A A T A C T T G A T G C A T T C A T A C A G G C A A G A A<br>T C C C A G C A T C C C A G A G A A G C T C T G T C T G C G A J G T G C A A G C C A T G G C T G C A G A C A T C A G G G A A G C T<br>G G T G C A G T T C T A G T C T C G C C T C T C G A T T T C C C T G C C A G C A G T C T C C T C T C A T T C T C T G G C C C<br>T C T G |
| WI-6303  | 96  | A C T C T G T C T G C | C C C A G A G A A G<br>C C C A G A A A C T T                | C A G C C A T G G C T<br>T T G C A G                          | A T G C T T T T G C A T G A T T C A A T A T T G C C T T T T C A G A G C T C T G C T G T A A A A A G T G G G T G C C A T A C A<br>A A C A G T C C C T T T C A A G C C C A G G T G C A T G C A T C C T G C C A A T C A A T C A C T G A A T G T C C A T T G T C C A<br>A A C A G G T C A A C C G T T G T C C C A T G A A A A A C T G G A T A A A G A G T T G C T G A T A G T A G T G C T G T C T G G T T<br>C T T C C C T T A C A T T C T T T G G G G G A  |
| WI-6315b | 193 | C T ...               | ...   | ...   | A T G C T T T T G C A T G A T T C T A A T A T T G C C T T T T C A G A G C T C T G C T G T A A A A A G T G G G T G C C A T A C A<br>A A C A G T C C C T T T C A A G C C C A G C G T G C A T G C A T C C T G C C A A T C A A T C A A T C A C T G A T A A T G T C C A T T G T C C A<br>A A C A G G T C A A C C G T T G T C T C C A T G A A A A A C T G G A T A A A G A G T T G C T G A T A G T C J A G T G T C T G G T T<br>C T T C C C T T A C A T T C T T T G G G G G A  |
| WI-6315  | 187 | T C ...               | ...   | ...   | A T G C T T T T A C A T T C T T T T G G G G A<br>C T T C C C T T A C A T T C T T T T G G G G A  |

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| WI-6375  | 28 A G A A                | GGTTTATTGCA<br>TATGGAAATC | AATGTGAGATC<br>TTTATTCTAAG<br>CTTTTT | AAGGTTTATTGCATATGGAATCAATAG/AGTATCTTTTACAAAAAAGGTTAGAATAAAGATCTC<br>ACATTTGTAAGGCACATATGAACAATTTATAGCAAGCACAAAGGCGAGTGAACATCAACAA<br>TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT<br>TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA/T/A/GCAACTGACAGTTTTTGAAG<br>GACACCAAGACAATAGGGCT |
| WI-6409b | 112 T A ---               |                           | ---                                  | TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT<br>TACAAC/AT/ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTTGAAG<br>GACACCAAGACAATAGGGCT   |
| WI-6409a | 73 A T ---                |                           | ---                                  | CTAATAATCTCTGGGCACATGGATTCCAAAGAGAGATTTTGCAGCAGATTTTCATTATAGTTACTTAA<br>CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA<br>GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG/TTATCAACCTTCCCTAAGCATCTGTCTGGTCCG<br>CAGC  |
| WI-6523  | 165 G T C T G             | GCTAATCCAGT<br>AGAGACTGAA | AGATGCTTAGG<br>GAAGGTTGATA           | TCTCTAGCCCTATTAGGCTACACTGTAGTCACTTCTATGAGAGCAAGGAAACAGGAAGATGGGC<br>TCTGGAGTCCAAACAGGATGTGGACGTCCCTGGTAGTCTCTCTTTTACACAACTTTTCCCTGAGA<br>ACTGTCCAGTCAAGTGGACCTTCAACAACACGACGCTAAACTCTGAGAGAAAC/C/G/CTG<br>ACTTTCAGAAAGCATAAAGCTGAGAAAAA  |
| WI-6554  | 195 C G ---               |                           | ---                                  | ATTGTAATTTAAATTTACATGGGCCTATTATTAAAGGACATGTGTAATGTTCCACTTTGTTTTAAA<br>/C/TTAATTAACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAAGTTTGAAAAATGGGCG  |
| WI-6558b | 68 C T ---                |                           | ---                                  | ATTGTAATTTAAATTTACATGGGCCTATTATTAAAGGACAT/G/C/TTGTAATGTTTCCACTTTGTTTT<br>AAACAATTAACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAAGTTTGAAAAATGGGCG   |
| WI-6558a | 42 G C ---                |                           | ---                                  | AACCAACAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA<br>AGTTGTCATA/T/C/JAGCAATGGATGCTGTGTCAGAACATACTGCCAATAAAGTTTAAAGAAAAAGGA<br>ACTCAATGAAGTTACTGTATATAAACAAGGAGCTCACAGCAGGGATGTAAGAGTTAATGGAAGAT<br>ATCGTGAGCCAAAC   |
| WI-6629  | 75 T C G T C A T A        | TCTTTTCAGAG<br>AATAAAAGTT | TGACACAGCAT<br>CCATTGCT              | CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATAAAGCTCCAGCTGTTTCTCTTGCTTTT<br>TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACAT<br>T/C/JACCCAACTTGAAGGTGATTGAACCCCAATAATGGGTGGGAAACACCAAAATGAGGTGGAGGA<br>ATGAGAAAGATGTGTGGCCCAAGCTATCTGGTTATATTTGATGTTGCCAAT                                |
| WI-6644  | 134 T C ---               |                           | ---                                  | TGCTAAACACCACCATTTAAGGAGAGTACTAGGAAAAACTACCAACACAGCATGTGAAACAGT<br>TGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGC/C/T/JGGCTAATACACTGCAATATTTTA<br>TGTTTAGCAAAATTATAGTGGTCTGTGTATTAACCAGAGAGCGGTATCTGG   |
| WI-6690b | 106 C T A G C C A C A G C | CAGACTCTGG                | TTGCAGTGTAT<br>TAGCC                 |  |

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|----------|--------------|----------------------------------|--------------------------------------|---|
| WI-6690a | 28 T C       | AAACACCACC<br>ATTATTAAGG<br>AGAG | GCTGTGTTGG<br>TAGTTTTTCT             | TGCTAAACACCACCATTATTAGGAGAGT/CJACTAGGAAAACTACCAACACAGCATGTGAAAC<br>AGTTGGCACGGTGTAAAGGGACAGACTCTGGAGCCACAGCGGCTAATACACTGCAATATTTA<br>TGTTAGCAATATAGCTGTGTGTATACCAGAAGCGGTATCTGG   |
| WI-6770  | 53 A G       | CAACCCCAA<br>AACATCACA           | GCTTTGGAGT<br>GTATAATAGTA<br>TGAATAA | GATGTTAATGACACAGATCTTCCAAAGTAATCCAAACCCCAAAACATCACA/GJAATTATTCAAT<br>ACTATTATACACTCCAAAGCAAAATACITCAACTGCAATCC  |
| WI-6686  | 151 A G A    | GCATTCTCCA<br>AAACAAAGA          | CCTGTGAAGTG<br>ACTATTCCAAT<br>GTT    | ATTCTGTAGGCAAGGTCAGCAATCAGGTAGCAGTCACTAATCTTGACCAATGGGTGAGTCAGCCTCA<br>TCACAGAGATTTTTTTTTTAATTAGATGAAATTCACATTTAAAAACATGTTAACTCCAAGCATCTCT<br>TCCAAACAAAGAAT/GJAACATTGGAATAGTCACTTACAAGGAC  |
| WI-6761  | 32 C A G     | GATCTAACAG<br>CTGCAGAAATG        | AAAAGCTGGG<br>AAGGAAGAAG             | CCTGAGAGGCAGATCTAACAGCTGCAGAAATGG/CJCTCTTCCCTCCAGCTTTTGTGAACAAAC<br>AATTCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGTTGTTTCAGGTACAAGTCTC   |
| WI-6844  | 225 T C      |                                  | ---                                  | TAAATACTGCCAACTAGCATTACGTCCACTCTTGCAATCATTAAAAACAAAGGGTATTTCCTCCTTG<br>GTATTTCAATGATGCATTATACAATAACGAAGTTAGAATTTAAATGCACCTGATTAATTATG<br>TAACTGGTAATTTGTTTTAAAGCATAATAATTTGGTCTCTTCTCATAAATGGAATTTAA<br>TATTTCTGATAGCTTGAGGT/CJATCATTAGTAGTGCAAAAGTGTG              |
| WI-6824  | 112 A G      |                                  | ---                                  | CGGTTTGTACACTTTAATGGTTTTTTTTAAGGATTTTTTTCAGGCTTTTCAGCCTTGCAGCAACATCAA<br>ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCCAA/GJACACCTTAGAAAAATTACAT<br>GACACGGAGAAAATGCGCTCTTGTCTCTTGAAGAGCTACAGTCTAGGGATTGACAACTCAGAT<br>CTTAGGAACTGGGCAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTGTG |
| WI-6889  | 139 T C AATC | GAAAAATGAG<br>ATGCAGTTAA         | TCACTTTGTGG<br>CTTTTAATTAT<br>TCT    | GTACAAAAAAGCTGAGAAAGAGCCAAACATGGAAGTGTCAAGAAAAACATTTCTGATAGTACGGACAA<br>AAGAGCTCCTCAATCAAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA<br>AAATTCT/CJAGAATAATTAAAGCCACAAAGTGAACCTGTGTCTGGGGCCCTATGTTGTAGATT<br>CTCT   |
| WI-6911  | 216 T C      |                                  | ---                                  | TCCCAGCTCATATTTTGGGCACAGATGGGCACTCAAATATCTGATGAACITGTGAACCTGAA<br>AAGAGGTCTCCTTAACAAGATATCATCTCCGAGAGAGAAGTCCCAACCATATAAATGTATGAT<br>CAAGTCCCAGAAAACTTGCCTCCCAAGGAATGTGTTCTAATTTGGTTTCAAGCACACTGGTTCC<br>CACTTTTACCACITTT/CJCATGACATTGGACAATAGTACTACTCTTTTCTAC      |
| WI-9413  | 112 G C      |                                  | ---                                  | GCCAGTCTCTAGTAAGTCTCTAGGGACATGACAGACAGAGCCCTGTCTATATGAAGACAAAC<br>AGGTGGCCATACITGGGTGGAGGATACCGTGTCTATCCAGATG/CJAAGATTTGGTGAAGGAG<br>ACCATGACAGATGACAAACGGAACAGTTTCTCAAAAACAGAGGTATGA   |
| WI-9557  | 74 C T       |                                  | ---                                  | AAAAGCTTTAAAAAAGTGGTGTCTATCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCCCAGCT<br>ACAGCCTC/TGGTGCATCTTAACCCCTCTCTTTT   |

|           |     |    |            |                                    |   |
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| WI-9617   | 37  | GT | ---        | ---                                | TGCTCTTTTATTTCACGTTTCACAACACACGCGCTG[G/T]TGGCAGCTTACCAAAGTGCCCGCAG<br>CGCCACGCTGGGCGGGAAGGTCTCATCTGTTGCTCTCTATGGACTGATTGAATTTGGGATGGCCAG<br>CTCCAGAATGTTCCACGTGGGGCACTCTGTGGGCAGAGAGGCTGAGCCCTTGCCACACTGGCAACCA<br>AAGAGGTTCACGATGACGCTTGCAGTGGGTCCAAAGCGGGTGTGCTGTG  |
| WI-9657   | 121 | TG | ---        | ---                                | AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGTACCATCCACTAT<br>CATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT/GJATAATTCTT<br>TGTAATAATAAATGTTTATAAATGTTTATGAAGCTCAITACATTATCTTTTTTAAAAAAGTAAAAA<br>TTTTAGACATATGACGCTTTTCATAATTAAATGCTTTTGATAIAGATTGAGG   |
| WI-13119b | 114 | GC | GCTGGGA    | AAAAATTAAC<br>CAGGTGTGGTG<br>T     | CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGTGACACAATCAAGACTCACAGTAGCCTCAACCT<br>CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTG/CJACACCACACCTGGTTAA<br>TTTTTTAATTTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGCTCTCAAAAAACAACCAACTAAC<br>CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT/CJACAGTAGCCTCA<br>ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA<br>ATTTTTTAATTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGCTCTCAAAAAACAACCAACTAA<br>C |
| WI-13119a | 51  | CG | ---        | ---                                | ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT<br>TTTT/C/TCTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAGAAAATATAAATAGT<br>TTCAGTATGTTATGTAGAGTCACATACATATGGCAAAAATATTTTAAATTGAGGGAATAGGCCAAT<br>TT   |
| WI-12988  | 36  | CA | CTCAGTACAA | CAAGGTGTACA<br>CTACTGATGCT<br>GTTT | TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA/CJAAACAGCATCAGTAGTGACACITTTGAT<br>AAAAAGGAATTTTAGCTTAGTAGAAAAGAAAGCCAAAGGTGAGAAATATATGAATATGTACAT<br>CTTTATGGAAACTGTTTGTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTGACACACACAAGT<br>AAA  |
| WI-13020a | 108 | GA | CTTT       | CATTATTAAAC<br>CCCTTGCAGA          | TGCTATTTCATGACAGACACGTGAGACAAATATCTTATTTTACAGATGGAATAGACCCAGACATTA<br>TTCAGTACTTTAACCACTAATAGTGGAAACCCTGAGACTTTA/GJATCTGCAAAAGGGTTTAAATAAT<br>GCAAAATACATATATTTCCATTTTACACCATAATTAAGTTTCCATTTTCTTAATAGAAAATGA<br>TAAAAATGTTTCCCAATAT  |
| WI-12837  | 87  | AG | AAAGTCCA   | GCCATAGGAA<br>ATGCTGTTTT           | TGTATAAAAAATCCAACTTGTTCACAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC<br>ATATATCAAGGTAAAGTCCA/GJATACAAAAAACAGCATTTCCATGGCCAGTGTTCACAGAAGT<br>AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCGAGGATGAGGCAAGCA<br>AGTTGTGTTCCA   |

|          |                   |                            |  |  |
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| L42611b  | 50 GC ---         |                            |  | GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTCTCTCAGGTTGCCTGTGCGCTCTCCTGGCCTCTAG<br>TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCCTCTCTCTCTGTATACCT<br>GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGATGATTACCA<br>CTGGAGCTTCACITTTGTTAC  |
| L42611   | 34 TC ---         |                            |  | GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTTCTCAGGTTGCCTGTGCTCTCCTGGCCTCTAG<br>TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCCTCTCTCTCTGTATACCT<br>GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGATGATTACCA<br>CTGGAGCTTCACITTTGTTAC    |
| WI-1172b | 179 C T A         | TGAAGAAATG<br>GCTGATACCA   | ATGTGCATTTT<br>TCACTGCAG               | TGAACGTGTGGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACAGTG<br>ACCACACCTCAAGCAATGATTATCCCTAGCAGCTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC<br>AAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCTCTGTCAGTGAAAAATGCA<br>CATGATGAGCCTGGAAACATGTTGT |
| WI-1172a | 17 C A ---        |                            |  | TGAACGTGTGGTTAAACATGAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACA<br>GTGACACACCTCAAGCAATGATTATCCCTAGCAGCTCAGATTATGTTCTTGAATACCATTTTCTGCT<br>TTCAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA<br>CATGATGAGCCTGGAAACATGTTGT   |
| WI-1177  | 35 G C A          | GCAGATTGGA<br>AGTGAGAAAA   | CACCTACATTT<br>CTGAATATTTA<br>GACTCTTT | AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTTCAG<br>AAATGTAAGTGTGCTGCCCTCACTGTTCTTTACCCACTTAATCTGCAATTTTGAAGAACTAGATTGAAT<br>TCCCTTGCAAAAACCCCTTGATCATGATACCCGAGTTAAACCGTTAATTTAAAGACATTTAAACATGG<br>CCTGGTG              |
| WI-1231b | 141 G A ---       |                            |  | TCCATGGTTTGGTTGCTACTGACTTGTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC<br>CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATCTCCTTCTTTCATTAATTTCTT<br>TCAC[G/A]TTATTCCTCACCCTGAACGCCCTTCTCCTCTCGTAGACATTTTAAATCCACTTTAC<br>ACATCGGACC               |
| WI-1231a | 126 T C A         | GGCTCTTTATT<br>CTCCTTCTTTC | CGTTCAGGGTG<br>AGGGAATAA               | TCCATGGTTTGGTTGCTACTGACTTGTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC<br>CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATCTCCTTCTTTCATTAATTTT<br>CTTTCAGGTTATTCCTCACCCTGAACGCCCTTCTCCTCTCGTAGACATTTTAAATCCACTTTACA<br>CATTCGGACC                 |
| WI-472   | 114 G C ACAGAAAAG | ACATACATAT<br>CCATTATACA   | GACCTTTCITT<br>TCCAGCCC                | GAAAGCAGGAGTGTGTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTAAATTTTATT<br>TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG[G/C]GGGCTGAAAAAGAAAG<br>GTCAAGTGAGATTTCAGATATCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT   |



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| WI-478   | 46 C T                  | GCATGCTGTG<br>TTACTCTATTT<br>TGTTCT | AAATGCCACAG<br>GTGGCT            | AAACCACTGCAACCTTCAAGCATGCTGTGTACTCTATTTTGTTCCTAGCCACCTGTGGCATTT<br>CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC<br>ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC<br>ACTGCCCA  |
| WI-533   | 29 T C A A C T          | ATCACAGCAG<br>AGTACCTTTCT           | CCTTCCAACCT<br>CTACACAATCT<br>T  | AGCCATCACAGCAGTACCTTTCTAACTT/CJATAAGATTGTGTAGAGTTGGAAAGGAGGACACAGGA<br>CTGTCTGTGGTATAATGACCCTGTGTCCAGTTAATCCA  |
| WI-601b  | 112 T A ---             |                                     | ---                              | TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG<br>TAGTGAGCGAACAGAAAGAGGTTTCATTGACTCTCTAACTGAGTAC/T/ACAAAACGAGCAGGTGCT<br>CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT  |
| WI-601a  | 74 C T ---              |                                     | ---                              | TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG<br>TAGTGAG/C/T/GAACAGAAAGAGGTTTCATTGACTCTCTAACTGAGTACCTCAAAAACGAGCAGGTGCT<br>CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT   |
| WI-863   | 107 A G C C T C A C C A | CTCCTTCACAA<br>CCTCACCA             | CTTCCCGGTAA<br>GCCAAGT           | AACAAAACAGACACCCCTGGCTCTCTCACAGTCCACATGGTGCCAAACAATCCACATTCTCT<br>ACATCTCCCCACTGGCTGCTCTTCAACACCTCAACA/GIACCTGGCTTACCGGGAAGCATAAA<br>GCCAAGCATTTAGTCTTTTATGCAACATGGTCTGGCTGCAATAC  |
| WI-919   | 36 G A C                | ACTGCTTGCTT<br>GTTGATTTAAT          | TTATTCTAATC<br>CCACATGACAG<br>C  | ACTCACTGCTGCTTGTTGATTAAATCAACCTAGCC/GA/GCTGTGATGTGGGATTAGAATAAATA<br>AACACAAAATGAAACACACAGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGCTAAAGAT<br>AATAACTTCAA   |
| WI-991   | 37 A T ---              |                                     | ---                              | TGCATTCTATTGCACCAATAATACTTCTGTACAT/AT/CATTATTGTATTTCATTATCACAAAAT<br>TATGAGTGAGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT<br>TTCCCAAGTCACAAAGTTAGTGACAGAGCCGGATTCCGAATCCATCAACTTGAATCCAGAGAAAAT<br>GTTCTGCATCACTGTACAACTGACTCTCTTTCTCTTTGAAAACAAGGC        |
| WI-1011  | 70 G C C C A            | CAGTATCTGA<br>AGTTTTGTCT            | AGGAACACCTA<br>CAAAATGACTT<br>CT | CTTCTGACCTGTTTGCAGTGGATACTGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTGTCTCC<br>A/G/C/JAGAAGTCAATTTGTAGGTGTTCTGGCGTGTGTTGCTACGTTTCCATTTCTCTAATACACTGC<br>CGTCTTAAGGGAGGGCTTGACAGCAATTTACAGATGGCTGTTTGTGCTGCTGTGCACTGAAG  |
| WI-5381  | 178 A T ---             |                                     | ---                              | TTCATGCAGAAAGGTCCATGAGTTTACAGAACTCAAGGAAGAAAGGCCCTAGAGATGACACCCAGAA<br>ATGAGAGTGGCTTGCTCATGAAAATTGGACAGCATGTTCCAAAGCAGAGGGGAACAGCATGGAGAAGA<br>AAAATCATACTCTATCCACGTGCAGAAACTGGCAATTAGTTTGT/ATTTACTAAACACACAAATGT<br>TTAACTTGGGGTCCACAAACAAGGATA/GTTGGCAATGGTATTCTGTGATG |
| WI-5791b | 76 G A ---              |                                     | ---                              | CTATGTATTCATCTAGCAAAAGCAAGACTATTGGATAAGTTTCAAAAGATGAGAACAGGTCCTA<br>GAACCTCAG/GA/JATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCCAAGGTA<br>AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTGCCACCCCTGTTTGT<br>TAGGAA  |

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| WI-5791a | 44  | C G   | ---       |                           |  | CTATGTAATCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTC/GIACAAAAGATGAGAACACAGGTC<br>CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCCAAAAGGTA<br>AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTCTTATTGCCCACCCTGTTTGT<br>TAGGAA |
| WI-5406c | 120 | C T   | ---       |                           |  | CACCTGTGCTGTTGCCATGGTGCCACAGACTCTCCAGAAGAGCCACTCCACAGATGCAACAGGCC<br>TTTTGAAGGAGCCCGATTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACC/CJTATGAGCCAC<br>ACTTCTCATTTCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAAAAGAGAGAGGCA<br>GG               |
| WI-5406b | 118 | C A A |           | CCAGGATGTC<br>AAGGTGAGAA  | AATGAGAAGT<br>GTGGGCTCAT               | CACCTGTGCTGTTGTCCATGGTGCCACAGACTCTCCAGAAGAGCCACTCCACAGATGCAACAGGCC<br>TTTTGAAGGAGCCCGATTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/AJCTATGAGCCAC<br>ACTTCTCATTTCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAAAAGAGAGAGGCA<br>GG              |
| WI-5406a | 42  | A G   | ---       |                           | ---                                    | CACCTGTGCTGTTGCCATGGTGCCACAGACTCTCCAGAAG/A/GJGCCACTTCCACAGATGCAACAG<br>GCCCTTTGAAGGAGCCCGATTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCTATGAGCCAC<br>ACTTCTCATTTCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAAAAGAGAGGCA<br>GG              |
| WI-5798  | 48  | G C   | TG        | TTTATTCTCCC<br>TTGTTTCTTT | ACTGTTAGAAA<br>ACCAGTATTTT<br>TCAAT    | CCATTCTCTCTCCCTCTCCCTTTATTCTCCCTGTTTCTTTTG/GCJATTGAAAAAATACTGGTT<br>TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA   |
| WI-5415  | 54  | T A   | TTT       | TCATCATGAAT<br>TCATCTTTT  | GGACTAATTC<br>TGATCCGATCT              | CCTGCTAATAATAATTTAAGCACGATTGTCTTCATGAATTCATCTTTCAGTTT/JA/JTAGATCGGAT<br>CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA  |
| WI-5437  | 41  | C T   | G         | TCCCAGAGAA<br>AAATCCAAGA  | AGTTTCTAAAC<br>ACAAAATAATG<br>GTTTAAAG | TGTTTTAACCCAGGCAGACCTCCCAGAGAAAAAATCCAAGAG/CJCTTAAACCATATTTTGTGTTTA<br>GAACTCCTGTGCCAACCACTCTTGATGTGAGTGAC  |
| WI-5481b | 131 | A G   | CTGCAGTCG | TGTCATTATG                | TTACTTCCAGG<br>CTCCAAGTATT             | AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC<br>TCTCTGTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGCTATTTATGCTGCAGTCG/A/GJA<br>ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA                                 |
| WI-5481a | 29  | G A   | AATTT     | CCAAATTCAC<br>ATTAGTTGATG | CCCATGCATTA<br>GATACTGTAAA<br>ATT      | AAGCCAAATTCACATTAGTTGATGAATTT/GA/JAATTTTACAGTATCTAATGCATGGGCATCTGTTTTC<br>AACTCTCTGTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGCTATTTATGCTGCAGTCGAA<br>ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA                                |
| WI-5492  | 38  | T C   | ---       |                           | ---                                    | TCATGAGTCTTTCTTCAAAGATGCTGTGTTAAAGTCCCA/T/CJCAAAGAAAGGATCCCATGGCCTAAT<br>GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCA  |

|          |     |     |   |                                    |  |
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| WI-5826  | 134 | T C | ---   | ---                                | TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTTCTATGCTTCACATTTATTTTTT<br>TTTCACTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTTCTTAGT[C]<br>TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCACAGGCCAACAGCCTCACTCTTCCTT<br>CCTTGGTGCAATTACTCTTTACAC  |
| WI-5546  | 40  | C T | A   | CCCAATACTTT<br>TTCAGGTGAA          | CCTGTATTTTA<br>GCAAAACATGGG  |
| WI-5552  | 97  | C T | T T T T A G A G T                                     | GGCACCAGCCT<br>T T T T A G A G T   | TGCACAAATGG<br>CCCAGG  |
| WI-5836b | 161 | C T | ---   | ---                                | TGTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGTGAGCGGGTATGGGT<br>GGGGCTATCGGCACCAAGCCTTTTAGAGT[C]CCTGGGCAATTTGTGCAC TAGTGCAGA<br>TAAGTTGATTTAAACACTCTGTGCCCTCAATTTTCTCACCTATAAAATAAGATAATAGTATCTAAAA<br>AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATACTCTGATGATCTGGTTGTATCCCTGAA<br>TCCTGCAATATACACATGATTCAATGAT[C]CCTATTTTGAAATAAGCTTTTGAATTTGTTTCCA<br>ATG |
| WI-5573  | 58  | C T | G T T C A T A A G G<br>A G G T G G G A                | TGAACAGTTGG<br>AGAGTAATGTG<br>TC   | TCGGGTATTAGGATGCGTTCAACCTCGATGATGATGGCGTTTATAAGGAGGTGGGA[C]TGACAC<br>ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG  |
| WI-5850b | 134 | G A | ---   | ---                                | CAGGACCTGGAGCCTTGTCTTGTCTTCCACCTCACTCTTCTGCTGCCCTGCCCATGGGTGGAGC<br>CTCTCTCAGGCTTCTCTATGCACGCGTCTATCTTATATGGGCAATATCCAATGTCCCATTC[G/A]<br>TTTTGCCATTTCTGTATATCAAAACAGAGAGCAGAGGGTGG  |
| WI-5850a | 92  | C T | ---   | ---                                | CAGGACCTGGAGCCTTGTCTTGTCTTCCACCTCACTCTTCTGCTGCCCTGCCCATGGGTGGAGC<br>CTCTCTCAGGCTTCTCTATGCA[C]TGCGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCG<br>TTTTGCCATTTCTGTATATCAAAACAGAGAGCAGAGGGTGG   |
| WI-5612b | 125 | A T | C T A T T A A T G A<br>G C A T C G T G T C A<br>T T C | TTCTCTTGAGA<br>AACCTAAAAAG<br>ACTG | TGCTGTATTGACACATAGTTATCTGACAGTAATCATCTTAACATCACAATAATCTTATTCTGCCTG<br>TCACACTAATTTGCAAGCATTCAAATTGATTGACTATTAATGAGCATCGTGTCAATC[AT]CAGTGT<br>TTAGGTTCTCAAGAGAATTATGCTGTTCTTCTCTGTAACCTCAAGTA   |
| WI-5612a | 44  | T A | ---   | ---                                | TGCCTGATTGACACATAGTTATCTGACAGTAATCATCTTAACA[AT]A/CACAAAATATCTTATTCTGC<br>CTGTACACTAATTTGCAAGCATTCAAATTGATTGACTAATTAATGAGCATCGTGTCAATTCACAGTGT<br>TTAGGTTCTCAAGAGAATTATGCTGTTCTTCTCTGTAACCTCAAGTA   |
| WI-5636  | 26  | A C | G C C A A T T T T A T<br>C C G C A A T A A A          | CATCAGGACT<br>TTGGGA               | TGAGAGCCAAATTTATCCGCAATAA[A/C]TTCCCAAGTCTCTCGATGGAGGCATTTCAGAAATCGGG<br>GCAGGGAGGAGGAGGAGGTGAGACAGATGTGAAGAAC  |

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| WI-5865c | 103 | C G ---       | ---                                 | TTAGAAACCTCCATTATTCTGCCATGGTAGACATCTTTTAAAGATCTTTTTTTCATTTATGCAATC<br>ACTGACTCACTCACTGCTCTATCAAAAATTAA[C/G]AAATATTAAATATTTTATTTACAGAGAA<br>CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA<br>GAGAAGACAGACAACATAAATCCAGG   |
| WI-5865b | 99  | T A ---       | ---                                 | TTAGAAACCTCCATTATTCTGCCATGGTAGACATCTTTTAAAGATCTTTTTTTCATTTATGCAATC<br>ACTGACTCACTCACTGCTCTATCAAAAATT[A/J]AAACAAATATTAAATATTTTATTTACAGAGAA<br>CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA<br>GAGAAGACAGACAACATAAATCCAGG   |
| WI-5865  | 165 | T A ---       | ---                                 | TTAGAAACCTCCATTATTCTGCCATGGTAGACATCTTTTAAAGATCTTTTTTTCATTTATGCAATC<br>ACTGACTCACTCACTGCTCTATCAAAAATTAAACAAATATTAAATATTTTATTTACAGAGAACTC<br>AGAAGCCAGAAAAATGACCAAGACACAGT[A/J]CCAGTCTCCATCTTCAAAAGGTCACAGTCTTCC<br>AGAGAAGACAGACAACATAAATCCAGG  |
| WI-5874  | 76  | T G ACAGAAAA  | CATAGCATGG<br>ATAATATTAT<br>ATATGT  | CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGTATTTTCATAGCATGGATAATATTACAGAA<br>AAAAAATTTGTTACATATCAAAATGACTGAAACCTTACTAGTAGCAATTTGTTTGCAATTTGCT<br>CATGGAGCCGACGTTTCCAGTCTCAGTTTTTCCATC[A/J]TTTTTTCATAATTTACTCTCTTTTCTGTC<br>ACAATGTTCTGCTCTGATTTCAACTCTCATTGCTGATGGATGGTAGTCATAAAATATGGGTGATTC<br>AGAAAAAAGTAAATG |
| WI-5752  | 36  | A T TTTTCCAIC | GACAGAAAAG<br>AGAGTAAAT<br>ATGAAAAA | TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAAAT[A/C/G]<br>CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAAGCCGAGTTTTCGATTTCACACA<br>GTTGCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCCACGAAA<br>CATTGTTGAAACGAAAGCCACGTTTCCGATTACACAGTATTGTCGT   |
| WI-5760b | 61  | C G ---       | ---                                 | TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAAATACCCAT<br>TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAAGCCGAGTTTTCGATTTCACACAGTT<br>GTCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG[G/A]TCCCACGAA<br>ACATTGTTGAAACGAAAGCCACGTTTCCGATTACACAGTATTGTCGT   |
| WI-5760  | 187 | G A ---       | ---                                 | AAATCTGGCCTTTTCTCTTAGGAGGAGATTTCTCACCATTGGGAATCTTG[A/G]TGCAAGTTAGAT<br>CCCACCTCACTATTGAGAAGCTAAAGTGAAGACTACTCATTTCTCAGTCTTCTTCTGCTG  |
| WI-5944  | 52  | A G GGAATCTTG | TTCTCACCATG<br>AACTTGCA             | GAGTTTAATGAATCTGTTCCCTCTAAACCTCTGTTCCCCCACTTCACATTCAGCAGATATT<br>CTTTCATGGGTTATTTTGCCCAAGTCATGAGGAGATGATGATTAATTTGATCATTTCAAGAGTGTGAG<br>TAATGCTTGGT[A/C]TTTGTCTGTGCGCGTATCTGCTCCCAATCACCATTCCACTTTATTTCCTATTAT<br>GCTGAATGAAACGGTTATTACAG   |
| WI-5967b | 148 | C T ---       | ---                                 |  |

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|----------|------------------|---------------------------|--|---------------------------------|---|
| WI-5967  | 165 C T ---      |                           |  |                                 | GAGTTTAATGAATCCTGTTCCCTCCTAAAAACCTCCTGTTCCCCCAACTTCACATTTCAGCAGATATT<br>CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG<br>TAATGCTTGGTACTTGTCTGTGCGCGTATC/TJTGCTCCAATCACCCATTCCACATTTATTTCCCTATTAT<br>GCTGAATGAAACGGTTATATTACAG   |
| WI-6093  | 53 G C ---       |                           |  |                                 | GGGTAAGATCCAGAGCCACAGGTGAACCTGCGCGTATTGAAGTCTTTGGGCCA/GCJGTCTGTAATG<br>ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTTCCAACTGTGCACTGAGCCCATTTGTAGGGA<br>GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTCAGCAAACCTTGATTGACGGTGAC<br>ACACATGCTTCGAGAAGGAATGAGG  |
| WI-6141  | 80 T C AGGTACTT  | CTTCTTAATTA<br>AGCATCTACA |  | TGAAAACCCCA<br>GAACAGTG         | GACTCTGTCTCAAGAAAAAATAAATGAATAATTGAATTAATTAAAGCATCTCTTAATTAAGCAT<br>CTACAAGGTACTTAT/CJCACTGTTCTGGGGTTTCAATCCTCTCACCTTTAGACTTCAGGAAAT<br>CAGAAAAATGCATGAAAAACAGGATTGTACATGCAGAGAAATAGGGGGAGATAAAAAATTTGTCTTTT<br>CTC   |
| WI-6450  | 45 T G TGTACA    | CCAATGACTT<br>ATTCTATATCT |  | TTGTTTGAAT<br>GTGTGGTACTT<br>CT | ATAGGACAGTTTTTCTTCCAAATGACTTATTCTATATCTTGTACAT/GJAGAAGTACACACATTTCA<br>AACAAGAGCCAGGCTATGCCAGGGTGGGATTATTTACGGTCATGGTAATATGCATGTAAAGACTA<br>TTTTACTGGCCTCTTTTATGCATAAACAAAGGATTGGTCTATTCAACAAACATGTGTCAATACAG<br>CAGTTGTCATGTCCTCTGGTACTAGAAATATAGTCTTTATAGAAATGTGGTTAGAAATAAGCCACA<br>AATTATTCTATAAACAAACA/CJJAAGGAACGAGGCTCAAAAGTGGAACAAACGGCCTTAGTTTC<br>TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA |
| WI-6461  | 88 C T ---       |                           |  |                                 | GAAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCT<br>ATGAAATAGTCTATTTCAGTGAAGTATCATATAAAGACATGCAAAACCTTTTCACAGTCTTTGT<br>CCTGG[G/JAATATCTCACAAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGG<br>ATTGTCCTTT   |
| WI-7466c | 141 G A TTGTCTGG | TTTTCACAGTC<br>TTGTCTCTGG |  | AGTGGCATGCC<br>AATTATAATT       | GAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCT<br>ATGAAATAGTCT/JCJATTCAGTGAAGTATCATATAAAGACATGCAAAACCTTTTCACAGTCTTT<br>TGTCCTGGGAATATCTCACAAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA<br>TTGTTCCTTT  |
| WI-7466b | 80 T C GTC       | GACTTCTGGG<br>CTATGAAATA  |  | ACTGAA                          | TGCTTTTTAAAAATAACAATGACCACCACTGACACCATAGTGTGTCTCCATTTGCCACGTCTTCCTC<br>AGTAGAATAAGACAGGGACTTTGCTGGCTGCTATCTC/JATTCCTTCAGAAAGACACTTGGCCCT<br>CATAGGCATTCATAGATATTTGTGAATGAATGTGCTTTTTCATATTGATTCCTACATTTGATACA<br>TTCTCAGGAGGGACATTTGGCCTAT  |
| WI-9814  | 104 C A ---      |                           |  |                                 | CCTCTAACAGAAAACTTGACTTCTCAACTCAAAATACCCCTCTCTAATAATTTT/JGJAGTAACCA<br>AAATATCTCTCAAAATAAATTAATCTTTTAATTAGAAAGAACACAGTGTAGAGGTAGTACATTCA<br>CCACC  |
| WI-9720b | 55 A G ---       |                           |  |                                 |   |

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|----------|-------------|-----|--|
| WI-9720a | 47 A G ---  | --- | CCTCTAACAGAAACTTGACTTCCTCAACTCAAAATACCCTTCTCTJAGJATAATTTAAGTAACCA<br>AAATATTCCTTCAAATAAATTAATCTTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA<br>CCACC   |
| WI-9825  | 123 A T --- | --- | CACGCTTAAGGCAGGATGTGGCTTATGAGATACITTTGCAITGTCTGCACACCTTGAATCTGCC<br>TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTAGGGTGTJATJGAGGATTAG<br>TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTTAGTTGCATT<br>TAAGAAITGCCAGTCTTTTGCTGCTGCATCATCTTGAACATTATCCACATG  |
| WI-9748  | 74 C G ---  | --- | CCACTTCAGTAAATCAATTTGTAGCACTTATTTCTAAAGATTTCTAAATTTTTATATGTTTACCCTTT<br>GTCATTJGJTCAGACCAAGTACATGTTTTCACACAGCCATCTTCTTTCTCGGAATCTTTCAGAAT<br>TACAGTTATGATGTCCTTTTATATTCCTCA  |
| WI-9943  | 91 T C ---  | --- | TGAGGCTATGATGCAGATTTGTAGTGACTAATACTATTAAAGCAATTTCAATGTTGTGGCACTGTT<br>CGTTGTGTTTTATATCCATCTTCJATTTTTAATTTTCTACTGAGCAGAAAAAATAATGTATACATT<br>AACCTTTGCTCCCTATTGTACCTTTTAAATTTGCAATTCACACCTTCTCTTTTGTCAATTTAGGGA   |
| WI-9891  | 39 T C ---  | --- | AGGGCTTTCACAGATCCGTAGCTCAACACTGCCTCTTJCIAGTGAGCCTGTGAACACCCCAAGAC<br>GGCTGGTCACTAGTGTCACTCTTCTTTCGGGACACTATCTTTAAAGAAAAAAGAGTGT<br>CTTTGAATGATCCATTTATCCCCAAATAATCTTGTGTTTAAATAATCTTTATAGGCCAAATCCAAT<br>GTGCTGAATATCTGCCAAGCATGTCTATTCTACACAAAAGGATTTGCCAA          |
| WI-9897b | 84 C T ---  | --- | CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATCTTGTCTCAACATCCTATTTTCTCTCAAAC<br>ATTTATCTAGCCTGTJATJAGTGCATCCAGTGAGGCTGTTTATTTCAATCTATGTGAAATTTTGAGCA<br>ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA  |
| WI-9897a | 83 A T ---  | --- | CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATCTTGTCTCAACATCCTATTTTCTCTCAAAC<br>ATTTATCTAGCCTGTJATJAGTGCATCCAGTGAGGCTGTTTATTTCAATCTATGTGAAATTTTGAGCA<br>ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA  |
| WI-9935b | 115 C A --- | --- | AGATAACCCCTGGAAACTAGAGAAATTAATAACGTGTGCAJCTJACCTCACCAGAACTGGAAGGAGT<br>CTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTCAGACACAGCCAGAAAGGCC<br>TGATATTAAGAGGCACCTTGCAATTA  |
| WI-9935a | 42 C T ---  | --- | AGATAACCCCTGGAAACTAGAGAAATTAATAACGTGTGCAJCTJACCTCACCAGAACTGGAAGG<br>AGTGTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTCAGACACAGCCAGAAAGGCC<br>TGATATTAAGAGGCACCTTGCAATTA  |
| WI-9983  | 146 C T --- | --- | CCGTGTTAGGTGCCAGAGTCCATGCTTTGGCCACAATGTTAGGCTGCCTCCCATTTCTTTGTCTTGA<br>TTCCCCAAACCCAGGTTCTCACCCCAATCTGATCAATGTCTAGCTAGGTGCTGGTGCAGGGTAA<br>AGCATTATGAJCTJAGACACAAAGACAAAGAGGTTAAAGTTGCTGTCTCAAGAGAGAGACATAA<br>AAACAAATGGATCTGGAACTAAGTAAAGGCTTCGAGGAGGAGGTGAGCAAAGG |

|           |     |   |   |           |                            |  |   |
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| WI-10019  | 139 | A | T | ATCT      | TGATGTAATGC<br>TATGTAGCAA  | TTGATTACTGT<br>GCTTAGGSA               | ATATCAGTGGTTGAGTATACAGCAATCTATTGTTTATTATGTGTGCTATAAAATCAATGGTTCTA<br>ACATTCAAAATAGATCTTTTGGCTCTCTGCTCAGATGCTTTCATGATGTAATGCTATGTAGCAAT<br>CTA/ATTTCCCTAAGCACAGTAATCAAGGCCCTTCTAGCCCA                                      |
| WI-10020b | 122 | T | A | TTT       | GCGAGAAAAG<br>AAATCATGAC   | GACTGTTAATT<br>TATTTAATCAT<br>TAGTCTGG | TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATATTGTTAACTGGCTGAAAAGAATTTAGGC<br>ATGCATAGAGAAATAGCAGTGTGTTTATTGGCGAGAAAAGAAATCATGACTTTT/TA/AAAAATACC<br>AGACTAATGATTAAATAAATAACAGTCTAGGGTCCGGAAGTGGCCTAAAGCACGTTAGTAGCCCT<br>CCTTAGA |
| WI-10020a | 39  | T | C | ATAAAT    | TGTCATCTTGA<br>CTCGTATTA   | AAATTCITTTT<br>AGAGCCAGTTA<br>AC       | TTTACTTCATTGTCATCTTGACTCGTATTAAATAAAT/TC/TTAACTGGCTGAAAAGAATTTA<br>GGCATGCATAGAGAAATAGCAGTGTGTTTATTGGCGAGAAAAGAAATCATGACTTTT/TA/AAAAATACC<br>AGACTAATGATTAAATAAATAACAGTCTAGGGTCCGGAAGTGGCCTAAAGCACGTTAGTAGCCCT<br>CCTTAGA |
| WI-10064b | 170 | C | T | TTACATG   | CCTTTAGATAT<br>ATTGTGATTGT | ACCTTTCTGAA<br>GCCAGATTTC              | TCTGAGTCTTTCTGAGACACTTGCCTGTCAGGGTAGCAGGATCAGGAAGGCATTATAATAAT<br>ATAATTTGCAGAGCATCTCTCTCTATGCACAGATATTGTTGAGACTCTGTTTAAATCCAGTATCC<br>CTACTCCTTTAGATATATTGTGATTGTTTACATGTC/TA/AAATCTGGCTTCAGAAAGGTTAGGTGTT<br>T          |
| WI-10064a | 54  | C | A | CAGGAAGG  | GTAGCAGGAT<br>CAGGAAGG     | CAAAATTATATT<br>TATTAT                 | TCTGAGTCTTTCTGAGACACTTGCCTGTCAGGGTAGCAGGATCAGGAAGGCATTATAATAAT<br>AATAAATTTGCAGAGCATCTCTCTCTATGCACAGATATTGTTGAGACTCTGTTTAAATCCAGTAT<br>TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT<br>T           |
| WI-10289  | 29  | T | C | CAAACTCTT | TCTCCTGTCCC<br>CAAACTCTT   | ATTCTTGTGT<br>ATTGAATGGAA<br>TTAA      | CCAGGGATTCTCCTGTCCCCTAACTCTT/TC/TTAAATCCATTCAATACAACAAGAAATTTATAGAA<br>TATGCCACCATGCCACAAAGACACCCCTTATATTAGT  |
| WI-1319   | 40  | A | T | ATTCTTT   | TGGCACTTAG<br>AACATAGTTT   | GCCACACACC<br>CTATGGT                  | AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATCTTT/TA/ACCATAGGGGTGTGGCTTATCT<br>TTTAACTGGCATGGCTTTAGTCTGTTTATAATTTGGTATCTTTTGGCACAAGAGTCTGTTCTGAC<br>AGTCTTATGATCTCTATTTTAAACATTAACACTGGTCAGATGTGTTTAAACCTGTTGAACCTGCAGC             |
| WI-10316  | 104 | T | C | CTCTT     | CTGTTGATTT<br>CTACCTCTATT  | GCTTTGGAATG<br>TATCCAAAAGT<br>TT       | AGCAACGTGTACAACCTTAGTGGGTGTAATCAGAGCATCTATATTATTCACCAGTCACCACCCTG<br>GACTATAGTCTGTTGATTTTCTACCTCTATCTCTT/TC/TTAAAGTTTGGATACATTCCAAAGCAT<br>CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAGCCCGAGCC                                    |
| WI-2572   | 61  | C | T | ---       | ---                        | ---                                    | AGTGAGTTGTGCACAATTTGGAGACATCTGTGACCCCACTTAAACACCTCTCCCCACA/CT/AC<br>AAAGTTAACACTTCAGTTACCAGGTGATGAGCAGA   |

|           |                |                           |                                       |   |
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| WI-10368  | 31 C T         | TGAAGCAACC<br>AGGTCTTGTT  | CAAGATATTAT<br>ATTTATTCCT<br>AAGAGGGG | GAGGAAGTGCCTGAAGCAACCAAGGTCTTGTTGCTACCCCTCTTAGAGAATAAATAATATCTT<br>GAGATAGGAGGAGCAGCCTGAGGACAGTCTGGTTTTGTTCTACCCACTGGAAGCAGAAATATCC<br>TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCCTGATGGATTGCCCTTCAGGG<br>T  |
| WI-10391  | 32 A G         | CTGTCTCAGGT<br>ATGACTCCCA | GGGAGTTAGGA<br>GTCAAGAAGTT<br>GA      | CTTCCCGTTCTGTCTCAGGTATGACTCCCAAGGTTCAACTTCTGACTCCTAACTCCCATCTCGGTG<br>TCTGCTTCCAGGGGACGCATCTGACACAGCCTTTTGCTTGCTGTGACAAACAGAACATTCGAGAAG<br>TGATGCTGGGTGACCTCCAGGATA  |
| WI-10567c | 146 A C GCAA   | GTACCCAGA<br>GTCTTCTAATA  | TGCCGCTTCCA<br>GTAGCT                 | AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTTCATATT<br>TTCCAAATTATTAATACTAGAAATTTTACCACACAGAAATTTTTTAAACATTTTAAAGTTACCCAGATCTT<br>CTAATAGCAACACAGCTACTGGAAGCGGCAAGAAATTTAACCCCT   |
| WI-10567b | 82 A C         | ...                       | ...                                   | AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTTCATATT<br>TTCCAAATTATTAATACTAGAAATTTTACCACACAGAAATTTTTTAAACATTTTAAAGTTACCCAGAT<br>CTAATAGCAACACAGCTACTGGAAGCGGCAAGAAATTTAACCCCT  |
| WI-10567a | 60 T C TTTT    | GGGTGCTCAAT<br>AAATATTATT | AAATTTCTGTT<br>GGTGAAATTC<br>TAG      | AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTTCATATT<br>ATTTTCCAAATTTAATACTAGAAATTTTACCACACAGAAATTTTTTAAACATTTTAAAGTTACCCAGAT<br>CTTCTAATAGCAACAGCTACTGGAAGCGGCAAGAAATTTAACCCCT  |
| WI-11153b | 84 C G TACTTTA | CAAACCTCAA<br>ATTGCTTTAAG | AAATCCAACA<br>GTCAAGGTCT<br>C         | CGTTGGGAATATTTCTATCTCACCTAAATATGCGGTGATTAATAATATACATTTTAAACAACTTCAAA<br>TTGCTTTAAGTACTTTACGAGACCTTGACTGTGGATTTTGGATTTTTCATTTTCTTTTAAATA<br>AAACATGTCATATTTAAGTTGTCAGCAAGATGACTTATATGTTAATTATCTGATATCAGCATCCCTT<br>TATGTATT  |
| WI-11153a | 33 C A AATTATG | GGGAATATTC<br>TATCTCACCTA | GCAATTTGAAG<br>TTTGTTAAAT<br>GTAT     | CGTTGGGAATATTTCTATCTCACCTAAATATGCGGTGATTAATAATATACATTTTAAACAACTTCT<br>AAATTTGCTTTAAGTACTTTACGAGACCTTGACTGTGGATTTTGGATTTTTCATTTTCTTTTAAATA<br>AAACATGTCATATTTAAGTTGTCAGCAAGATGACTTATATGTTAATTATCTGATATCAGCATCCCTT<br>TATGTATT  |
| WI-2616   | 125 T C ATCC   | CACAAATGTA<br>ACAAGAATTG  | CCATGGCTGTA<br>GTCCAGT                | GTTGTGAAACTCCAGTATCATTTCCCTCAAACCCAGCTTAAATCACAATCACTTTTCTTCTCTGTA<br>GAGCTCAAACCTCAGTCTGAATGAAATTTGCTGCACAAATGTAACAAGAAATGATCCTATTC/ACTGGG<br>ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG   |
| WI-11163  | 58 C T TGAGA   | CAAGTGAATT<br>ATGACCAAAA  | TGCTCTTTCA<br>TTTGAGGTTTT<br>T        | TGACTCAAAGGAAACACACACAAAAAGTTTACCACAGTGAATTTAGCCAAAAATGAGA/CT/AAAT<br>TTGTTAAAAAAAACCTCAAAATGAAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTTGT<br>ACCTACAAAAATAGGGATAGTCATGGTTTGGCAGACTTTTCTTTCTTTTCTTTTGT/GCTCTTA<br>GAATCCATTTGCTTTTGGCCAGCATTCCTCTCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT<br>CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGAGGACTATTCACCCCATGGGTGAT<br>AGAGAGGATTAAACAGGGTGATGCTGCAATGGGAATTTTGAACCC |
| WI-10656  | 59 T G         | ...                       | ...                                   |   |



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| WI-11169b | 154 T G T T T T             | TTAACCAAGA<br>GTTTTTCATTC   | CTAACTTAAAA<br>ATCCTCATTTCA<br>AAATATAA | CAGCATAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA<br>CTGACTTTGAAAAAATAATTTAAGCCTAAAGTAGTCTTTTAAACCAAGAGTTTTTCATTTCTTTT<br>TTTAAAAAAGAGCAGACAT/GJTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGATT<br>TTTAAGTTAGCAT                |
| WI-11169a | 95 A G T T G A A A A        | AATAAGTGAA<br>AGTAACTGAC    | AAACTCTTGGT<br>TAAAAAGCAC<br>TACTT      | CAGCATAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA<br>CTGACTTTGAAAAAATAATTTAAGCCT/GJAAAGTAGTCTTTTAAACCAAGAGTTTTTCATTTCTT<br>TTTTTTAAAAAAGAGCAGACATTTATCATGTGTTCTGATAAATTTTTTATATTTTGAATGAGGAT<br>TTTTAAGTTAGCAT              |
| WI-10685  | 25 A G ---                  |                             | ---                                     | CAAGTGCTGGACCTTGATAGGTG/GJACCGGCTGAAGGTTGGACAGTTGTTGGTTAGGTTGGAG<br>ACCAAAATTCAGTCACTCTGTAATATAGATCTTGTCTTTGGGTTTACCACAGGGTCACTAAAG<br>AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATCCAAAATAGCCATGGGTTTGGACAAAATAC<br>AAGGTTAGTGCTCTCTAACTTTAATGGGCATA |
| WI-10686  | 133 C T A A G G             | TGCCCTGTGC<br>AAGG          | CAATCTCTAAA<br>TTCATGTGTAG<br>ACACA     | AATAACCTGTGGCACATAAGGCAATACTGAGCCCCATACAGAGTGTTTATGTTAATATATGAAA<br>AAAGTCAAGAGAACAGATGATATAGTTCTGCTAGAAATCTGAAATCTGATGCCCTGTCCAAAGG[<br>C/TJTGCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAGGG  |
| WI-11175  | 77 T A A                    | AAATGATTCCT<br>TCTGCTCAAG   | CTGTTCTCACA<br>TTCCTTTTGAA<br>AA        | GGTAGGATGATCTAGAATGCCACTTTACAGCCACTGAAATATATTGCCCTCCCAATGATCTTTCTG<br>CTCAAAAGAT/GJTTTTTTAAGTTATCTACTTATTTATCTGCTTTTTTCAAAAAGAAATGTGAGA<br>ACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATAATTAATAAAGTAAGAAAAAGAGCCAAATT<br>TGGGC                        |
| WI-10694  | 144 A G T A T G A G T T T C | TGCAAAATGCTT<br>TGAATTCATCC | GGCATTTTGTA<br>AAGGAGGAAA               | TAGAGAGGCTTTTCAGTTTCAGGTTGGAGGGGTGGTGAGGTGAGATTCATCTTAGAAGCACTGGC<br>TATGTACAGAAAGATAAACTCTGAGAAAGAACTCAGTTCTAAAGTTTCAAGTCTTTCGAAATGCTTTA<br>TGAGTTTTC/GJTTCCTCTCTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGGCTTTCT                                    |
| WI-2716   | 23 T C C                    | AGAAAAACAG                  | TCTGTTGTCA<br>TTC                       | GTGAATTCATCCAGAAAAACAGCT/GJGAATGACAAACAGAGAGAGAAAGATAAAGGTTTTTGT<br>ATACGACAAGTGGCTCAAGCAATTTTCTCTGTCCAGTGCATGGAGCAGTG  |
| WI-10719  | 115 T C G C C A T T C T A G | TGACTCTCAAG<br>GCCATTCTAG   | GCACTGCCAGC<br>AGCC                     | CAGGCCCAACTCTGTCTAATTAAGTGTTTGAACACAGACACCTCAGTCACACAAAAGTTTCTTTGTATGT<br>GCCCAACATAAACAGTTACTGGAGGATGACTCTCAAGGCCATCTAGT/CJGGCTGCTGGCAGTGCTT<br>TTCAGCCTGCTGCCCATAACTAA  |
| WI-10721  | 40 A G C T T G C C A        | TGGCTCTGCTA                 | GAACTCCAC<br>ATAAATAAAT<br>CTCA         | CAACCAATTCAGATTTAATTTTGGCTCTGCTACTTGCCA/GJATGAGATTTATTTATGTGGGAGTT<br>TCTGAAGATCCCATGGTAAATAGTATTCCTCTTCCCTGCTTAGGTTTGAAGAGATTGAA   |

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| WI-11204b | 88 T C ---        |                            |   | GCACACGAAATTGATTAAATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG<br>AAAAGAAAAACTTTACACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT<br>CAAAAAATTTTAATTGGGAAGAGATTTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTCAGAAG<br>GCAACATC |
| WI-11204a | 80 T A AACTT      | GTAAAAAGGG<br>TGAAAAAGAAA  | ---<br>TGATCATTAA<br>AATGTACATAA<br>TACCTTT | GCACACGAAATTGATTAAATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG<br>AAAAGAAAAACTTT/AJCACCTTTTATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT<br>CAAAAAATTTTAATTGGGAAGAGATTTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTCAGAAG<br>GCAACATC  |
| WI-10732  | 80 C A ATTGGTCACT | GCTGTGCTTC<br>GCTGTGCTTC   | AGAACAATG<br>CATAACAGAA<br>CTTTAA           | ACATGTATTTCCCTTAGTGGTCAGCCCTTCCCTACCCCAAGAAATATCCCTGGTTTATGCTGTGCTTC<br>ATTGGTTCACCTC/AJTAAAGTTCTGTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTTCCA<br>CACCACCTGTGTTAACTGTC   |
| WI-11206  | 127 A T ACTC      | GGTTGTGTTTT<br>CTGTATGTACA |   | TAGTCTTTTCTTTGTACGAGTGTCAATAAAGAAATACCACCTCTGTACATTTGTAAAGATAGCACAG<br>AGAGAAGCATTACAGGGCACAGCACAAACATGAGGTTGTGTTTCTGTATGTACAACTC/AJTCCAA<br>CCATTAGGATTGTCACTCTCATATATAGACAGAAATTCAGTGGTGGTGAATTTGAATCCACACATGGA<br>ATAAGTCTA |
| WI-11215  | 68 C T ---        |                            | ---   | GAAAAAAAGTTTAAATTGGATTGCTTAGTTTGCTTAAATTTGACCTACTTTTCAGATTTATTTTAGT<br>[C/T]ATTTTCTATAATATTTCTGTAGTGATGGATTTCTATAAATTAAAGGAAACAGATATTT<br>ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTATCCAAAGCCCATTCACCATGT<br>TTT             |
| WI-11219b | 89 G A AGAGAA     | GAGAGAATAT<br>TCCAAAAAGT   | GGTCTCTAAT<br>TTTCTCACT<br>TTCT             | ATGAAAAATGCATTAGAAGAATTGGAGGATAAAATTGAGAGAATATCCAAAAAGTAGAGAAAAA<br>GAGACAAAGAGATGAAAAATAGGA/GA/JAGAAAGTGTAGAAAAATAGAGGACCATCTATACAG<br>TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC<br>AAACATCTC          |
| WI-11219a | 18 G A ---        |                            | ---   | ATGAAAAATGCATTAGAA/GA/JAATTGGAGGATAAAATGAGAGAATATCCAAAAAGTAGAGAA<br>AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATAGAGGACCATCTATACAG<br>TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC<br>AAACATCTC           |
| WI-11222b | 136 G A/GGCTGG    | CATACCACTGC                | CCTGGTAGCCA<br>AGTTGTGA                     | AGCCACAGTGAATCAATTTACACTACCGAAATCAGCAAAATGCTAAAAATGGGCTTTGGATTTTGT<br>TTTTGTTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACCAAGCATACCAGTGGGCTG<br>G/GA/JTCAACAACCTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTTGCTTTCACAGGCTACTGG<br>AAAGCC   |

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| WI-1122a | 25 C T  | GCCACAGTGG<br>AATCATTTAC<br>A        | TTTtagcattt<br>GCTGATTTCG             | AGCCACAGTGGAAATCAATTTACACTA/C/TJCGAAATCAGCAAATGCTAAAATGGGGCTTTGGATTTT<br>TGTTTTGTTTTTCCATAGACCCACCGTTGAACCTATTGTTAAACATTTACCAGCATACCACCTGCGG<br>CTGGGTCAACAACCTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTACAGGCTACTGGA<br>AAGCC |
| WI-10775 | 39 C T  | TTTATGCCATA<br>TTAATTCAATTA<br>CACTC | CTAGATGTATT<br>TGCTAAGAAA<br>ATATGATG | TTGCAAGTTTGTTTTATGCCATATTAAITTCATTACACTC/C/TJACATCATATTTCTTAGCAAAATACA<br>TCTAGACACCTGGCACTCAGTAAGGGATATTCCTGGCAGCATATCATTTGTTATCATTAGACATTGCA<br>GGAACCAACCATATGGATGGATAAATGTGTGTTTAAATGAAGGCAAGCAATTA                       |
| WI-11226 | 165 A C | ---                                  | ---                                   | TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTAAGTAAAAATAAA<br>GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAAGAAAAATGTCAGTGGTTGC<br>TAGTACAGGAATCAAAATTTGGACTATGAACA/CJGACATAGTTGCTAAGGATATTCACAAAAATTAT<br>TTCATGA  |
| WI-10778 | 62 A G  | GCAAGGGAGG<br>AACATTTACA<br>G        | CTGGTGACATC<br>AGAGATGGAC             | CAGTGGCTGGCTACTGACAAAACGTAAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/A/GJG<br>TCCATCTCTGATGTCACCAAGCAGGGCCAGGAAGGTTGATCTGGAG   |
| WI-10789 | 21 C T  | GGGACACACT<br>GCTCTAGACC             | TTGAGGGACCC<br>TGGGA                  | TGGGACACACTGCTCTAGAC/CJ/TJCCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCT<br>GCCCTGGGGACGCAGAGGCATCAGGGCTTAGTCTCTCTGGGACAGTGAAGGGGCCACCAACC  |
| WI-10810 | 58 C T  | CATCTTCATGG<br>GCAGGAATT             | CAACCCCTAAG<br>AAACACAGAA<br>ATG      | ACAGAAAAATGCCTAGGCTTGTAGCAAGAGAGAAAGCATCTTCATGGGCAGGAATTC/TJCATTT<br>CTGTGTTCTTAGGGTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGTATCCAGCAACATT<br>TCCGTAACCTACCCCTCTAGAAATCATGCAAGAGAAATGATGA  |
| WI-10828 | 23 T C  | ---                                  | ---                                   | GGACCAACAGAAATTAATCTGGCAT/CJAGGGTTTCTTAAACATTTCTGCAGAACATTAGTAAAGT<br>TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATTTCTTTAGTAGAG<br>GACTTCTAAAGGCTATAATATTTGGATACATTAGGCTCATTATGAATCTCAAAGGAGCATGTAGT<br>AGGGCATATCTAA |
| WI-10832 | 91 G C  | CATTAATCTGC<br>AGGCTCTCC             | CCTAACTGCAG<br>GTGACTTAGAA<br>A       | TATGCCCTTCCCAACGAGCCATCCACGCTGCTCTTAGCACAAAAAATAGAAATACATCATCTGAAATG<br>GGCACATTAACTGTCAGGCTCTCC/GC/JTTTCTAAGTCACTGCAGTTAGGTCTGCAGACACTGTGTA<br>TACCATATAAATCTGATTTCTGAGCAGGAGGGGAGGATGAGAGAGGGCTGCTCCGTGAAATAC<br>TAGTTCGG   |
| WI-10834 | 96 C T  | AGAAATTAAT<br>GTTCAAAAGT<br>GTGTTAAT | TGGCCCTATAA<br>AATTGGTATTA<br>AG      | GATTTGAGTATTATCAAAATGGCCAAAGACCATTAAACAGATTTAATAGTTAAAGCCAAAACTATA<br>AAGAAATTAAGTGTCAAAAGTGTGTTAAAT/CJ/TCTTAATACCAATTTTATAGGGCCACCATTAACTT<br>CTGAAGAAAGGTGAGCATATGCAACTAAATTTCTAAAGTCCAGT                                   |
| WI-2287  | 24 T C  | ---                                  | ---                                   | GGATGATGTTCTGTGGTCCCTTTAT/CJAAAGCCCTCTTGATCCCAATGTGTAATTTATTTATCT<br>TGGTATTTCTCGCTTACCCTAGTACCTGTCAAGTGTCCACCT   |

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| WI-2296  | 81 A  | G | TGTTACTTTGA<br>TTCTTTGCTCT          | GCAAATCACAC<br>AGCTAACTGG       | TGGAGGGTTAGAAATCAGGTGGCATCCTAGAAAGGTCTCAGGCTTTAGAATAAGTTGTTACTTTGA<br>TTCTTTGCTCTGAC(A/G)CCAGTTAGCTGTGTGATTTGCAGAAGTTACATTTGTTTGTG   |
| WI-2300  | 77 G  | T | GGCAGAGAAG<br>CCAGTCATAC            | GGTTGGGTCAA<br>TTTTAAAGCA       | TTTCATCATGCTGCTCTTCCCTGGAAATTTCCCTTTATTGAGCGGGCAGGTGGTAGGCACAGAAGC<br>CAGTCATAC(G/T)TTCCTTTAAATGACCCCAACCATTTACTAAGAATAGCATTCA   |
| WI-2371  | 55 G  | T | GTCTTGTTCTT<br>CCAGCTTCT            | CAAAGATTGAC<br>AGCCACCAC        | CAATGATCCCCCAACATTTCCAGGGAAGGTCTGGTCTTCTCCAGCTTCT(G/T)GTGGTGGCT<br>GTCAATCTTTGACATTTCTTGTCTTGACGCTGTATAATTCOAATCCTTGCCTCCAGCTTTACATGATGT<br>TCTCTCCGTGTGTGTG   |
| WI-2395  | 122 A | C | GAACATATTT<br>GTAGAAAAAT            | TCACCTTTCTA<br>TTTATTCTGAA      | GGGGGCACAATTTAGCTACAGTGCATATTTAAAGATAACATAGAAATATCATATAAATTAACCTTGGTTTAC<br>TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTATCCAA(A/C)CTGAATTC<br>AGAAATAATAGAAAAAGGTGAATCATCTTATATCATTAAAGAAAGCTAAATTTATTAGTAACAATCTTTA<br>CATTTACACAAACCCA |
| WI-2437c | 192 G | A | ---                                 | ---                             | CACCAGCCACCACCTTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT<br>CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA<br>ATAGTGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAAACATCACAGTG(A/G)GCTGTG<br>GTGCCAAGGACGCATTATG       |
| WI-2437b | 179 G | A | ---                                 | ---                             | CACCAGCCACCACCTTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT<br>CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATCCCAATG(A/CTC<br>TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAAACATCACAGTGGGCTGTG<br>GTGCCAAGGACGCATTATG       |
| WI-2437a | 128 G | A | ---                                 | ---                             | CACCAGCCACCACCTTACAACTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT<br>CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATCCCAATG(A/CTC<br>TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAAACATCACAGTGGGCTGTG<br>GTGCCAAGGACGCATTATG       |
| WI-2440  | 71 G  | A | GCAACCTACT<br>GACAAITTA<br>TTTTAGTT | AACAACCTGTC<br>TATTGGTCTCA<br>C | CAGTAGGAAACGGGTCTTCTTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA<br>GTTG(A/G)GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT   |
| WI-1356  | 123 T | C | TGTTTAGGAA<br>ATAATGACAA<br>GAAAA   | TGGTTACAAC<br>GTACCAACAT<br>G   | CTGTAACCTACACACATCCTCCTGTAACTCTAGGTTACTTGTAAATACAAAAACAATGTAAATGCT<br>ACATAAATAATTGTACATACTATTTGTTAGGAAATAATGACAAGAAAAAGCC(T/C)GTACAT<br>GTTTGGTACAGTTGTAACCAGCCATTTTCCCCCAATATTTTCAATCCACAGTTGGTTTAAATCCACAG<br>AAACCACGAATG                    |
| WI-2886  | 46 C  | A | CAGAGTCTGG<br>GGGAGAAGA             | TTGCCATGCTT<br>TATCTCGTT        | ACAGTTAAGAAAAAGGTGCAGCCGTTGCAGAGTCTGGGGGAGAAGA(C/A)ACGAGATAAAGCATG<br>GCAAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA<br>TAGGAGGAGGGCTAGGCAAGGAAGGTGTGACAGAAACAGAGGAGCGTT   |

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| WI-2906b | 77  | T A ---        |                       | ---                         | CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATCTGCTGGAACCTTGGCTGGAATGCTCTTTCCCTCTG/A/GAGCTTTGCTGGCTTACTTTTCTTTTCTTTAGGTTTACAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA  |
| WI-2906a | 50  | A C TCTTGCTGG  | GACACCTTCAT           | AGAGCATCCAGGCAAGT           | CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATCTGCTGG/A/CJACTTTGGCTGGAATGCTCTTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTCAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA  |
| WI-1736  | 175 | C T ---        |                       | ---                         | TACTCCTCATTCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCCCTAAATAGATTTCCACCCCGACACTATTTACACAGAAACAGCATGGAGCAGTTTGGAGTCTGGCTCTTAGAGAACCTTACTTAAGGACAGTGGTTTTCOCATCTGCTTCCAC/C/TAGAGATCTAGGGTGTCTTTTGAACCACCTTGG |
| WI-1851  | 136 | G A GTGTTAAGTA | GCATTGAATT            | CACTAGCAATGTTAACTGAAGTTG    | AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTATCTGGGGAGGACACAAACATTTAGACCATAGCATTGAATTAAGTATAGATGTGTTAAGTAAATTATTAACATGGTACA/G/AJACAACCTCAGTTTAACATTGCTAGTGATCCATGTGGATACCATGTACCTTCTTACATCATGTGA         |
| WI-3000  | 62  | G A AGAGACCCC  | CCCAAACAC             | ATTGACTAAGACTCA             | CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTACAGACCCAAACACAGAGACCCCG/G/AJTGAGCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT   |
| WI-1754  | 177 | G A TAGTC      | TTTTCTCCCTTCTTAAAGAGA | AAAGTCGAATTGGCTCTGG         | ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACTTAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTTCTCTTTCTGTTTGTCTCCCTTCTTAAAGAGATAGTC/G/AJCCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT   |
| WI-3167  | 37  | T A TAGATTG    | AAATTCAACCACAGATCTAT  | TGTGATAGTTTGAGATGGGTG       | ACAACACAGCAAAATTCACCCACAGATCTATTAGATTCT/AJACCCCATCTCAAAACTATCACATCAAAGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA   |
| WI-3208  | 140 | G A AGATAAAGA  | GTGGAGTGGGC           | TCACTCAAACCTAGGGCTTGG       | CAAGCACACATTCAAGCAGTGGGAGGTAGGGAAGGTGGGCAACTTGGCAGCAGAGAGAGGGAAGAAGTTCAAGACCGTGGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGGAGTGGGCAGATAAAGA/G/AJCCAAAGCCCTAGTTTGTAGTGACACTGTGGGGATTCAAG                            |
| WI-1775  | 47  | C T TTTTCTCTG  | CCTGCATGGTC           | AGTTGAGATTTATGACAATGATGTAAA | ACTCCACCAACAGTTTGTGAGCCAAACCCCTGCATGGTCTTTTCTCTG/C/TJTTACATCATTTGTCATAAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA   |
| WI-3402  | 55  | G A ACAT       | AGCATATTCA            | GAGGACTTAAAGAGGACATTTG      | CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTTCATTGATTTCCCTTACAT/G/AJCAAATGCTCTTTTAAAGTCTCAACTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCTTAGGA  |

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| WI-3416  | 33  | C T | CCAAAGTTGTA<br>GCATTCAGAA            | ACGAGCACAA<br>CTACCTCTAAG<br>AG | TCCTGGTTCTCTCCAAAGTTGTAGCATTCAGAAGTC/TCTCTTAGAGGTAGTTGTGCTCGTCGTTAA<br>TATGTTTTCAAGATAGTATCTCCCTGTTGTCACTTCTCTCCAAACAAGTGTACCAACAGCATTTGTTAAG<br>GAAATGTGCAATGCTTGCTACCTCTGACGCACAACATAATTAATCCCATTCCTCTAAAGACACAGG   |
| WI-3453  | 70  | C T | TTCTTAGGCC<br>ATCAGAGAA              | TCAATTTTCCC<br>CATGACTTC        | TCCTATTCCTACAACAACAGAAATTTAACAAATTTGAAATCAGCTACTCTCTTAGGCCCATCAGAG<br>AATC/TJGAAGTCATGGGGAAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG<br>AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAAGAC   |
| WI-3474b | 109 | G A | ---                                  | ---                             | CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA<br>GTCAGTTTCCCTAAATTTTAGCACAGTATTTAATGAGGTGGT[G/A]TGGGAGAAAAATTTGATGGTTGCG<br>TAGTTGAGTTTCTGTCCACC  |
| WI-3474a | 90  | A G | AGTCAGTTTCC<br>CTAATTTTAGC<br>AC     | CAACCATCAAT<br>TTTCTCCCA        | CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA<br>GTCAGTTTCCCTAAATTTTAGCAC[A/G]GTATTTAATGAGGTGGTGTGGGAGAAAAATTTGATGGTTGCG<br>TAGTTGAGTTTCTGTCCACC  |
| WI-3502  | 79  | C T | CCTGGGTTTCT<br>GGATGTCT              | GGGTGACCTG<br>TCCTCA            | TTTGACCCCATACATGAGAATAAAACCATAAGAAATGGTGGAAAAATAAAACGGGAGAGACCTGGG<br>TTTCTGGATGTCT/TJGAGGACAGGGTCACCCCAAC  |
| WI-3600b | 146 | G C | GGTTCTAAAC<br>TGGATATAA<br>CATCT     | CCAGTGCAGCC<br>TTCCAT           | TCACGGCAAGTTCTGCAGCAGTGTCTTACTCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCTG<br>ATAGTTCTGTGAGCCACCTAAACTCGTTTCTCGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGGATA<br>TAAACATCTG/CJATGGAAGGCTGCACCTGGATGAGGTACAAA  |
| WI-3600a | 78  | T G | CCATGCCCTG<br>ATAGTTCTG              | GGAAACGAGTT<br>TAGGTGGCTC       | TCACGGCAAGTTCTGCAGCAGTGTCTTACTCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCTG<br>ATAGTTCTGTG/JGAGCCACCTAAACTCGTTTCTCGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG<br>ATATAAACATCTGATGGAAGGCTGCACCTGGATGAGGTACAAA  |
| WI-3678  | 125 | G T | ---                                  | ---                             | TAAATCATGCTTATTTTACAAGGTATCCACTCACAATAGGCAATTGATGTGATCTCTTTCTGTAA<br>GAAAAGCTCTCATGCTCTTCTGAACCTTCTACTTACTGTGCTGTATGATGCACCTG/TJCCCTTTGG<br>ATAGATGGTTGATAGGAGATGGGTTGTTAAGACACAAATTTACCTTGTGTGTTTCAGGCAGAAATAG<br>ACTCTCTGTGTAATCACTGAATGAGTTCCTCAAGCCTTATGCTTAC |
| WI-3687  | 67  | A C | ---                                  | ---                             | AAAGCGATGTTGAGATACCACATTCATGAAAAAGTAAAAACACACACACAAAAATATGACATAAAA<br>TJAC/JAAAAACTACTATAGTTTATGAAAATGACTTCCAAAATCAGAGAAAAAGTCACCTTAAACAGG<br>ATTCTCAATTCAATCCAGAATACTCCTCTGTCATCTTAACTTTGACTGCACAG   |
| WI-3735  | 72  | T C | CCTCAGTTATG<br>TATCAAAATGA<br>AAAAAC | GGCTCACCAAT<br>CATTTGTTTT       | TCTAAAAATGTGAAACCAAAGAAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA<br>AAAACT/CJACACCGTTCAATGAAAAAACAATGATTTGGTGAGCCATGTCCCCCTTATTTAATGAAAA<br>GATCTTGGGCAATTAATCTC   |

|         |     |              |                            |                            |        |   |
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| WI-1819 | 51  | C T ---      |                            |                            |        | GAAAAAGCAGGAAGCCAGGAGGACAAACATTTTGA AAAAGTCTTTCAGCAC[C/T]TTCGTGGATCCG<br>AATTTAGTGTGATTTGGCAGGCAATCGGGGTAAACATGTTCCAGTGTTTTAACTTGCACAGAATTGC<br>CAGATTAGCGATTGTTGACTTGTCCTCAATTAATGAATGTGGA AAAAAAAGGGTGGTAACCTGTT<br>AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGAATACC |
| WI-3746 | 116 | G A ---      |                            |                            |        | GGCCTATTACATGACACTGGCCCAAGATCTTGCTCCCTTCTTCAATAGATAGACTAACTAGAAA<br>ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTG[C/G]A]GCCCCCAGGATAAAGCA<br>GGCA  |
| WI-3867 | 49  | T C CAA      | ACAGTCATTT<br>AGTCTTCTCTGA | TAAGATAACC<br>ATACTAGGTAC  | ATCCG  | AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA[T/C]JGGGATGTACCTAGT<br>ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAAGACACAGT<br>CATTAAAGTGGAGAAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG<br>CATC  |
| WI-3898 | 25  | A C G        | TGACCAATGTC<br>TTTAGAAGCA  | TCGTGGTGTG<br>CTCTCC       |        | CAATGACCAATGTCTTTAGAAGCAG[A/C]JGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG<br>GTGAAGATGAAGCAGTGTGACGCAGCCACAAAGGTGAGGAAGAGCAAGGGTGTGCTGGCCACT  |
| WI-3901 | 114 | A G ---      |                            |                            |        | GGACCATTTGCCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCCTAACACTGTGACCTCAGGCA<br>AGTCATGTCTGCTTCTGAAACCTCGGCTTCTCACCTGACAAGTGG[A/G]TATCATGTGCTACACTGC<br>AGTGTTTATAATGCTGCAT  |
| WI-3914 | 99  | C T GC       | TGATTCTTCTC<br>AAGACTCACA  |                            |        | CTGAGGAGATTGATGCTACTTTACCTGAGGAAACCTTTTATTACCTCCCTGAGTTTGTGCTTGCAA<br>GACATTGCTGATTCTTCTCAAGACTCACAG[C/T]ACCATCCTTCTTACTTGTCTAGACCTATAACTAG<br>ACTCAAGTCCCGCAGGCCCCCTTAAAGGTAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA<br>CAAAAGAG   |
| WI-4019 | 33  | G A A        | CCAGAGCGT<br>CCTATGAATC    | AACAGCAATA<br>ACAGGAACAA   | ATG    | CCACTCCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTTGTTCTCTGTTTATGCTGTTACAGAGT<br>GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTATAGATGCTGCAGGAGACGAAGGGTC   |
| WI-4091 | 84  | A T          | TTGAGTCTTA<br>GTCATTGCATG  | TGAGTTCCTAT<br>TAAGTGACAAT | ATTGTT | TAATTCACATTGCTCTGTTTGTGCAATTTATTGCTTCTCTTATGTAACACAAATCACCACATTGAGG<br>TCTTAGTCATTGCAATG[A/T]TGATAACAATAATTGTCACCTAATAGGAACTCAAGCATAGTTATGTT<br>ACATTTATTGCTAACAGCAG  |
| WI-4160 | 117 | A G CAACAGAA | CCTATAATTTA<br>GCAACAATAT  | TGCAGGTAGAA<br>TTTTCTAATAT | AGCC   | TCCTCTCTGTAATAGGAAGTCTGATTAGATGCCTTTTGAGGTAGTTGGCTTCTTAAGATGGTAATT<br>ATCTGTCCAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA<br>ATTCTACCTGTCATCCCCCTGGATCTGAACGTTCTTCATGATACT  |
| WI-4168 | 32  | A G AAACA    | GGTGAGAGTC<br>AAATTGATAC   | ATTGCCAAACA<br>GATTTTCAGA  |        | CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[A/G]TCTGAAAATCTGTTGGCAATCTATTAAAGG<br>CAAAATATACCAGCAGTGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT  |





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| WI-5204  | 54  | C T | ---         | ---                                 | TAGATTTTGATTGATGACAATAGGGAAGCCCTTTGTTAAATTTGGGTTTTGAAGAA[C/T]GAAGAAAA<br>TGGAAAGGGAAGAATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAAATCCCAGTTTGACTGGA<br>ATATAGGTGATGICAGGGTIG  |
| WI-5215  | 70  | A G | CTCAAAAA    | AGATAATTTTG<br>TAAAGATAGTT<br>TTCCG | TTTTCCCTTATTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA<br>TAT[A/G]GCGAAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT<br>GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAAT                                 |
| WI-4448  | 112 | T G | ATATAA      | ATATAAGAA<br>ATCTTTACATG<br>GTTCTTT | CCCTGAAATGTGCTTTGCTTCTCTCCCACTCTAGGGAACCTTTCCATGTGAGGTGAAGGTTTTGA<br>AGAGTACTTTAATTAACTTGATCAAAAGAGATGGGGTATATAA[T/G]AAAGAAACCATGTAAAGATTT<br>CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGTCTATCAGTAAA                            |
| WI-4456  | 49  | C T | TATAGTTCC   | TTTCCTGTTAT<br>GCATGAACCTTG         | ACACATTTCACTTTGCTTTAAGTTGAATTATTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA<br>CAGGAACACCCAGGTGGGCAATTGATTGAATTGT  |
| WI-4461  | 49  | A G | CTTCC       | TTTGACCTTTC<br>ACCAATTTCA           | CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAATTTATCCTTCC[A/G]GTGAAATTTGGTGAAA<br>GGTCAAGAATGAATTCACCTTTTAGATTCTCGGAAATTTATTTGCGATGATAATGCAATGGGC  |
| WI-4465b | 75  | G A | ---         | ---                                 | CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAGAAAAACAGTTAGTAAT<br>TCACCTTT[G/A]TATTCTCTACCTCAGGGAATC   |
| WI-4465a | 41  | A G | ACACGAAAGT  | GGTGAAGATT<br>ACTAAGTGT<br>TCTTT    | CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAGAAAAACAGTTAGTAAT<br>CTTTCACCTTTGATTCTCTCTACCTCAGGGAATC   |
| WI-1949b | 160 | T C | TAATC       | GAGTGAATAA<br>ATGAATGCCA            | GGGGTTAGGACCTCGAGATCTTTGAGAAAGCACAATTCAAACCAATAATGGCAGTGCACAGGTAACCA<br>GTGGTGAGATGCTCTGAGT[G/C]AAGGCTGCTGACATGGTCAATGGCTGAATATATGTTGAAGAAAT<br>GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG<br>CACA    |
| WI-1949a | 86  | T G | ATGCTCTGAGT | CCATGTCAGCA<br>GCCTTG               | GGGGTTAGGACCTCGAGATCTTTGAGAAAGCACAATTCAAACCAATAATGGCAGTGCACAGGTAACCA<br>GTGGTGAGATGCTCTGAGT[G/C]AAGGCTGCTGACATGGTCAATGGCTGAATATATGTTGAAGAAAT<br>AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG<br>CACA |
| WI-4529  | 64  | T C | AAGATG      | CCAAGTAAGT<br>CTATCATTCTG<br>AAAA   | TGAGAGAGTTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATCTGAAGATG[T/C]<br>GAGTTCTCTTTATATCCTATGATTATTTTTCAGGAAGTGTATTTTGAATATAAACTCCTGGGT<br>CCCATCCAGGCTAGGGTCAATGGCATGCCATCGGTGCTGGACAAGATGGGCCCTAGGATCATTTT                |

|          |     |               |                       |                       |   |
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| WI-4540  | 110 | A G C A T C C | G C A C C A T G T G G | G A C A A T G C A G C | A G C T T T C C T T T C T T A A A A A T T G G T G C C A T A G T A G T G G C T T G C T G T G T G C A T C A G G A A G C A A G C C T A T T G C T G G T A A C A G T A C T T T G C A A T A A G C A C C A T G T G G C A T C C [A/G] T G C A T G G C T G C A T T G T C C A G T C A A T G A G A C A A C T T C C T A T   |
| WI-4582  | 226 | T C ---       | ---                   | ---                   | A G C A A G C A T C T G G C A A G C C T G G T G A C C A G A A C A T T A A T T C A C C A A A C A C C A C C T G C T C C A A T G T C C A T G T T A A T G C A A T T A G A A G A C T C C A G T A G C A T C A A G G C C A G T T A A C T T A T T C C T G T A C A C A A T A A C T T T A T G G A C A G C A T T G A A T C A A T C A A T A A T G A C T C G G T T T G G C T G T A C A A G C A T A A C A G A A C G C T T G C A A A A T A T G G T T [C] C C T C C T T G C T A G A A A C C A T T T G A T |
| WI-1965  | 105 | G C A G       | G C C A T T G A G G   | G A A T G G A T G G G | C A A A G G T T A G T T A A C T T G G G G G C A A C A C A A A G T T A T G A G T A C T C A A T A A C C T A T G T T C A A G G G T A A C C A A C A C C T T T T G C C A T T G A G G A A G T T T A A A G [G/C] A G A G A G A T G A C C C A T C C A T T C C T G G G C T T C T A T A T G A C A C C A T A C T A T T C C A C A C A G A T G T G G A G T C A T T A T T T G G T T G G T A T G A C A G T C A T G G   |
| WI-5248b | 99  | C T T T G     | ---                   | T C A T C T C T C T   | C A T G G   |
| WI-5248a | 38  | G C           | A G T T T G T G C T G | T T T T A A T T T T C | T G T T T A A A A A C C A T A C A G T T T G T G C T A C G T T G T T A G A G A C A C C C C A G A A A A T T A A A A C G C C T A C A T T T T T C A C T G T T T C T A T T G A C C G T A C T T G [C/T] C T T T G C T T T T T T C C C T T C T C T C T T T T T C T G C C T C T T T T A A C T A T T   |
| WI-4596  | 69  | T A           | T G A A G C A G A A   | C A G G A G A T G G G | T G T T T A A A A C C A T A C A G T T T G T G C T G C T A C G T T G T T A [G/C] A G C A A C C C C A G A A A A T T A A A A C G C C T A C C A T T T T C A C T G T T T C T A T T G A C C G T A C T G C T C T T T T T T T C C C T T C T C T C T T T T T C T G C C T C T T T T A A C T A T T T G A C A A G A T T C T C C T T T T T A A C A A   |
| WI-5252  | 119 | A C ---       | ---                   | ---                   | G A A A T A G G G C A A A A T T A A G A C T T C A A T A A T T A A G A A G T C T T G G G A A A A G G A T T T G T G A T G A T C A T T G A A T C T G T T T A A A T A C A G A A T T A A C T G A A T A C C T G T G T G A A T C A T T G C T T T T A [C/T] A C C A T G T A C A T A T A T G A A T T A A C A A T G T A A A A T A G T A T G A C T A A G A A A A T T T G G G C C C T   |
| WI-4606  | 61  | A G C T       | G C A A T G C T A G   | T T A G G T G C T T A | T G C A A A A A A G G A A A A T G A T A A C A G G A C T G T T G T T C A A G C A A T G C T A G A A A A A T T A T G C C T A [A/G] C C A A G T A G A C A A C T T A A G C A C C T A A G G C A G A A T G A A G T T T C T C T C T T G T C A T T A A G T C C T C T A T T C A A T T A C C A T T T A T C G G G T A A T T A A C A C T G G A A A G T A A T G C C A G G C T A A T T G T T A G A T T A T G A T A A T T A C A C G C T T T T G C T A T G C T   |
| WI-5257  | 77  | C A           | G A G G C A T G A A   | C C A G G G G C A G A | C A A T G A G A A G T T A C C A G A T G C G G G G C A A A T T A A G C A T A T G A A A A T A C C A A G T G T T G G C A G A G G C A T G A A G C A A A G A G G [C/A] C T T T C A T C T G C C C C T G G T G G G T T T T C A G T A A C T G C A A C A T G C T T T T G C C T C C C G C C T C C G G A T G A A A G A T A C C C T T C T A T G A C T C A G C A A T T C C A C T C C T A G G T A T G C A C C C T A A A C A T A G G G T G C A A A T   |
| WI-4649  | 50  | C T           | G A G A C C A T T C T | T A C T T A C A A G A | T C A C T G T T T A G A A A T T C T C T C C T C A G T G A G A C C A T T C T T T C C G A A T G [C/T] G A T G A T T T C T T G T A A G T A C A C C T A G T A C A T C T A T G A G C A C A C A A T T A A C A A G T A C T T G C T A C C T G A A T T T G T A T T T T T T A A A A A T C C T C C C A A T A T T G   |

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| WI-4650 | 148 | A | GCACAAAGAA<br>AGTATAAGTT<br>GTCTCTT | CTGAAGTGTTA<br>AACTGGATTGG<br>G       | AACTGTGGTATGTATTGTTGTGATTTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG<br>GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAGACACAAAGAAAGTATAAGTTGTCTC<br>TTATATTGCTTTT[A/G]CCAAATCCAGTTAACACTTCAGTAACGTT  |
| WI-4677 | 82  | T | C<br>AAA                            | TTTCAACAGTG<br>TCATTATTCAA<br>CTT     | AATTCAGATTTTGAACATACGTGACATTTTGGAAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAAT<br>GAGTTGAAATAAATGT[C/A]AGTTGAATAATGACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA<br>CATGAAAGGAGACTAGAACACACAGCAGGTTTATAGGGGAATACTCAT   |
| WI-4698 | 135 | C | G<br>---                            | ---                                   | ATGATGCTATCATGAGGAATTTCTGAGAAAAATTTTACCTGGCAATGATTCAAAATAAGATTGTGTC<br>TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTTCTTTTGACGGGAAGAAAACTTCAA<br>C/GTTGAGAAAGGCTTAGATTATATCGCTGAAGCCCATCTG   |
| WI-4722 | 88  | G | A<br>AACACCACAC                     | AATATGGAATC<br>TGCATTGAGTT<br>G       | CTTCCATTCTGCCAGTTAGATGACTGCCTCTCCACCAGCTAGAAAAAGATGGGAGATTTATTTTC<br>TGCACTATGGAACACCACAC[G/A]CAACTGAATGCAGATTCATATTTGAATACTGGGAAATCAGTGA<br>AAG   |
| WI-2020 | 145 | C | A<br>---                            | ---                                   | GCCACAGTAAAGAGGAAAAATGGAGCCATGTAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA<br>TAAAGGTCAGTAAATCACTTTGATGGTTGAGATTTTCAGAAAAACGTGAAATTTATGAGTAACCATGGG<br>TCAACTATGAT[C/A]CCAAAAACAGCAGTGTGTCTAAAAAATATGATAGTTTCTTCTCCTGTCCACC<br>GCAATGAAAAAGGAGTT |
| WI-2028 | 176 | T | C<br>CCTGTCTCATC                    | GGTTGGAAACT<br>CAAATTACCTA<br>GAA     | GACTACAGCGCACAGACAGGCAATGTGTGGCTTGACAGGTTTGGTTTGTGTTTAAAGTTAGATT<br>TGAATCCTTTAAAGAAAGAAAAAGTGGCTCTTCAAGTTTACTACAGACCTCATCTCCTGGTTCTCTTG<br>CACCCAGTCCACTTCACTGTTTACGTTCCCTGTCTCATCT[C]TTCTAGGTAATTTGAGTTTCCAACC<br>TGTGG                  |
| WI-2033 | 183 | T | C<br>A                              | GGGTGCTAGA<br>ACTAATCCCTC<br>CGTTCTOC | ATGTGTATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAAATATAGTATTCACAGATGG<br>GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAAGGTTATACAGGACCAAGTTGGAAATTT<br>AGCAATTTCTGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTGGAACC<br>ACTGATATACCAAT        |
| WI-4745 | 131 | T | C<br>---                            | ---                                   | TTATGGATACATGTTTCTGGTGAAGGACAAAGATTGAAGCAAAAGGACAAAGGAGATCAACTGGG<br>TAGAATAACTCATCGATCCACAGGCTCTTCCACCATTCTCCATCTACTTTCTACTCTGA[T/C]<br>AGGCAGACTTATATGAAAAAAGGGA   |
| WI-2034 | 150 | T | C<br>CCAAGGAC                       | GGGTAAAGAT<br>AGAGTGCAGGT<br>CC       | CCACGACTATGCTTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCAAGA<br>CCTCCTTCTCGGGTTTCAGTGAAGAACGATGAACCTCTCATCTTCTACAGCAGCTGGACTTCACCA<br>CAGTGCACCAAGGAC[T/C]GGACCTGCACCTCTATCTTTACCCCTTCCGACACCCAGATGCTGAGATGCC<br>ACACTCTGAGTG       |

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| WI-2038  | 155 | C T   | ATTAAATTAG | TGTCCTTTAAA<br>GTGTGTAAGT  | ATTCCTCTTG<br>AAAGAAACAT<br>CA       | TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTCACCATTGCTGTTATTGCTCTTGCAGTGT<br>ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAAAACTGTGCTTTAAAGTGTGTAAGTATTA<br>ATTAGATTTCTATTTTGTATACTCTTCAAGAGGAAAAATTTGTGTAAGAGGATTCCCAATT<br>TGCAATTCATTGGC |
| WI-4782  | 113 | C T   | AATGC      | GATGCAGAAG<br>ATAACTAGAA   | GAACTCTCTG<br>GTTATTTTCT<br>GTTG     | TCATTGACTTTTAGAGTTCTTCACTTATGCTTTATTTCTTTAGGAAAAAACTAGGCTAGGAGAA<br>CACAAATTCAGGTTCTCTCCAGATGCAGAAGATAACTAGAAAAATGCCTGAAACAGAAAAATAACCA<br>GAAGAGTTCATTATGGTTTTTTTCCAGAACGATTAC  |
| WI-4788  | 65  | A G   | TTCC       | GCATAGAATC<br>ATCTTGCTAAG  | GGATAAAATT<br>AAAAATTTGGC<br>ATAA    | AGGAGAGTTTTGGCTCTTTCCGGACTCTTGGAAATTCAGTGCATAGAATCATCTTGTAAAGTTCCJAG<br>JTGAAAAAAAATTAATGCCAAAAATTTAAATTTATCCAAACTTTTAAGTCGAGATTATAATTGATATTT<br>AAAAAACTATATTGAGTCTTTCTTAAAGAGATGGCGTATCACTCTA                                |
| WI-5300  | 38  | T C   | CACTTCATTC | TCCAGAGAC                  | CTACTCTTTCT<br>ATTCATAATC<br>CAAAAA  | CTTACTTCCAAAGTGTTTTCCAGAGAGCCACTTCAATCTCTCTTTTGGATTATGAAATAGAAAGAGT<br>AGGTGTTATTATCTCTTTTACCAAGGTGAAATTTAGGGCTCAGAGACAAGGTAGATGATGAGCCCA<br>AGGTCAGTGACAGAGCCA  |
| WI-4818b | 121 | G T   | GGCCTGTT   | TGATAATGGG                 | CCTTCCTTTA<br>TATGTATGCCA<br>GA      | TATAATGTTTTGTTCCATAGTGGCATAGACTAGGTTATGTCCACACATGAATAAACAACTCTTATATA<br>ATAATTTATCAAGAAGGAAAAATATACATATGGGGTGATAATGGGGCCCTGTTGCTCTGGCATA<br>CATATAAAGGAAGGCTAA   |
| WI-4818a | 43  | A G C |            | TTGCCATAGAC<br>TAGGTTATGTC | CATATGTATAT<br>TTTCTCTCTG<br>AATAAAT | TATAATGTTTTGTTCCATAGTGGCATAGACTAGGTTATGTCCJAGJACATGAATAAACAACTCTTAT<br>ATAATAATTTATCAAGAAGGAAAAATATACATATGGGGTGATAATGGGGCCCTGTTGCTCTGGCATA<br>CATATAAAGGAAGGCTAA   |
| WI-5317  | 139 | T C   | GTAGCAGGT  | TTCCATTTCTG                | GATGCAAGA<br>AGAAATGAGTC<br>C        | TTTTTCCATTTTGTGATTCCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT<br>AATATAATAATATGATGTTATATATTACAAATTTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT<br>ATACTCTGGACTCAATTTCTTCTTGCATCTATTTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG              |
| WI-4888  | 56  | G A   | AAAGATAACA | GCAAGATATA<br>AAGATTAAAG   | CAATCCACTA<br>CCTCATTTAT<br>CA       | AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA[G/A]ATGAAT<br>AAATGAGGTAGTGGAAATGCTTGATAACTGGAGTAGTGCCTT   |
| WI-5328  | 44  | A G   |            |                            | ---                                  | AACATTTTTAACCATGCTACATTTAGAACACTGAAAGACAGJAGJAAAAAAAAGAAATATTTTG<br>CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAAAAT<br>AGAAACACGTGATCTGGAAGGAG  |
| WI-4897  | 93  | A G   |            |                            | ---                                  | GCTTTTTGAGTTAAGTCTTTTGTGAGTGTGCTTTTTCCTCCCACTAGGTACTCTCGGCCCAAT<br>CCCCAAAAGAAAAATAAGCGCTTGGJAGJGATAAACACATCTTC  |
| WI-5345  | 29  | G A   |            |                            | ---                                  | CCCTGCTATAGGTGAGTTTAAAAATCCTGJAGJCCCTGCTATGGTTGCTTGTGAAGCCACATCCAGT<br>GAGGTATATTCTGCTGCATTTTCTATATCACTCAGCTTCAGATCCACTCCATCAACTTGCAG  |





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| WI-7593  | 46 G A ---       | ---                               | TTTGTGCTCTGGACACCCACTGCTCCAGGATGAAAGGAGAG[G/A]ATGAGATCAGTTTGGG<br>CACTTCTCTTGAATATAAAGATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCCAA   |
| WI-6962  | 78 A G ---       | ---                               | AGTGATCTTGGGGAAGGCTCCAGTGTTATCTGGACCAGTTCCTTCATTTTCAGGTGGGACTCTT<br>GATCCAGAGA[G/G]ACAAAGCTCCTCAGTGAGCTGGTGATATATCCAAAGACAGACCCCAAGTCTCC<br>TGACTCCTGGCCTTCTATGCCCTCTATCCTCTATCATAGATAACATTTCCACAGCCTCACTTTCATTCCAC<br>CTATTCTGAAATATTCCCTGAGAGAGACAGAGATTAGATAAGA |
| WI-7059  | 43 C G GCCATC    | AAGGCACCCA<br>GGTCA               | GCAGAGAAGAGAACCATGCCAGGGAGAGGCCACCCAGCCATC[G/G]TGACCCAGCGAGAGCCAA<br>CTATCCCAATATACCTGGGTGAATATACCAAATCTGCATCTCCAGAGGAAAATAAGAAATAAA<br>GATGAATTGTTGCAACTCTTAAAAAA   |
| WI-9063  | 53 A C TT        | CACTTCACTGA<br>AAGACACCAT         | AGCAGCCATCAGATGCTGTTTTCACCACTTCACTGAAAGACACCATTTAT[A/C]ATCCCAAGGG<br>CAGAAAGTAGAAGCTTACTTATTAATGTTTGACACAATTTGGAATTGTC   |
| WI-7079  | 293 T G ---      | ---                               | AAGGGCATTGAGACTATAAGCAGTAGACAATCCACACATACCATCTGTAGAGTTGGAAGTGCATT<br>CTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTCTTCTTCTTCCATTGCT<br>TATCTTGAGCACAAATGATAATCAATTATACATTTATACATCACCTTTTGACTTTTCCAAAGCCC<br>TTTTACAGCTCTGGCATTTCTCGCCTAGGCCTGTGAGGTAACTGGGAT         |
| WI-9074  | 38 A G AAAAG     | GGTAAAAGTT<br>CTTTTGCTCT<br>TT    | TGGATGCCGAGTAAAAGTTCTTTTGTCTAAAAGAA[G/A]AGGAACTAGGTCAAAAATCTGTCC<br>GTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAATGTAACTGT   |
| WI-7104b | 249 C T ---      | ---                               | GGAGTTGCCCTTCTTAAGGAAGGAGATCTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA<br>GAAAGAGAGAGTGCAGGAGACCTGAGGGCAGCCGTTCTTCTTGGACTGAGAGAGGAGGCC<br>CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT<br>GTGAGGCTTGACACAGGTGGGGCCACAGCACAGCATCTTTG[C/T]              |
| WI-7104  | 157 C A ---      | ---                               | GGAGTTGCCCTTCTTAAGGAAGGAGATCTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA<br>GAAAGAGAGAGTGCAGGAGACCTGAGGGCAGCCGTTCTTCTTGGACTGAGAGAGGAGGCC<br>CCAGGCTGGAGCAGCATGAGGC[C/A]CAGCAAGAAAGGCTTGGTTCTGAGGAAGCAGATGTTTCAT<br>GCTGTGAGGCTTGACACAGGTGGGGCCACAGCACAGCATCTTTGCT           |
| WI-8974  | 34 C T AAGAACTCA | CCTGAGCCTC<br>GCTGGC              | CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTAGCCCTACACCAGTTTCCACC<br>TGGAGTTCATGCAAGGGCAAGGAGTGCATGCAAGCTGTTAA   |
| WI-9161  | 61 C T CTTGGC    | GCTTACAGGAG<br>AGACTAGACA<br>GGAA | CTGTGAGGGTGACGTTAGCATTACCCCAACCTCATTTTAGTTGCCTAAGCATTGCCTGGC[C/T]TTC<br>CTGTCTAGTCTCTCTGTAAAGCCAAAGAAATGAACATTCCA  |
| WI-9014c | 93 T C ---       | ---                               | CCCTGTTCCCATGCTGACCTGTTTCTCTCCCAAGTCACTTCTCTGTTCCAGAGAGGTGGGGCTGGAT<br>GTCTCCATCTCTGTCTCAACTTTAT[C/G]TGCACTGAGCTGCAACTCT   |

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| WI-9014b | 44 C T ---  | ---                                 | COCTGTTCCCATGCTGACCTGTGTTTCCTCCCCAGTCATCTTC/TGTTCCAGAGAGGTGGGGCTG<br>GATGCTCCATCTCTGTCTCAACTTTATGTGCACTGAGTGCACACTTCT   |
| WI-7023b | 206 C A --- | ---                                 | TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCCCTGGTGCT<br>CAGTGCCCTTTAAGTGCAATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGTCCCC<br>TCCTTTTGGCCCCAGTATTATGCGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTTCAACAC<br>A/C/AJACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA |
| WI-7023a | 56 A C ---  | ---                                 | TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/A/CJCCCTGGGT<br>GCTCAGTGCCCTTTAAGTGCAATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGGTC<br>CCCTCTTTTGGCCCCAGTATTATGCGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTTCAA<br>CACACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA   |
| WI-7093  | 54 C T ---  | ---                                 | CTGAAATCCCTCTCTGCOCTGGCTGGATCCGGGACCCCTTGCCCTTCCCTTC/TJGGCTCCAGCC<br>CTACAGACTTGTGTGTAACCTCAGGCCAGTGTCCGACCTCTCTGGCCCTCAGTTTCCAGCTATG<br>AAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAGAAAGCTGGAGGAGGCGGTGGGCCAAT<br>GGGAGAGCTCTTGTTATTATTAATATTGTTGCCGCTGTGTGTTGTTA                |
| WI-9171  | 62 G A ---  | ---                                 | ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAGAAAGTAGAGATAATAATCA[G/A]<br>TTCTTTACACCGATGGTAATTAAAGCTTGATTACAAAGACTTCAIGC  |
| WI-9174  | 47 T C T    | CTAGGACCCC<br>ATTCTCCTATT<br>ACTG   | GTGTGAGACCATCATGGTGCCAGCTAGGACCCCATTCCTCTATTAT/CJGAGTCCCTGTCTATATA<br>CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAATTGAG  |
| WI-7753  | 52 A G      | CCATGTTCCGA<br>GAAGAACAGA<br>A      | AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAGAACAGAT/GJATCCCTGTATT<br>TCAAGACCTCTGTGCATTTATTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCTCAGGCTA<br>AGCTGCCGGTTCTTAATCCATCCTGCTAAGTTAATGTTGGGTAGAA  |
| WI-9186  | 76 G A      | CCACTTCTCCC<br>CGCA                 | AAAGAACTACAGAGGACGATGTCCAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCACCT<br>TCTCCCGCA[G/A]ACCTAGGTGACACTTTCCCTTTCACTT   |
| WI-9193  | 94 G A CA   | AGAATATTGT<br>CTGCCTTAAAG<br>CA     | TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTGAGCAATTGACAGAGATAA<br>CTCAGAAATTGCTGCTGCTTAAAGCA[G/A]TACCCCTTACACACACACCCCTGTCTC  |
| WI-9015  | 48 C T ---  | ---                                 | TTTGATTGATATCGTGAATCTCAGCCGAGAAATTCATTCCAGGTAGCTGGCACCACTAAGAA<br>CTTTCCCTAAAGAGATAAACACAAAATCCATTCCAGGTAGCTGGCACCACTAAGAA  |
| WI-7254  | 37 A G      | GGTCTGAGAG<br>AGGAGCAC<br>CATTAGGGA | GGAGCCAGGAGACAGCAGGGTCTGAGAGAGGAGCCAC[G/G]TCCCTAATGACACCCACTCTAGCC<br>CTGAGGCTCGTCCCTCAGACTGGGAAAGAGTCCAAAGGAGGGGAGGAGCAGCCACTCTCAATGC<br>TCAATGGCTCCCTGAAATCAAGACAGG   |







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| WI-7424 | 131 T A | CAAGAGAGAG<br>AGAGGAAAGA<br>A AAA | TGCAAGAAA<br>GAATGAAAGTT<br>G | CCAGGAGCACTAGAGAGGGGGGAGAGCAGAAGTTAGAGAAAAAAGCCACCGGAGGAAAGG<br>AAAAAATCGGCCAACCTAGAAACGTTTTCATTCGTCAATCCAGAGAGAGAGGAAAGAAAA<br>TTA)ACAACTTTCATCTTCTTTCACAGTTTCATAAACATTCACATA  |
| X86400  | 118 A C | ---                               | ---                           | TCCTGCAAGAAGTTCTCAAGCCTTTTGATTTTGTGCAATAAAGTACAGCTTTGCATAAGAGTGA<br>TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTAATTTTAAAGTGAGA)C)TCTTTTAAACACCT<br>GTTAAATTTAATGTAGCAGTCTGAGAATCTAAATATGTACCACTCGTTTATTTGTTTCATTCATCCA<br>TCCCTTTCCCATGAATATTTCA                                |
| WI-8053 | 242 T A | ---                               | ---                           | GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCAGCTATGAATAAAGGCTGAG<br>TTATCACTAAGCAGGAGAAAGCATTAAAGTGTCCTCATTAAGGGACITTTTATCAACCTAA<br>TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAITTTATACATGCTGAAAAGGGTCCACA<br>ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAA)T)TTCAGAAC               |
| WI-6190 | 165 G A | ---                               | ---                           | TACAAATGAATGCTTTTATTTGGGTATGCATCCACATTCAGCATTTAGTGTCTGAACAGCAAG<br>TGAAAGACGCAGCAATTTGCCAGGAGTCAAGCCACCAATTTCCGGGATCTGCTGTGCACACCGG<br>GTTCTTCTTAATCCCTGCTGAGGATCTTG)G)A)GAAGCAGCAGCAGCACCACCAAGGCATGCA<br>COGGATTCAGGTTCTTTTGTCCAGTTGTCAGATTCCAAACTAGACCCCA            |
| WI-6275 | 148 G C | ---                               | ---                           | AACAGTCACCACCAACCATGACATGACAACTGCCAGGCAAGGCTTGTCTCCCTCCCTTTCGCTCCC<br>ATGTGCTAGTCAGCAAGGTGGGGAGGCACCGATGTTAGCTTCGCCAAAGGGAGTATTACAGAGA<br>GAGGCTTGGGAA)G)G)GAAAGGAAACCTGGACAGGCTTTTACGACTGAGAAATCACTTAAAACTG<br>ATTTGCTTTTCAGTAACTGGTATGTCGAA                           |
| WI-6421 | 41 G T  | ---                               | ---                           | ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGTTG)G)GGCTTCTGAAAGAAACCTTGC<br>TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGGCTCTCACAAAA<br>GAATATTTGGGCGAGAACCTTGAAGTGGCCACGAGGACATCCCAATATCCCTCCTCCTCAGGG<br>CTCACCCCGACATCCTCAGCCCAATGAAGGCTCTGAA                        |
| WI-6905 | 215 T A | ---                               | ---                           | GGGTGAGACGGGTTTATTGTGCACATTTACACAGCTCACAGCGTCTGGGCTGGCAGCGGCCATGCTC<br>CTGTGGTGGGCTGCTCTACAAGGGCGTTCACTTTCTTCCACACACTATGTACAGTCAAGTGTCCAA<br>GGTGATGGGCTACAGTGTGTCATCAGTGAGTCTGTACACACATTTTACATAAATACACACGACTC<br>ATACATGA AAAA)T)A)JAGAGCCTAAGGGCCTGTATTTTAAATGAGAAAAA |
| WI-9420 | 202 G A | ---                               | ---                           | AACCTGTTTACAAAATAGGCTTTCACAACTTCATTACTGAATTTGTAAGTCAATGACTGTGTTGTTT<br>TAAAAATGTACCAAGGAAATACAAATGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC<br>AGAAATAAGGATACCTGCACAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG<br>G)A)GCATCTTCTCACCTTAACCTGACAGCTGTGCAAGATGCCTCAGTGTG  |

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| WI-9448  | 184 | G A --- | --- | TGGGGCTGCTTTTAGACTTCATTCTTAGAGCAGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC<br>TGCCCTTGCCCATGGTGGTTAAACCTACATAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC<br>TTTTAAGAAAAATGGCTTGGTTCCAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA<br>TCTCTGGCTTGGATTTTATCCAAGGCAATGTTCTTAAGTGGCCGTGAGCAG |
| WI-9470  | 204 | G A --- | --- | ATGTCAGAAGAGACACAGACAAGGAGTTTTCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA<br>GATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCAGGCTTTTCTTGTCAGTCCGCTTA<br>TGAGATCAGGAATATGATCTCCCTAAAGCCCCAGATTCTACTAGAGCGCTGGGGACACTGATGAC<br>AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACAGGGCTCACCTTCCCAG   |
| WI-1245b | 201 | G T --- | --- | GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAGGAAGAGTAGGTGTTAATGGCA<br>TCCTAGGGCAATGGTAGGTCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGGT<br>TTATTAATTCATTATCATCTGACAGCCCTTCTTATAACGTACATCCTTGCCTCTCTGAGGCG/G<br>TCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA                    |
| WI-1245a | 85  | T C --- | --- | GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAGGAAGAGTAGGTGTTAATGGCA<br>TCCTAGGGCAATGGTAGGTT/GCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGT<br>GGTTTAAATTTTCAATTTATCATCTGACAGCCCTTCTTATAACGTACATCCTTGCCTCTCTGAGGC<br>GCTAAGATCCCAAGGTGGCTCCTGTATCCAGAAA                  |
| WI-1031  | 149 | G A --- | --- | TTCAAGTAAAGGACAGGCTAGAACAGCGTTCCCAACCCCTGGCACCATAACAGTGGAGTGGACAAA<br>TAACCTTTGTTTCAGGGGACTGTCTACACATTTGGGATGTTAGCAGCCTCCGTGGCTTCTACCCA<br>CTAGATGCCAGCA[G/A]CACAAACCCCTCCCAACAATCATGACAATGAAAATGCTTTAGACATT<br>GCCAAATATACCTTGTGGACAAAATGGCCCTGATTGAGAACCACTGGTT     |
| WI-5385  | 110 | G A --- | --- | AATGAGTCATTGTGGAGTTAGAGGAGTTACTGAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG<br>GAAAGTCGATAAATTTAACATATGTTTCTTCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA<br>TTCCTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCCTGAC<br>CCCTGCTACGGGAACAATTGAATGCA                       |
| WI-5403  | 199 | T G --- | --- | ACCAACCCGTTGGCAAAGGCTCCCCAAGACTCACCAACCTTTGGTGCTTACCCTATGCCGGGTG<br>GGATTGAAGAAATAACCATAAATATAATTGCTACAATTTTCCAGTAGTTACCAGGCACAGCCTAT<br>TGGAGAAATCATAAATGTAAACCTACAATGATTGCTCTGCTGGCTTGGTGCCAGGCATAGAGTT/G<br>JGGCCTACAACCCATTTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT |
| WI-5801b | 157 | G A --- | --- | TGGTATTTTCTTTTCTTAAATGTTATGATTAAATAGTGCTTTGTAGAAATTTGAAAAAATGTAAA<br>TCAGAGAACAGAAAAATAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG<br>GGAAGAAAGAAAGAGCCCTGGGA[G/A]AGGGAATGAGAAAAAGCACACCAGAAAAAAGTGTGT<br>GGCTTAAGGGGAAGCCCAAGGAAAGTTAAGT                           |

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| WI-5801a | 48 A G ---  | --- |  | TGGTATTTTCCCTTTCTCTAAATGTTATGATTAAATTAGTGTCTTTGT[AG]GAAATTTGAAAAAATGT<br>AAATCAGAGAACAGAAAGAAATAAAGTATAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCC<br>TAGGGAAGAAAGAGAGCTGGGAAGAGGGAATGAGAAAGCACAACCAAGAAAAAAGTGTGT<br>GGCTTAAGGGAAGCCAAAGGAAAGTTAAGT                          |
| WI-5696  | 61 C A ---  | --- |  | TTCTATTTAAATCTGTGCCCATTTGCAAGACTGCATTAGTCTGCATGAGCCTTAGTTTC[CA]TAA<br>AAGCCCCCTCACACCGAGGACAATGTTCAGAACTAAATGACTGCAGGTGAGCAATTTCTCTGTATTA<br>TACAACTGGACCAAAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC<br>TTATAATAGATTATAAGGCTGTGGTGAGTTTATTTAACTT            |
| WI-7461  | 153 C T --- | --- |  | TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC<br>AATTCTAAGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTCG<br>TGGCAGGGACTGTGTCTC[CT]GTTCCCTGTTGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG<br>GAGGCCCTGAGTAGCATGTGCTGCA                         |
| WI-9716  | 221 G A --- | --- |  | AGAAGACAGGAGCACTGGGATCAAGGACTGATAAAGTCTGAGGCTTTAATGGTCCCTTGCTCTAAC<br>GCTTTGGTATACTTCTCTTTCTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT<br>ATTCTGATGTTTCAGATGTGTAATCTCTACATCTGGAACACTAGATGAGTTAGGCTCTCTTCATCT<br>CAATTGAAATTTCTAGA[AG]A/AAACACCTAATTGGCTCATCTTGGATCA |
| WI-9760  | 49 C T ---  | --- |  | TTTTGGTTAAGTCTTGTGAAGCCACACAGAAGTATCTCTCTTTAC[CT]AAGTGTACTTTTGCA<br>TATATTTATGGGATGATCTATCCCTACTTAAGATTCTCTCTCAGGTTAAATATTCATTTCTCT<br>TTGTCAGGAGTTTCTTATTTGGCTTCTTTCTAAACCTTAAACCATCTGCTTATCTCTGCTTGACA<br>CATGCTATTTAATCAAGGTGACATT                                 |
| WI-9855  | 31 A C ---  | --- |  | GAAAACTCGTTGGCTCAAAGGAAACTGTAG[CA]AATCTTTTTTTTTTTTTTTTAACTC<br>AAAGAGTGGAGTTTGCAATTGACCTTGATGGCAGCTGCTCTTTTGTGTTGGTAAATCCTCTAGT<br>GGGCACCTTGCAAAAGCAATTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAG<br>TAGCAATGGAAGAAAGGTTAATGGA                                   |
| WI-10312 | 41 A G ---  | --- |  | AAGCCCCAGTGGGAAAAGCAGACAAACACTCCAAGAATAC[CA]GAGATATAAACATCATCATCA<br>GTAGAGATGGATGACCTAGGAGGTGATGCTGATGAGGATGTCAGACCAAAAGACATTTGGGTCT<br>TGAGGTTGAATAGGAGTTTGTCTGTGAGTCTTGCCAGTCCCATAGTAGGTTGCCATAAATAAAC<br>AGTGAATAAAGTGAAGTACAGACAGAAAGAAATTTCA                    |
| WI-11152 | 179 C T --- | --- |  | GATCTTTGGCAGATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACAGCCCTA<br>ATTATAGAAACAGACTCTACAAGGACCAAGTTAAAGGTCTGCACCCAGGGGACTGGGTGGCCAAAG<br>TCAGTCAAGGCATAAAGGGGGACAAGTGGGACAAAAGGCTTGTCAC[CT]CTGTCAGAAACATTGAA<br>AACAGCCAGTACATGCCACTGATAGA                          |

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| WI-1968          | 167 A G --- | --- | TGGTGAGGAGCTGTAAAGGCTGAAAGAATAGTCTCTGCTGGTCTTTGTTGGAATGGATGAGTCCT<br>TTTACAAAATTTTCTCTGGCATGGGTGTTATGTTAGAAATCATGGAGTTGGAAGACTTAGATTCA<br>ATTTGGGGCTGTACAGTTTACTGGAAGTTGT[A/G]TGAACCTTGAGCAAGTGCTCTTAATGTCCTCA<br>GCCTCAATGCCCTTCCCTGTAA                              |
| WI-4701          | 198 G A --- | --- | GGGTTCAATTAACAGCCTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGATAG<br>AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACACACATTAAACTCCTCCCACTCTA<br>CCGCGCAAGTCTACCTTTGGTCTTTTATTCTGCTAATGACCATACTATTCCCAATTAGA[G/A]<br>CCATGTCATTTTCAGAAAAGCAGTATA                              |
| WI-4823          | 164 C A --- | --- | TTTATCTTCCAAACCATGTGTGTTTCTTCACATACTTTACGTAATTTAAATCATGTCATTTAATTA<br>TGCACTTACTTGTGGCTACAGACATTGCTTCCAAATTTGTAATTCCTTAACACAGCAAGCATAACT<br>GATGTCCATCTTGTATTCCTAAA[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGT<br>CTTCTCTGTTTCACTCTCTGTTTCCCTATTCAGCATTCATGATTA          |
| WI-4860          | 72 A G ---  | --- | AAAAAACAACTTCATTTGACATTTAAGAAGATAAAGAAAAACAACGATCCACTGTGTGTTGCTT<br>GATTT[A/G]GGAGATAAACCTGATCTCTAAGAAAAATTAACCAAGCAGTACACTAAAATAGCCT<br>TTGTGTGTGTTTTCAGGAAAGAAAGCCAAATCCAACTAAGTTGCTAAGAAAAATAATGTTTCATATCA<br>CTCTAATCTCCACATAGAGCATTAATATAGCA                     |
| WI-9705          | 111 C A --- | --- | TGAAGGACCAGTTTCAATGCCTACCAAGTTAAAGTAAATCGGAGGGGAGGAGTAGGAGTTGCTT<br>CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGCTGCC[C/A]AAAAATTTGTTAACACTGATGC<br>TGCTCAAAACGCACATAGAAATCGGTGGTAGATTGCGGTTCTAGTAAGTAGCTAATGTTTAGATA<br>TGATTGTTGAATATTGTTGCTGTGTTCTGGTG                  |
| TIGR-<br>A004Z48 | 177 A G --- | --- | CAAATAATCTCTGCTTAGAAGTTGCTTAGGGCCATGGATTTCATGTAAGGTGGGCGAGGTGGACTG<br>AAGATCTGTTGGCAGGCTCACAGACGGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCAT<br>CTTGGCAATACGGTTATCCCGTGTCTTCATACGCCACAG[A/G]TCTCCAATTTTCAGGGGCTCCC<br>GTGGGATGGTGGAGCCAAATGAAGACCAGGTAGATGATGCCACCTAGAGATG |
| U17579           | 34 T G ---  | --- | GGGATTCAATGTGTCTGTCTCATCCAATAAGCAC[T/G]CATGACCTCAGCCCCATACTCTTTCTCCC<br>TATGTTCCAGAGACAGAATAGACCTGGCCCTTCCTTCTAGGGGATCACAATAATTGGAAGGATGAG<br>GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC<br>TGGGAGAGGGATCCCTTCTAGTTGA                         |
| WI-7747b         | 88 T G ---  | --- | GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA<br>TATATAATTTTAAATTTGAT[T/G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAATT<br>ATTTCTTTGTTGTTTGGGTATCCTGCCAGTGTTGTTTGTAAATAAGAGATTTGGAGCACTCTGA<br>GTTTACCATTGTATAAAGTATATAATTTTTTATGTTTGTCTGA      |

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| WI-7747a | 44 T C ---  | --- | GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCTGCT/CJTTCGTTAACTGTGTATGTAC<br>ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAAGAGCTTCATGCCCTTTGTAAAGTT<br>ATTTCTGTTGTTGTTGGGTATCCTGCCAGTGTGTTTGTAAATAAGAGATTTGGAGCACTCTGA<br>GTTTACCAATTTGTAATAAAGTATATAATTTTTTATGTTTGTTCCTGA       |
| WI-7189  | 197 T C --- | --- | TCAGAAATTTCTCTTCAGCTCATTTTGTCTCTCTCACAAATTAAGGAGTAGGTTAAGTGAAAGGT<br>CACATACCAATTTATTTCCCTTCAAAACAATAATATTTTACAGAAGCAGGAGCAAAATATAGGCCTTT<br>CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAAGCCTACAACATTTTTCJAG<br>TTTGCAAAATAGAACTAATACTGGTGAAATTTACCTAAACCTTGGTTATT       |
| WI-7850  | 57 G A ---  | --- | AGCCCACTGGACTCATGGATGTGCACCCTTTGCTCCCTGCTCTTTCTGCCCTCTGG[G/A]CTCATGTA<br>TCTGGCAGCTCTGGTACCCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCCTTGCCCTTGAAGCT<br>GAGAAGCACAGGGCAAGGAGCCAAAGGACCACAGAGCCTCAGCCAGGATCCGCTCCTCATTTT<br>ATTGGTATGATGAATGGGAATGAAATCAGGGGGCTGCTACTAGAGCC       |
| WI-7907  | 69 G C ---  | --- | CTCTCTCTCATCCCATCACCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAGAGGTGGGAGGAGG<br>G[G/C]JAGAAAGTGAAGGAAGATAGGAAGGATATTACCTCTCTGTATTATTTTAAAGAAACATTTGTTT<br>GGTGGCAGCAATCTCCCTGTCCCTATCACTGTTAGAGGCCATAATTTATATCTATAAATATATTAAAA<br>AGCAAGTCAAACTTGGATGTATCAAGGTAATAATTTATGTCAAAGTTTAAAT |
| WI-7919  | 242 T C --- | --- | GAAGGCAGCTGGATCACTTCCGCGAGTCTTGGGCGGCTTTGCTGTGGAACACGAGAGCTCCTCCT<br>CAGGGCCTGGCACTCACCTTCTATTCTGTATGATGATGATTTGGTTAAACACTGTCAAAATAATAGAGAT<br>GTGCCAGATTTAGATTTTCTACCCCTAACTGTTTAAATTTGTAACCTTTATCCCATTTGAAAGTGCA<br>AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAAAT/CJACAACCTTT  |
| WI-7928  | 101 T G --- | --- | CTCCCTTCTATGTCTCAGCAGCACGTTGGGGCACACTTGTTCATCTTCTGACCCGTTTGTGGGCTA<br>TTCCCTGCGAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGGAGAAAGCTGTA<br>TGCAGGATGCTCACTGATGTTTGCACCTTTAAACTGAAATTCAACTCTTTATATAGGATTTTCTTTT<br>CTATCTCCATCTCCTCATTAAAAATACGTACATTTGAGGTAATGGTA         |
| WI-7936  | 131 T A --- | --- | TTTTGAGTCAAAAGACTTAAAGGGCCCCAATGAATTTATATACATACTGCATCTTGGTTATTTCTGAA<br>GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACCCCAACACTTACACCAAACT[A]<br>ACTGAATGAAGAAGTATTTTGGTAACCCAGGCCATTTTGGTGGGAATCCCAAGATTGGTCTCCCATATG<br>CAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA     |
| WI-7944  | 99 T C ---  | --- | TACACGTTCCAGCCCGTTGCCCACTCATCTGCGCTTTGCTTTGGTGGGGGCAGATTGGGTGG<br>AATGCTTTCCATCTCCAGGAGACTTTTCATGT/CJAGCCCAAGTACAGCCTGGACCACCCCTGGTGTG<br>TGAGCTAGTAAGATTACCCCTGAGCTGCAGCTGAGCCTGAGCCATGGCAATGGACAGTTACACTTGACAGA<br>CAAAGATGGTGGAGATTGGCATGCCATTGAAACTAAGAGCTCTCAAGTCA     |

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| WI-7805 | 101 A G --- |  |  | TTTCTAGGCTGTACAGTCTGATGCATGATTTTATATAATATTTTCACTCTTGGAATTTGGATCTTT<br>TTTACTTTGAGCATATATTTAGAAATATGTGT/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG<br>AAGGAGGTTTATTGTGGAATAGTTTAAACAGTCAGGAAGGTAACCTGGTCAGTATTAATGTGTAGC<br>CCTACCAAAAATAGCCAGTAGTATCTGAAAAATGAAAAATAAATGAAGTAT     |
| WI-7416 | 137 G T --- |  |  | GGCCAGGAGATTAGCAACAAGGATTCACTCTGTACTTACTTGGCCCTTTTATCTTCCCTCTTGCCC<br>CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTTGGCAGTGCT<br>[GT]CTACTCCCTCAGGTGCAGCATACATAACCAAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC<br>CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAATGTCAATCAG |
| WI-140  | 252 C T --- |  |  | ATTTGAAGATTGGAGGGCTTGCAGAGGAAAAATAGATTTCAATTGGATCCCAAACTATAATGACA<br>AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAGTGAAATGCAAGTTGTACCAGTAAAGTTTATA<br>TCTCCATTCAGCCAGCTCATTGGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG<br>GATGAAAAATTTAGTTAAAAATGTGTCAATTTGCTGTATTGGCATTCCTTC/     |
| WI-198  | 218 C T --- |  |  | GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTCCCGGATCAAGTGTGGCAAC<br>CATGATGAAACTCTTGCCATGGTTTGTAGTACCCCTGGACCAAGTAGTCAATCCATCTGACTTTAAAA<br>TTCTAACAGCCCTTGATGGGACAATCTCTGTAAGACTAACCACTTCCCTATCTTATCTTCAGCTA<br>CCTGCTTCCCTTTC/TTGTTTAAACAAAGCATAGAAATATCTGAACAAC      |
| WI-205c | 146 T C --- |  |  | TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCCTCATCTCTTAACATGACTTGGTCGG<br>AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT<br>GCATGAGTTTGTC/JCCAAAGGCTTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT<br>ATCTTACTTTTGTAAAAAACTGCATATGCCTTTATTTTGTAGTTCCC     |
| WI-205b | 146 T C --- |  |  | TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCCTCATCTCTTAACATGACTTGGTCGG<br>AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT<br>GCATGAGTTTGTC/JCCAAAGGCTTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT<br>ATCTTACTTTTGTAAAAAACTGCATATGCCTTTATTTTGTAGTTCCC     |
| WI-234  | 165 G C --- |  |  | GAAGACTGAGTTTCCAGGAGGTTCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA<br>GGGATTCAACCTGTTTGAACCCCAAGTNCCTTCCAAGAGGTCTCAGACTACCTCCTCCATCTCCCCCT<br>CTCCCCCACAACACACAAATACAGAGATTG/JAATTCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC<br>AATCATACACAGTAATCTCTTGGTGTCTTAGTTTCTCAAAATGGAAATGG  |
| WI-276b | 25 A G ---  |  |  | AGCTTTTGAATCCAAAAACACAT/GJCTTGACTCTCTTATCCTCCTCTTGTGTAACTATCTCC<br>CTGAGGCAGAAAAATACAGAACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT<br>CGGTCAATGTATCAAGCATCTCTCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC<br>TCTGGCAAGGGCTTGTCTTATCCTCCTTGTCTATCCCTGATGACTGGGCAAA         |



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| WI-276  | 25 A G ---  | --- | --- | AGCTTTGAAATCCAAACCACATAG/GJCTTGACTCTCTTATCCTCCTCTTGTTGTAACTATCTCC<br>CTGAGGCAGAAAATACAGAACCCCTGTGGCTCCCTGAACGGAGGAGGATGGGGCGGGGAGACAT<br>CGGTCAATGTATCAAAAGCATCTCTGCCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC<br>TCTGGCAAGGGCTTTGTCTTATCCTCTCTGCTATCCCTGATGACTGGGCAAA     |
| WI-427  | 59 G A ---  | --- | --- | TTTTCCCAATCCACAGGTAAAACTAATAATGGATGTATAGAATTTAGAACTACTCCG/AJGTTT<br>TTTCCCTGGGGAAAATATTCAAAAACATTTGTGCTGCAATCAGGTTAAAGACATAGTGTGCCA<br>TTTGTCATCAGACAGGTAGAGGCCGTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT<br>ATTCATTTATTAGAGCCAGGGTCTTGCTCTGTCAACCCAGCTTTCAGTGCAGT  |
| WI-562c | 106 T C --- | --- | --- | CTCTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGCGCTGTCTC<br>AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAAAA<br>AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTTATGGCCACAGCCAAAACCACTCT<br>TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC  |
| WI-562b | 106 T C --- | --- | --- | CTCTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGCGCTGTCTC<br>AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAAAA<br>AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTTATGGCCACAGCCAAAACCACTCT<br>TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC  |
| WI-562  | 103 T C --- | --- | --- | CTCTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGCGCTGTCTC<br>AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAAAA<br>AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTTATGGCCACAGCCAAAACCACTCT<br>TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC  |
| WI-597c | 141 A G --- | --- | --- | GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG<br>ATGAGGAAGAAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT<br>GATACATG/AJGTAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC<br>TTGATCTAATATTCTTCACAACATAATACCTGAGAGAAATAAGTCTATTAAAT |
| WI-597b | 141 A G --- | --- | --- | GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG<br>ATGAGGAAGAAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT<br>GATACATG/AJGTAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC<br>TTGATCTAATATTCTTCACAACATAATACCTGAGAGAAATAAGTCTATTAAAT |
| WI-597  | 136 A G --- | --- | --- | GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG<br>ATGAGGAAGAAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT<br>GATACATG/AJGTAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATAAC<br>TTGATCTAATATTCTTCACAACATAATACCTGAGAGAAATAAGTCTATTAAAT |

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| WI-611  | 66 G C ---  |  |  | TTCAAAATTTAACACCATTTGGGTATATTATAATTTTNGCTCTATCCATAGTTCTAACCCCTCTTCTCT[G/<br>CJACAGTGAGACACCTGCTCTATTGTCTTGACGTATTACGTATTTCGATTCAGTCACCCATCTGGA<br>ACCAAGGTTTCATTCTGCTGACCCCTCCCTCCTCACCCCTACTTGGGCTCTGACTTCCTTCTCTGGGCT<br>GAACCTTCTGCTGGGCTGTCCGCTTCTCTGCTTGGGCTCCATAC |
| WI-681b | 156 A G --- |  |  | TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA<br>GGGATATTGTGAGAAATCAATAAGTTCATACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA<br>TCCATAATTGTTATAGCTATT[G]TTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA<br>CACCACGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCATGGTTT   |
| WI-681  | 156 A G --- |  |  | TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA<br>GGGATATTGTGAGAAATCAATAAGTTCATACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA<br>TCCATAATTGTTATAGCTATT[G]TTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA<br>CACCACGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCATGGTTT   |
| WI-867b | 119 G A --- |  |  | AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG<br>CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G]ATTTGTGTTGGC<br>CAATAATATCTCCCCCAGGACGCTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC<br>AGTGCTATGGTTTGAATGTGTCCCCCACAAGCACACATTAGAACTTA       |
| WI-867  | 113 A G --- |  |  | AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG<br>CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G]ATTTGTGTTGGC<br>CAATAATATCTCCCCCAGGACGCTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC<br>AGTGCTATGGTTTGAATGTGTCCCCCACAAGCACACATTAGAACTTA       |
| WI-867  | 119 G A --- |  |  | AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG<br>CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G]ATTTGTGTTGGC<br>CAATAATATCTCCCCCAGGACGCTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC<br>AGTGCTATGGTTTGAATGTGTCCCCCACAAGCACACATTAGAACTTA       |
| WI-871b | 123 C G --- |  |  | TCATCAGACCTGAGATTCAGGATGAAATCTACCAAAGGTACCACAAATGTAACCTTGTCCTCAACCGA<br>ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCCACCTACCTCATG[C]GJAACGTGT<br>GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGAATGCACGTATTGGCCTGAATTGTGTACCC<br>TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGATTTGTACATAA   |
| WI-871  | 123 C G --- |  |  | TCATCAGACCTGAGATTCAGGATGAAATCTACCAAAGGTACCACAAATGTAACCTTGTCCTCAACCGA<br>ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGCACCCACCTACCTCATG[C]GJAACGTGT<br>GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGAATGCACGTATTGGCCTGAATTGTGTACCC<br>TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGATTTGTACATAA   |

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| WI-884  | 198 T C --- | --- | --- | AGGTTCTGGACTTGATGCTGGGAAACAATTGGGTNCTGGGAAATTCCTATTTTGGTNTTTCACAGAT<br>CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTCTGATCTATTGGGA<br>ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G<br>ATCCGGCATGCAACATTTATTCAGTGAAACATGATGAAAATGAACATAAT |
| WI-921b | 205 G A --- | --- | --- | CACTOCCAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA<br>TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATACTGG<br>CAGTGATCCCTCTCAGCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGAACGATCCATCTAG<br>TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATCTTCCGAG        |
| WI-921  | 205 G A --- | --- | --- | CACTOCCAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA<br>TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATACTGG<br>CAGTGATCCCTCTCAGCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGAACGATCCATCTAG<br>TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATCTTCCGAG        |
| WI-945c | 90 G C ---  | --- | --- | GGCTGGGATGAGAGGTCTACTTGTGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA<br>GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGCCTGAGTAATAAGAAA<br>AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAACANTAGGTGCAGCACANNNGGTT<br>TTCTCTGGTCATAGAAATCTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA   |
| WI-945b | 90 G C ---  | --- | --- | GGCTGGGATGAGAGGTCTACTTGTGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA<br>GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGCCTGAGTAATAAGAAA<br>AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAACANTAGGTGCAGCACANNNGGTT<br>TTCTCTGGTCATAGAAATCTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA   |
| WI-960b | 167 C T --- | --- | --- | TTGCTTCAAAGAAAGTTCTGCTCAGGAAGTTATTCAATCAGCAACCTAAAATGTTTTTGGATACAT<br>ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC<br>CTGAGGAAATTTATCAAAGATGTTAAGTTAICT[C/T]CTTAGAGGTATAAGTCATATAGGCATATTCT<br>ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA              |
| WI-960a | 155 G A --- | --- | --- | TTGCTTCAAAGAAAGTTCTGCTCAGGAAGTTATTCAATCAGCAACCTAAAATGTTTTTGGATACAT<br>ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC<br>CTGAGGAAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT<br>ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA              |
| WI-1121 | 181 T C --- | --- | --- | TCCACTGAGTATGGCTTTCAGTAGTTTTTATTATGATGCTGCCTAGGTACATTTGTTTTATTGTTCTG<br>CGAATTGTTGATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTTCTGTGTTTC<br>CTTCTAAAGATACAAAATAAATGTAACATTAGACCTCTCAGTAT[C/G]GCTGTTTTTACTCTCCTCTG<br>ATTTTTTTCATTATTTTATTGCTCTGGCTTCATTTTGTAATNG    |

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| WI-1147b | 204 | G A | --- |  |  | TTTGCCATTATTTGAAGATAACCCACACCTTGGTGTCCAGGGTTTCACAGGATTAGTGGTCAGTCA<br>CATAGGCATATAGTACCTGTATGACTTCTATTCCAGCCACCGCAAACCTTCTCCTCCCTGCTGGCTC<br>CTGAGCCAAAACAGGCATTTACCATAAATCACCTTTGTTAGGATGAACCTTATCTGGCCAAACGTGATA<br>C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA |
| WI-1158b | 147 | C T | --- |  |  | GCATTGAGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGTCTATGTGAGGCCCTTGGTTGAAGA<br>CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATGCGCCAGGTGGC<br>TAAGTGCTGGGGC/GTCTGGGGTCAGGCTGCCCTGGGTACATCCTGGCTCCAAACGTCTTTGCTATG<br>GCT   |
| WI-1158a | 124 | C G | --- |  |  | GCATTGAGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGTCTATGTGAGGCCCTTGGTTGAAGA<br>CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATGCG/GGCCAGGT<br>GGCTAAGTGCTGGGGCTCTGGGGTCAGGCTGCCCTGGGTACATCCTGGCTCCAAACGTCTTTGCTATG<br>GCT  |
| WI-1304  | 124 | T C | --- |  |  | AAGTTTACAGAAAAAATACCGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA<br>TCATCTCAANGTNCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATGN/T/CJGNCANT<br>AAAATGATTTGAAATTTGGGAATAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG<br>GCC  |
| WI-1305d | 202 | C T | --- |  |  | TTCTCAATCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG<br>ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA<br>TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNATATG/C<br>/TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA   |
| WI-1305c | 46  | C T | --- |  |  | TTCTCAATCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAG<br>ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC<br>ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNINATA<br>TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA    |
| WI-1305b | 153 | T C | --- |  |  | TTCTCAATCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG<br>ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA<br>TCCACTGCTTTCANTAA/T/CJNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNINATA<br>TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA  |
| WI-1305  | 202 | C T | --- |  |  | TTCTCAATCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG<br>ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA<br>TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNINATATG/C<br>/TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA |

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| WI-1306b | 248 A G --- | --- | TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAATAATGGACAATCTTGNGNNNTNG<br>GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA<br>AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGGCCCTNNTTCTGTAGGCTTTTCAGT<br>CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCTTJAGJGC  |
| WI-1306  | 240 A G --- | --- | TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAATAATGGACAATCTTGNGNNNTNG<br>GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA<br>AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGGCCCTNNTTCTGTAGGCTTTTCAGT<br>CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTJAGJCTTCCTAGC    |
| WI-1307b | 118 T C --- | --- | GACAAGGCTGGTACTAGTTCCAAATTCCAAATCTATGTACACTTTCTCTCACATTTCTCAAGTGGACA<br>GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGTAGGCAATJ/CJGTGAGATTGTCTTT<br>CCTACCCCTTAAATGTATCTTNCATTAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT<br>TCITTTGGGTGTTGTTGTTGCTGTGTTTCTCTCTGTAAGNTGTTT         |
| WI-1307  | 118 T C --- | --- | GACAAGGCTGGTACTAGTTCCAAATTCCAAATCTATGTACACTTTCTCTCACATTTCTCAAGTGGACA<br>GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGTAGGCAATJ/CJGTGAGATTGTCTTT<br>CCTACCCCTTAAATGTATCTTNCATTAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT<br>TCITTTGGGTGTTGTTGTTGCTGTGTTTCTCTCTGTAAGNTGTTT         |
| WI-1325b | 169 T C --- | --- | GAGAGATGGCCAAAGACAAGCAGAGGGGAGAGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN<br>ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC<br>ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC<br>ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT     |
| WI-1325  | 165 C T --- | --- | GAGAGATGGCCAAAGACAAGCAGAGGGGAGAGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN<br>ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC<br>ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC<br>ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT     |
| WI-1327b | 162 T C --- | --- | CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCTGTTATTTGTAAA<br>ACACCAAGTGGGGTTTAAATGGAATCGGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC<br>CAGCGACACTATGGAGCTGAGAGTCTGTC/CJGAAAGTTGGGTAGTACCAGGCTCCCCAAATGTAGT<br>TCITGNGCTGAAAGTCTCTCTACTGAAAGGCAATGGTTCATCTCTAAG |
| WI-1327  | 175 C G --- | --- | CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCTGTTATTTGTAAA<br>ACACCAAGTGGGGTTTAAATGGAATCGGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC<br>CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGT/CJGTTACAGGCTCCCCAAATGTAGT<br>TCITGNGCTGAAAGTCTCTCTACTGAAAGGCAATGGTTCATCTCTAAG |

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| WI-1341b | 136 G A --- | --- | TATCAGCATGATTGGCTGTTGGACACAAAGTCAATTTGTACTTTTGNNGNNCTCTTTCTNITT<br>ACCTGATCCACTATCTTCTCAAGATCANGTTCAAATTTGGCTTCTTTGTTNAATTATACCCCAAGC<br>[G/A]GGATTGTGATGGATCTGTTTATTTTCCTGTCTTGGAAACAGCAGAGTCGTCTCTGNGAGTNTG<br>GTTTCAGGATTGTCTCTGTTTCCACAGCCCACTTGCACCTAGCAAGTGT     |
| WI-1349e | 192 G C --- | --- | CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA<br>GCAACCCAGCTTTGAAATGGATGAGGCGAGGTGGTAGGTCTGGCCTGTGAGTTGATATATATG<br>GCAGGTCTCAACAAATGATGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA<br>ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATA |
| WI-1349d | 264 C A --- | --- | CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA<br>GCAACCCAGCTTTGAAATGGATGAGGCGAGGTGGTAGGTCTGGCCTGTGAGTTGATATATATG<br>GCAGGTCTCAACAAATGATGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAAATA<br>ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATATGAT |
| WI-1349c | 192 G C --- | --- | CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA<br>GCAACCCAGCTTTGAAATGGATGAGGCGAGGTGGTAGGTCTGGCCTGTGAGTTGATATATATG<br>GCAGGTCTCAACAAATGATGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA<br>ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATA |
| WI-1349b | 264 C A --- | --- | CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA<br>GCAACCCAGCTTTGAAATGGATGAGGCGAGGTGGTAGGTCTGGCCTGTGAGTTGATATATATG<br>GCAGGTCTCAACAAATGATGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAAATA<br>ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATATGAT |
| WI-1349  | 264 C A --- | --- | CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA<br>GCAACCCAGCTTTGAAATGGATGAGGCGAGGTGGTAGGTCTGGCCTGTGAGTTGATATATATG<br>GCAGGTCTCAACAAATGATGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAAATA<br>ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATATGAT |
| WI-1403b | 57 C T ---  | --- | TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT<br>GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT<br>AAAGTTTACATCAACATAAATCTTGGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTCA<br>TAATCCCAAAAGTGCCAAAAGGGTTGTATCTGATTGT          |
| WI-1403  | 58 T C ---  | --- | TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCTT/CJCCGAA<br>TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG<br>TAAAGTTTACATCAACATAAATCTTGGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTC<br>ATAATCCCAAAAGTGCCAAAAGGGTTGTATCTGATTGT          |

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| WI-1417c | 31  | C T | --- |  |  | CAGCCGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGGGGCGAGATGTGAGCCACGGG<br>GGTGACAGCATGCCTGCTGGCATTGGAGGGCCCAAGAGGAATCCAGTGGCCCTCTCAATGACTTG<br>GGTCTCGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGCGGTTGC<br>AGGCGAGGCCCTTAGGTCGGTATTAAAGTTTGGCTTGTAGAAAAAGTCGC             |
| WI-1417b | 31  | C T | --- |  |  | CAGCCGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGGGGCGAGATGTGAGCCACGGG<br>GGTGACAGCATGCCTGCTGGCATTGGAGGGCCCAAGAGGAATCCAGTGGCCCTCTCAATGACTTG<br>GGTCTCGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGCGGTTGC<br>AGGCGAGGCCCTTAGGTCGGTATTAAAGTTTGGCTTGTAGAAAAAGTCGC             |
| WI-1729  | 172 | A   | --- |  |  | CCATGAGCAACAGCATGTTTCTACTCTGTGATGTATGTTAGGGGGCATGTATCTGTATTTCTT<br>TTTTATTCTCTCCAAAGAAATTTCAATATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAAGA<br>TGTTGGAGAACTGAAAAAGAGAGCTTACATGACCCCAATAGCAAACTCTCCACACATTTCCAGCA<br>GATGATGTGCTCTCCGTGGTNACCTTCTCTCCACCACATCACCTGTGTTTT         |
| WI-1732b | 122 | T C | --- |  |  | TGCCCTACTTCTTGTTCATTCCACCATTACATTTGTAAATGGAACTTCTAGGAGGTAGAAGGA<br>TATGCTGATCAAAAAAGGGGACATATCAAGGAGTNCCTGGTCAACCCCTTTC/JATTTCAGTCT<br>CTGCCACATGTCTAGTAAGTGTGATGGTGATCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC<br>CTTTCACACTACTATCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG           |
| WI-1732  | 114 | C T | --- |  |  | TGCCCTACTTCTTGTTCATTCCACCATTACATTTGTAAATGGAACTTCTAGGAGGTAGAAGGA<br>TATGCTGATCAAAAAAGGGGACATATCAAGGAGTNCCTGGTCAACCCCTTTC/JATTTCAGTCT<br>CTGCCACATGTCTAGTAAGTGTGATGGTGATCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC<br>CTTTCACACTACTATCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG           |
| WI-1750  | 97  | A G | --- |  |  | GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCCAAAAAAGGTTTAAAAATCTGTGTGGA<br>CATAATGTTTGAATTTGCAGTTCACCTTGG/JGJTAAAGGTGTGCTGTTTCTGGCAAGAGTCAG<br>TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCTGACTGAG<br>CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA                       |
| WI-1780  | 31  | A G | --- |  |  | GGTACACAAAGAAATGCTTCTGGAAATCTAC/JGTAGCCCTTAACAATTTGGCTGAGTATTAATC<br>TGTACATGTGTAAATGTGAACCCACCATGAAGCTGGGCAAGAACAAATTCCTAGGAAAGTACAATTAC<br>TGGGAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCTCCATCA<br>ACTGGAGAGACCTTGTGTAGTACAGAGGACATTCAAGAAATAATCATAAAAAT |
| WI-1803c | 77  | A G | --- |  |  | CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCGAGAA<br>CCATTATGAT/JAGTAGGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG<br>GGTGCTAATTTCAAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCCTCAA<br>GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATACTGGAATCA    |

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| WI-1803b | 77 A G ---  |  |  | CCACTCAGTAATAATAGTGTGGAGATAAGTATATGTTAGGCACATAATAATTATTTTCAGGCAGAA<br>CCATTATGATAGTAGGTAGGATAGGCATCACACTTGGGAGGACATATTCTGGAGTNAGATATCCTG<br>GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCTCAA<br>GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA |
| WI-1837b | 112 C T --- |  |  | TTTACTTGGGATTTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA<br>AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATACGCTTCTGTCCCCAGTTTATTTTTT<br>AAGGTTTTTTTTCATTCACCTGATGCCAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT<br>CGTGAACAACCTGGGAAGTCTGGGAACGTTTACGTTTCTGTGTGGCT       |
| WI-1837  | 112 C T --- |  |  | TTTACTTGGGATTTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA<br>AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATACGCTTCTGTCCCCAGTTTATTTTTT<br>AAGGTTTTTTTTCATTCACCTGATGCCAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT<br>CGTGAACAACCTGGGAAGTCTGGGAACGTTTACGTTTCTGTGTGGCT       |
| WI-1840b | 79 G T ---  |  |  | TCACCTAGGGAGGTCGCTAAATGTAGCTTCATTAGACACCTCAGACCTATTGGATCAGGATCTT<br>TCAGGTAGCAGTGTGAGAACTCTGAATATTACGACATACAAGTGTGACAACTCTGTTTAGTAT<br>ATTTATCTCCAGAGTGTGTTTGAATTTACTAAAAGTTCTTAAAGAGCCATGAAGAAATTATAAGACT<br>ATCGCA  |
| WI-1840  | 79 G T ---  |  |  | TCACCTAGGGAGGTCGCTAAATGTAGCTTCATTAGACACCTCAGACCTATTGGATCAGGATCTT<br>TCAGGTAGCAGTGTGAGAACTCTGAATATTACGACATACAAGTGTGACAACTCTGTTTAGTAT<br>ATTTATCTCCAGAGTGTGTTTGAATTTACTAAAAGTTCTTAAAGAGCCATGAAGAAATTATAAGACT<br>ATCGCA  |
| WI-1879b | 110 C T --- |  |  | GGGCTCACTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG<br>CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTATGCTGCTGCNAAATAAACTCCCAAAA<br>AAGTGGTTAGTCCACAGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTCT<br>CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT           |
| WI-1879  | 110 C T --- |  |  | GGGCTCACTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG<br>CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTATGCTGCTGCNAAATAAACTCCCAAAA<br>AAGTGGTTAGTCCACAGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTCT<br>CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT           |
| WI-1900b | 119 C T --- |  |  | TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGTCTGCATAATGAATAATCAACTGGACAACCCNG<br>CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGGCTGCTCTGAGAGGT<br>AAAGTCCCTGCCCAACCGGCACAACTAGAGAGCAGCAACAGGTGTTGAACCCAGCTCTGCT<br>GACTTCAGATCTGTGTGCTTAACCTGCCATGAGAAACCACTTTCTTGTCTCC        |



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| WI-1900  | 119 C T | --- | --- | --- | TGTTCTGGTCCAGGCACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG<br>CTNAGGTAGNTACCTNGGCAATTAGCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT<br>AAAGTGCCTGCCCAACGGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT<br>GACTCAGATCTGTGTCTTAAGTCCATGCAATGAGAAACCACTTTTCTTGTCTCC     |
| WI-1943c | 165 C T | --- | --- | --- | ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT<br>GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGTACTTTTCAGAGTCAAGC<br>AGCAAGCCAAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA<br>TACAGGGCACCGNTGAGCAATCCAGATGACTCCAAAGCCCCGGCTGGAGTAT |
| WI-1943b | 165 C T | --- | --- | --- | ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT<br>GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGTACTTTTCAGAGTCAAGC<br>AGCAAGCCAAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA<br>TACAGGGCACCGNTGAGCAATCCAGATGACTCCAAAGCCCCGGCTGGAGTAT |
| WI-1943  | 164 C T | --- | --- | --- | ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT<br>GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGTACTTTTCAGAGTCAAGC<br>AGCAAGCCAAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA<br>TACAGGGCACCGNTGAGCAATCCAGATGACTCCAAAGCCCCGGCTGGAGTAT |
| WI-1960c | 270 A T | --- | --- | --- | CCAGGTGAGGCTGAAAGAGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATCTGGAGAAGCACCCCT<br>GCAGAGCTTCATCTGTTTCAAAAGTGTGCCATGCANGGCTNCTGGGTTGTGAGCTCATNGCTGAG<br>TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAGCTCTGACTAGACCTTGGCA<br>GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCCAATTT    |
| WI-1960b | 270 A T | --- | --- | --- | CCAGGTGAGGCTGAAAGAGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATCTGGAGAAGCACCCCT<br>GCAGAGCTTCATCTGTTTCAAAAGTGTGCCATGCANGGCTNCTGGGTTGTGAGCTCATNGCTGAG<br>TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAGCTCTGACTAGACCTTGGCA<br>GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCCAATTT    |
| WI-1977  | 203 T C | --- | --- | --- | CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA<br>TTCTGGGCATTCTTCATAGAGNTTGTCTTGTAGTCTCGTAATAATACTGTGCCCTAGGAAGGTTGTT<br>TTTCTACTGCGTCTGTGAAAGCCCTTCCCCTCGAGTGATACAGTACTTCCAGTTATGGAGATTIT<br>/C/TAAACAAACAACACTGGCTGAGGCTGTTGG                      |
| WI-2012  | 102 T C | --- | --- | --- | AAATTTAGAGCCAGAGTCAAGTCAAGTAAATGATTATAAAGTTGAAGTAAATGCAATTGTAGTTTCATGT<br>TTTCTCTTAATCTGCACAAAAGTCAAGTAAAAATC/TCTTTAAATCAGTTACCAGAGGCAATACCT<br>GGGTTAATGTAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACTTTTTTCTACTCTCATTT<br>GGCTTACCAATGCTTCCACTGGATC                         |

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| WI-2013  | 127 C T --- |  |  |  | CTTTAGAGGTGGTCATTTCCGTTCCCTTCTGGAAAGTGATTGCTGTTTAAAGAAAAATAGATGCAACG<br>TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATAGTACACTGCTCTCA<br>CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC<br>CCTTTCACTGGAGGGATATCTCAGCTTCTGAGCCCTGGTTACTGCAATCC  |
| WI-2032c | 166 G A --- |  |  |  | ACAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC<br>TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC<br>ACATCACCCAACTGGTTTCTAGATGTACACGAGTGTGGGACCTCTGTCTCAACCTCCGACTTTTCAC<br>AGATCATTTGGTTAGGCTCACCTTCCCTGTAATGCTTCTGTTTTCAAAGGG  |
| WI-2032b | 219 C G --- |  |  |  | ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC<br>TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC<br>ACATCACCCAACTGGTTTCTAGATGTACACGAGTGTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA<br>TCATTGGTTAGGCTCACGCTTCTCTGTAATGCTTCTGTTTTCAAAGGG |
| WI-2032  | 219 C G --- |  |  |  | ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC<br>TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC<br>ACATCACCCAACTGGTTTCTAGATGTACACGAGTGTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA<br>TCATTGGTTAGGCTCACGCTTCTCTGTAATGCTTCTGTTTTCAAAGGG |
| WI-2054b | 188 C T --- |  |  |  | CGTTTCTTCTACATCTTGGGNNACATAAGANGAAAGAGNAGCTGCTTTTGTGGTAGTTTGGCT<br>CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA<br>TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTTCGTTCTGCTGCCCTCCAC<br>CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGCTTT    |
| WI-2054  | 183 T C --- |  |  |  | CGTTTCTTCTACATCTTGGGNNACATAAGANGAAAGAGNAGCTGCTTTTGTGGTAGTTTGGCT<br>CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA<br>TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTTCGTTCTGCTGCCCTCCAC<br>CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGCTTT    |
| WI-2573d | 129 T C --- |  |  |  | TGGGATTAACCCCTGTTTCTTCTCCAGTTCAAGTGTGCCCTTAATGTTTGTGCTAGAAATTAACA<br>TTAACAGCAGTAAATAAGTCTTTAAATGCACCTTGCCGTTCAACAGGTGTTCCGCTGCTTTTCJGA<br>TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT<br>GAAGTGAATGATTGCTTGCACAAAGGTCAATATGGCTGGGCTTGGACGAG      |
| WI-2573c | 165 A C --- |  |  |  | TGGGATTAACCCCTGTTTCTTCTCCAGTTCAAGTGTGCCCTTAATGTTTGTGCTAGAAATTAACA<br>TTAACAGCAGTAAATAAGTCTTTAAATGCACCTTGCCGTTCAACAGGTGTTCCGCTGCTTTTGATAT<br>CATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT<br>TGAAGTGAATGATTGCTTGCACAAAGGTCAATATGGCTGGGCTTGGACGAG       |

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| WI-2573d | 129 T C --- | --- | TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA<br>TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTT/CJTG<br>TATCATCTGATCTTCCCAACAGGGCTATTATGCCTAGGTAGGGTAAGCAACAGAGGCTGTGT<br>GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG             |
| WI-2573c | 165 A C --- | --- | TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA<br>TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTTTGATAT<br>CATCTGATCTTCCCAACAGGGCTATTATGCTGCCTAGGTAGGGTAAGCAACAGAGGCTGTG<br>TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG            |
| WI-2573b | 165 A C --- | --- | TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA<br>TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTTTGATAT<br>CATCTGATCTTCCCAACAGGGCTATTATGCTGCCTAGGTAGGGTAAGCAACAGAGGCTGTG<br>TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG            |
| WI-2573a | 129 T C --- | --- | TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA<br>TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTCCGTGCTTT/CJTG<br>TATCATCTGATCTTCCCAACAGGGCTATTATGCCTAGGTAGGGTAAGCAACAGAGGCTGTGT<br>GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG             |
| WI-2868b | 60 A G ---  | --- | GACTTCATGCTCATGAACAAGCATTTGCTTTAATTTACAGACATTAAAGAACAGCTTTCCJAGJCTC<br>CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT<br>ATCATGGAAGCCCACTACTCTATTAAACGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA<br>CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC |
| WI-2868  | 60 A G ---  | --- | GACTTCATGCTCATGAACAAGCATTTGCTTTAATTTACAGACATTAAAGAACAGCTTTCCJAGJCTC<br>CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT<br>ATCATGGAAGCCCACTACTCTATTAAACGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA<br>CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC |
| WI-2870b | 131 T C --- | --- | CATGCTGTGTAACCTCTGTGCTGCTGCTGCTGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC<br>TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C]<br>AGAAATGAATAGAGCCCATTTTAAATTATATCAGAGCTTTATGTCCACTTCTGTTCCCTGCCATCAC<br>TGGGCTTTTACAAAGGAGGCTTT                           |
| WI-2870  | 131 T C --- | --- | CATGCTGTGTAACCTCTGTGCTGCTGCTGCTGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC<br>TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C]<br>AGAAATGAATAGAGCCCATTTTAAATTATATCAGAGCTTTATGTCCACTTCTGTTCCCTGCCATCAC<br>TGGGCTTTTACAAAGGAGGCTTT                           |

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| WI-2954c | 49 T A ---  | --- | TTAGCACACATATCTGTGTGGGACTTAACTGAGACAAGGCATAAAAAA/T/A/CAGCACCTGGGGCA<br>CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT<br>CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAAATAAGTCCA<br>GAG  |
| WI-2954b | 41 A G ---  | --- | TTAGCACACATATCTGTGTGGGACTTAACTGAGACAAGGC/JA/AAAAAATCAGCACCTGGGGCA<br>CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT<br>CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAAATAAGTCCA<br>GAG  |
| WI-2954a | 38 G T ---  | --- | TTAGCACACATATCTGTGTGGGACTTAACTGAGACAAG/JT/GCATAAAAAATCAGCACCTGGGGCA<br>CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT<br>CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAAATAAGTCCA<br>GAG  |
| WI-2971b | 62 T C ---  | --- | ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/JG<br>CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACCTCCTCCTCTTAAATAAACCTAAC<br>ATTTCCTTTGTCCCTGACATTCTGAAGGCCACGCTGGTCTAGATGTATGTCCTCAGATTGCAATCCT<br>AGTTCITTAATGTTATTCTGAAGAAAACCTTTTACTTAGGGATTGTCT |
| WI-2971  | 62 T C ---  | --- | ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/JG<br>CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACCTCCTCCTCTTAAATAAACCTAAC<br>ATTTCCTTTGTCCCTGACATTCTGAAGGCCACGCTGGTCTAGATGTATGTCCTCAGATTGCAATCCT<br>AGTTCITTAATGTTATTCTGAAGAAAACCTTTTACTTAGGGATTGTCT |
| WI-2995d | 133 A T --- | --- | TTCTGGGAAAGAAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGCC<br>TCCAGTTTTNATCAAGATAAGACCTGGAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTTJA<br>/TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCCAATGGGTAAA<br>GAATGAGACAGAACTAGCAGAAAAGTGT                             |
| WI-2995c | 151 G C --- | --- | TTCTGGGAAAGAAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGCC<br>TCCAGTTTTNATCAAGATAAGACCTGGAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTTNA<br>AATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG<br>AATGAGACAGAACTAGCAGAAAAGTGT                                 |
| WI-2995d | 133 A T --- | --- | TTCTGGGAAAGAAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGCC<br>TCCAGTTTTNATCAAGATAAGACCTGGAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTTJA<br>/TAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA<br>GAATGAGACAGAACTAGCAGAAAAGTGT                              |

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| WI-2995c | 151 GC --- |  |  |  | TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC<br>TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGAGCTGGANTTTTTTNA<br>AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG<br>AATGAGACAGAACTAGCAGAAAGTGTT                                     |
| WI-2995d | 133 AT --- |  |  |  | TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC<br>TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGAGCTGGANTTTTTTNA<br>/TJAAATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA<br>GAATGAGACAGAACTAGCAGAAAGTGTT                                 |
| WI-2995c | 151 GC --- |  |  |  | TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC<br>TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGAGCTGGANTTTTTTNA<br>AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG<br>AATGAGACAGAACTAGCAGAAAGTGTT                                     |
| WI-2995b | 151 GC --- |  |  |  | TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC<br>TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGAGCTGGANTTTTTTNA<br>AATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG<br>AATGAGACAGAACTAGCAGAAAGTGTT                                     |
| WI-2995a | 133 AT --- |  |  |  | TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC<br>TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGAGCTGGANTTTTTTNA<br>/TJAAATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA<br>GAATGAGACAGAACTAGCAGAAAGTGTT                                 |
| WI-3147  | 85 CT ---  |  |  |  | GTGTGCAGTTTCATCTCTGGAGTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCAC<br>ATCTCACTTAGCTCTT[C/T]CTGCCATATCTCTGTTTCTTACTCTCTATCTCTGAGACTTCTTCT<br>GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTNAGGGAACCTTGACCTAAGACAGAA<br>ATCTAGTACCAATACTTTGCAAGG                                  |
| WI-3234b | 68 TC ---  |  |  |  | ATTCTGTAATGTTTTCACTGCTTCCAGTAAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA<br>T/CJGACAAGCAAGAAACAACAACAGAAAAGCCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG<br>TATAATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCCTTAATAAGCATAATCAAAAATTTTAC<br>TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTATATCTTTAT |
| WI-3234  | 68 TC ---  |  |  |  | ATTCTGTAATGTTTTCACTGCTTCCAGTAAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA<br>T/CJGACAAGCAAGAAACAACAACAGAAAAGCCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG<br>TATAATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCCTTAATAAGCATAATCAAAAATTTTAC<br>TCAGTAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTATATCTTTAT |

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| WI-3292b | 106 G A --- | --- | GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC<br>TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTG/AJGGTATTGGATGGGATTACTT<br>GCCATGAATATTTCCATTGTTTCTCATTAATGTTATTAAATTAAGTAAATATTATTNCCATGA<br>GACACAATGGAAAAATGGAAACATTCATGGAAAAAACCCATTTCATC                 |
| WI-3292  | 106 G A --- | --- | GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC<br>TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTG/AJGGTATTGGATGGGATTACTT<br>GCCATGAATATTTCCATTGTTTCTCATTAATGTTATTAAATTAAGTAAATATTATTNCCATGA<br>GACACAATGGAAAAATGGAAACATTCATGGAAAAAACCCATTTCATC                 |
| WI-3355  | 19 G C ---  | --- | CCATGAACCATGGGCTACA/GCJATATTCTTAACTTCAGAGTCCCTCCTTACTGGAGGGATCCA<br>CTTTTAAATATGATTTCTTGAAGTGGCTGCATACTATTCTTCCAAGCACTTAAAACTCATCAGAA<br>AAAAAATCATCAAAAAGTCGAAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA<br>ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTGTAGATGACTTTNNAGTTG |
| WI-3408  | 194 G A --- | --- | CCATGAAGAATGAGTTCCCTCCCTCCCTGGGTACGCTAAGAATAGCACACCCCTTGAGAAATTTNACT<br>TAGCACGTGGCATTGTAATGGCTGGATTTCTCCGCTCTAAGACACACCTTATGCTTTCNAAGCTTT<br>CTGGAATGGGATGAATCTNACATTCATGTCACCCCTGCTGGGATCAGTCTCC/G/AJTGCCCC<br>ATCTCTGNAGAAGCCACTGGGAAGTCGAAGGAGTGAATCAAAATCAGG       |
| WI-3505b | 131 G A --- | --- | TAACCTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAAATTTT<br>GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACATTACCTATTTTNAACCAAC[G/A]<br>AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT<br>GTTTAAATGGGAAATATGTTTGCATAT                           |
| WI-3505  | 131 G A --- | --- | TAACCTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAAATTTT<br>GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACATTACCTATTTTNAACCAAC[G/A]<br>AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT<br>GTTTAAATGGGAAATATGTTTGCATAT                           |
| WI-3564b | 177 C T --- | --- | GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGTCACTAAATGTTTGGAAAAATAAAGT<br>GAAATCAATGTGCTTCCAGTGATTCACATGGCAGTGCACAGAGGGCTTGAGCGCTGAGCG<br>TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTT/AACAAGTGTGTTGTGGTGCATC<br>AGTGTACACATGCTACCTTCTTCACAAAAA                                |
| WI-3564  | 177 C T --- | --- | GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGTCACTAAATGTTTGGAAAAATAAAGT<br>GAAATCAATGTGCTTCCAGTGATTCACATGGCAGTGCACAGAGGGCTTGAGCGCTGAGCG<br>TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTT/AACAAGTGTGTTGTGGTGCATC<br>AGTGTACACATGCTACCTTCTTCACAAAAA                                |

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| WI-3649  | 64  | A | G | --- | --- | AATGTCATGCTGTGACTGAACCTGTCTAACACCTTTCCTAGTATCCCTTAGTGAAGATTCAAC[AG]<br>AGACCAGTTTGCCTTCACTTAGTAGGCCAATGATAGACTTTTAGGTCTACCAAGGTTACCTGC<br>ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTCTGCTGCCTGGTC<br>TTCTGTTTTACCATAATATGATGACATGCAAACTCAGAGCCTTTTA              |
| WI-3674b | 133 | G | C | --- | --- | ACAGTACATGCCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA<br>ATTTAACTACCAAGCGGAGTGCTTTATAGTAATTAATAATGTTTATTTAGAAAAATAACAAAATG<br>/CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACCTTGGTCAAAATGATTGTT<br>AATCTTAATTAATTGTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAAG    |
| WI-3674  | 133 | G | C | --- | --- | ACAGTACATGCCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA<br>ATTTAACTACCAAGCGGAGTGCTTTATAGTAATTAATAATGTTTATTTAGAAAAATAACAAAATG<br>/CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACCTTGGTCAAAATGATTGTT<br>AATCTTAATTAATTGTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAAG    |
| WI-3682  | 137 | G | A | --- | --- | CAATATAGACCAAAATGACTGCCACAAAGAGAAAATTAGTGGATCTACATTTAGAAACCACATGTTTT<br>ATTGGCTCTCTCTTCTCTCTCTTTTATGCTCTCTCCAACCACTTACCTTTATCTTTTCAA<br>T[G/A]AGCAATTTGTCCAAITTAAGTCAATGAAAAATAATGTACATTTTCAACAAGTATACATTAA<br>GCCCTGCAAAAGTCTTATGCTAT                                    |
| WI-3854b | 194 | G | A | --- | --- | GGTATGTTGAGGTGAGTCACTAATGGTCACTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGGA<br>CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTCTTGATTAATAACTC<br>TGGTTCAGGAAGGCAAGGCGAGTTATGACCACCTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAA<br>GTTAAATGGCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA |
| WI-3854  | 194 | G | A | --- | --- | GGTATGTTGAGGTGAGTCACTAATGGTCACTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGGA<br>CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTCTTGATTAATAACTC<br>TGGTTCAGGAAGGCAAGGCGAGTTATGACCACCTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAA<br>GTTAAATGGCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA |
| WI-4039  | 210 | G | A | --- | --- | AGCCAGCCACATCATGTTGAGTCTGCTCATCTTCCATCTTATTTCTCTACTGCTTCACTTCACTT<br>CCATTAAACAAGAACTCTTGATTACATTTGATGTTTGGTTACACTACAGAATCCAAGATGACCTC<br>CCCATCTCAAGGTCAACTAATTAACACCTTAATCTATTGCAATCTTTGTCAATACCATAACATATT<br>CATGG[G/A]TCTGGGATAAGGGGTAGACATTTTATGGGAGGCATTA           |
| WI-4110b | 130 | T | C | --- | --- | GAAAAATGATGTTTTGATTTCCCTTCCCTATCTTCAGATTTATGGAGTGTCAATAGAAAACTGATAGT<br>AACCTTTTATTTGATGAAACTCTGTCTATAATTAACCTTCCCTCTCTGCTTTATTTTGGCTT[C/J]ACA<br>GTTTAGGTAAATAAAGATGCCCAAGAAATTCAGTATTCAGGTACAGTAAAAAGTAGCAACCATGGG<br>GTAGGGACAAGTNCAGAAAAAGGAGGAGGTTGGGGTTTTCTGGGAAGA  |





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| WI-4230  | 93 T   | --- | --- | AGAGACGTTGAATGGGGACATCTTTCTATTTTCGATTTTAGTTTAACATTTTGATAAGAAATTGATGAAA<br>GTTTGTACATTCAGATTATCTTTATAGCAGCAGAAGTCTGGCAAATAATAACAGCACACTGACT<br>TTTCCATGGTAAAAAAGAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATTTCTGAAT<br>ACATTTTAAATGGAGGAGAATGAATAGTGACCTTTTGAATTTTGAATTTATGG |
| WI-4241  | 118 CT | --- | --- | GAAATTCATTGAAGTTTGGACCTTGAACATGATCTCATTAATACCTTTTNCCTGTAGTGGTTGTATTT<br>CATTTTGTACAAACAGAACAGACGAAATTTCCACTTAAATTAATCTC[CT/TAAGTATCTATGAT<br>TTAGCACTGTTAGCACCCAGAACTGTGAAATTAATCTCTAGATAATCTTCAGAACTCTAGGATGGAAG<br>AA  |
| WI-4271b | 151 A  | --- | --- | CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT<br>CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG<br>GGACTGAATCCAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTTCTGCTCAGG<br>CTCTAGAAGGTCCAGTCAGGGGC                                       |
| WI-4271  | 151 A  | --- | --- | CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT<br>CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG<br>GGACTGAATCCAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTTCTGCTCAGG<br>CTCTAGAAGGTCCAGTCAGGGGC                                       |
| WI-4389b | 156 GA | --- | --- | AATCGAAACATTGATTTTGTAAAGGAACACATTTATGATATTTGTGCCAGTTTAGCATAT<br>GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAAGAAAGGATATTATTCATAACCTTTTGA<br>AGGTAAGATGTGAACCTATACA[G/A]JNCGAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA<br>AGAGGTATTGTAGGAACCTGGAAGCGGTAA                                 |
| WI-4389  | 156 GA | --- | --- | AATCGAAACATTGATTTTGTAAAGGAACACATTTATGATATTTGTGCCAGTTTAGCATAT<br>GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAAGAAAGGATATTATTCATAACCTTTTGA<br>AGGTAAGATGTGAACCTATACA[G/A]JNCGAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA<br>AGAGGTATTGTAGGAACCTGGAAGCGGTAA                                 |
| WI-4488  | 31 A G | --- | --- | GATGACAAATTATTGTGATTTGGCATTTTAA[G/G]GTACCATTCATTTCTTCTGGCTTTCGIGGTT<br>TGTTGTTGAGAAGTCAGGGTTAGTCGATTGCTCTTTCTAGTCTTCTCAGTAGGAAGACTGATC<br>CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAAATTG<br>TATTATCTATGCTTAAATGCTCAG                                 |
| WI-4491  | 145 GC | --- | --- | ACCATCAATGTATCACCCTCTAAAATTTATTAGATGATTAACTGGCTCTGTAAAAAATAAAAAACCT<br>GTCCTGGACATTGAAAAATAAACATTACTATTGGTCATTTCTGCTACTTACAAAGGACTGCACTA<br>AACAAAGTTAAG[G/C]GTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACGTCA<br>TTTCTGTCCCATAAATAAAATTTTACATGCGT                      |

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| WI-4584  | 144 | A G --- | --- | TTGGTTGGCATTAGCCTCATAACAACATTTACAAATCAATTTGTTACTCTTATTTTACAAACAAG<br>AAAAATGAGGCTTAACATCACACTCTGCTAGTCGAGAGCCAGATTTGAACCCAGGAATCCATT<br>CACCGGTAC[G/G]TGCTACCTGGTAAAAAATGTTTAAATTAATCTATGGCATTAGATTTCAAAGA<br>GTCCTAATGTGGTTTGAAAATAGGTGTCCTTAATTTGTTATCAGTATGC               |
| WI-4639  | 185 | C T --- | --- | TTTTCGCAATTTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCAATTTATTCAGTACAATA<br>TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCATTAC<br>TGACCATAATGACTTGGGAACATTATCTCACCCTATCTGAGTCTGATCC[G/C]TCATCTTTAAATTTGTA<br>AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA |
| WI-5327  | 63  | A ---   | --- | AAATGAATCCGCTTTAGAGCAAAATACCAGTAAGGCTGGTGCAAGATGGTGGCTGAGAGA[A/-]<br>JGATTACTCATAAAAGCATATTAAATTTTATAAATATGGAATAATTAACCTAGATAATTAATGTGAAT<br>TGAGTTGAAGGTTGCATGAGAGTAGGAGGAGGTAGTTCTACTTATAGGGTTTATATAAGTNTGCT<br>TCAATAGAATGGCTCTTTGGATGACAATGATGAACCTGTTCTAAGCAGACAG        |
| WI-5390  | 87  | C T --- | --- | GCTTTGAGAAATGAAAAGGGGAGCCTGGACCATTGCAGGGCTTCTCATCTCTGATTATTTGTGTAT<br>TTATTGTTCACTTATTTAT[C/T]GCTGTCTCCCTTCTGGTATGCTTGTGCATGAAACAATGAATTC<br>CCAGTGCCTGGCCGATTGCTGGCTCCTAGAGGTGTCAGAAAAAAGTTTGGTGAATAGAAATTG<br>ACGAATGGGTTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT           |
| WI-5404b | 87  | G A --- | --- | CCTTGCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAGAAATCAATTTAAGCAGT<br>GCAACATTAATTTAATTT[G/A]AAAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAATTTG<br>AATCTTCTCTCAGCAGTTCCATGGTGGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT<br>GCTACTTATATGGAAGGGTTTATAGAGTTTCATAACAA                           |
| WI-5404  | 87  | G A --- | --- | CCTTGCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAGAAATCAATTTAAGCAGT<br>GCAACATTAATTTAATTT[G/A]AAAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAATTTG<br>AATCTTCTCTCAGCAGTTCCATGGTGGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT<br>GCTACTTATATGGAAGGGTTTATAGAGTTTCATAACAA                           |
| WI-545b  | 77  | A C --- | --- | TAGGAAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTTCACCACCTCACACTGCCGCCA<br>TATCTCCTC[G/C]CCAAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATGGGACTATTT<br>GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC<br>GAGATACACCATGAATTTTATTTTCATTCA                           |
| WI-5545  | 77  | A C --- | --- | TAGGAAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTTCACCACCTCACACTGCCGCCA<br>TATCTCCTC[G/C]CCAAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATGGGACTATTT<br>GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC<br>GAGATACACCATGAATTTTATTTTCATTCA                           |

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| WI-5860b | 134 A G --- | --- | --- | ACTCAAGTTGGGGATAAAATCAGAAGTTTCTATGTACAACCTAAATTTTCTAAGATTTTATTGT<br>TTCTTTTATATAAAATGATTTGTTTCTCCCTAACCAACCTTCTAAGTGAAGAACTAC(AV<br>GJTATAGTGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTAAAGGGAATCA<br>ATTCCAAATCATCAACTTCTGTAT   |
| WI-5860  | 134 A G --- | --- | --- | ACTCAAGTTGGGGATAAAATCAGAAGTTTCTATGTACAACCTAAATTTTCTAAGATTTTATTGT<br>TTCTTTTATATAAAATGATTTGTTTCTCCCTAACCAACCTTCTAAGTGAAGAACTAC(AV<br>GJTATAGTGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTAAAGGGAATCA<br>ATTCCAAATCATCAACTTCTGTAT   |
| WI-6106  | 208 C G --- | --- | --- | GCAACAACCTATTATACCTGATCCAAACCCAGGTCTACTAACATTAAATCAACCCCTAACCAATAC<br>TATATTTGTCCTGTTCTGAATTTATTTCAATTTAGAATCTGATGAGATTTAGCATGGGATAAGTGCAG<br>TGCAGAGATAGTAAACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATTCTTACAGAG<br>TAATTIC/GJATAGTAGGTCACCACAAAGTCTATATTGTATGTGAAGGAAAG |
| WI-6109d | 129 T C --- | --- | --- | AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC<br>ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAACCTAA<br>AAACCTATATTNCTGTCCTTGTGCATCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT<br>GNAAAATTATCCCTGAAAAATTTTATACCA                             |
| WI-6109c | 147 T C --- | --- | --- | AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC<br>ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAACCTAA<br>ACCTATATTNCTGTCCTTGTGCATCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG<br>TGNAAAATTATCCCTGAAAAATTTTATACCA                               |
| WI-6109b | 147 T C --- | --- | --- | AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC<br>ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAACCTAA<br>ACCTATATTNCTGTCCTTGTGCATCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG<br>TGNAAAATTATCCCTGAAAAATTTTATACCA                               |
| WI-6109a | 129 T C --- | --- | --- | AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC<br>ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAACCTAA<br>AAACCTATATTNCTGTCCTTGTGCATCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT<br>GNAAAATTATCCCTGAAAAATTTTATACCA                             |
| WI-6112  | 96 T C ---  | --- | --- | AATGCCATACACCTTCCATCATGCTGCATAACTGATTGATTCATATGCTTATTGTTAGCACCTGTC<br>TTCCAACACATGCTGTTTGTTCATGAT/CJGCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC<br>AGTGAACAGTATTGACTAAACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG<br>GAAC  |

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| WI-6244  | 103 | T C | --- |     | TAATTGCACAACCTTACATATCAGGGTTTCTGATTGAAAGGAAGAGAATATTCCTTTCTTTAGTGATT<br>GCTTAATATTAATTCATAATAAGTGCACCATCTCTTCGCTCCTTATAAATGTGTTTAGAAGAAGG<br>AAATTGAGTGTGGGAATTAGCAACAGGAGACATTTTATATACTCCTACAGTGGGGAAGACTT<br>CCTATTTCTTTCCCAAGGATGGATACATTTCTAC                       |
| WI-6268  | 124 | C T | --- | --- | CTGGCCTTATAATCCCAAGTTTAGGATTAATCTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT<br>GTCTACAAGATTTCCTCCTAGTAGGGCTTTGGGTGTGGCACCGTTGGCTCATTC/C/TACTCTCCCT<br>GGGTCTTATTGACTTTCAGGGAGCCTAGAAAGAGCTGGACAAAACCTGCTCTTTGCAGAAAGAGTCG<br>GGTTCCAAAGATTTCGTACGATTTTATA                     |
| WI-6336b | 234 | C T | --- | --- | AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC<br>ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAATCAATTAAACAACTAAACAGCTT<br>ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTATAGATCACATGAAATGGACCATGTG<br>GTACCCCAAGTGCATTATGCTTGGTAGAGCC/C/TTGAGGACACTGACAGT  |
| WI-6336  | 234 | C T | --- | --- | AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC<br>ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAATCAATTAAACAACTAAACAGCTT<br>ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTATAGATCACATGAAATGGACCATGTG<br>GTACCCCAAGTGCATTATGCTTGGTAGAGCC/C/TTGAGGACACTGACAGT  |
| WI-6381  | 92  | C A | --- | --- | TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCACAAATTAAGTTATGAGTATTTATACAATTA<br>CAAAAATGNTTCATGTTTAAACAA/C/A/GTATTTTAAAGCTCAAAACATTTTAAACAGGCACAAT<br>ATTCTAANGGCATATGCATTCACCATGGGCTTTGAATGTCCTCACTCCCACTTCACAAATCAAAATC<br>TACAGANGCGCAAAAGATCAGAGTTCAG                      |
| WI-6436  | 198 | C G | --- | --- | GGTTGAGGCATTGGGAAAGGCAGAAATTTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT<br>TCAGAGGCAAGTCATGACAGACAGGAAATACAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA<br>ATTTGGTGTCAATAAAGAAGTTTAGACTTTGGTGTGTAGTAGTGTAGTAGGAGGTT/C/<br>G/ATTTGGTGTATTCACAGACAAGGTGATGTTCTAAGATTGATATTTATTGT          |
| WI-6449  | 186 | C T | --- | --- | GAGGCCTCTTTGCTTTTCCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT<br>GTATGGCTAGTGTGTTGCTGATTGGTGGTGTCTCAGACTGCCAGATTGTTAAATATTTTGAATAATC<br>GTATCTGGTTCTATTTCATCTGCATTCTCTGATCTTATGCTGGCTCTATT/C/ATCCCTATTCTCTGA<br>TCTTATGTCAGACCTGAAGTTCCCTAAATTTTCTGTGGTGTATTATA |
| WI-6449  | 186 | C T | --- | --- | GAGGCCTCTTTGCTTTTCCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT<br>GTATGGCTAGTGTGTTGCTGATTGGTGGTGTCTCAGACTGCCAGATTGTTAAATATTTTGAATAATC<br>GTATCTGGTTCTATTTCATCTGCATTCTCTGATCTTATGCTGGCTCTATT/C/ATCCCTATTCTCTGA<br>TCTTATGTCAGACCTGAAGTTCCCTAAATTTTCTGTGGTGTATTATA |

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| WI-6463  | 72  | T C | --- |  |  | GCTGGAGAGAAAGACCTCCAAAGAAAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAAATTGAAA<br>AGAACAT/CJTGAAGAAATTAAGTAGAACTCAAGAGAGCCAAAGTCCCAATTTGTGTCATTA<br>TAAGAAATATTTGAATGGAAATCTTAAGAAATGATTTTATTGATCAGTTAAATGTTCTTCTCTCCTC<br>CAGTCCCATTTATGACATTCGGATGCTG                             |
|          |     |     |     |  |  | AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC<br>AGAGGCAAA/C/TGTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTCTTAGAGCC<br>AAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG<br>AGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA  |
| WI-6474b | 76  | C T | --- |  |  | AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC<br>AGAGGCAAA/C/TGTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTCTTAGAGCC<br>AAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG<br>AGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA  |
| WI-6474  | 76  | C T | --- |  |  | AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC<br>AGAGGCAAA/C/TGTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTCTTAGAGCC<br>AAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG<br>AGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA  |
| WI-6478b | 175 | T A | --- |  |  | GAACTCAATTAACCTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT<br>TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTCGAGGCCGTGCTATATGCTTTATTTGTGA<br>CACTGTCTATTTACCTCCCCCAATAGTGGAGAAATCAGAGT/A/GCTCCTTGTGAGTGTGCTACAGA<br>GAAGATATACAGGATGGAAGACAGCTCCTCGTAGGACCTAGACACAACCTG    |
| WI-6478  | 175 | T A | --- |  |  | GAACTCAATTAACCTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT<br>TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTCGAGGCCGTGCTATATGCTTTATTTGTGA<br>CACTGTCTATTTACCTCCCCCAATAGTGGAGAAATCAGAGT/A/GCTCCTTGTGAGTGTGCTACAGA<br>GAAGATATACAGGATGGAAGACAGCTCCTCGTAGGACCTAGACACAACCTG    |
| WI-6559  | 149 | G A | --- |  |  | CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC<br>CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA<br>TTAGCAATATCTTA/G/A/TCAAATTTTAAAAAGAGAACAGAGAAATAAGGAAGGCCCTAACAGAGGAG<br>TTAAATAATTTGTGCAAAACTTATCAGTTCTTC                 |
| WI-6564b | 54  | G A | --- |  |  | TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCCTATGC/G/A/CACTGGCTTTG<br>TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT<br>GCTCGCCTCATTTNCTCAGAAATGAAAGGCAATTTGATTATNAATTTTGTGTTGGGCTGTGTAAAG<br>GTTCTTGGCAGGAGAACATGCATATGACTTTAAAAATAAGACCAACA |
| WI-6564  | 54  | G A | --- |  |  | TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCCTATGC/G/A/CACTGGCTTTG<br>TAGGCATTCACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT<br>GCTCGCCTCATTTNCTCAGAAATGAAAGGCAATTTGATTATNAATTTTGTGTTGGGCTGTGTAAAG<br>GTTCTTGGCAGGAGAACATGCATATGACTTTAAAAATAAGACCAACA |

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| WI-6608b | 46 C    | --- | --- | CTAATCACAGTAGCACTGAACATGGCTCTAGTAGTGAGTGGCCCTCAGT[C/-<br>JAGTTACGGCAGCTAAAGGGAGGGGATTCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG<br>GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG<br>GTAAACTGCAAAAAAGAAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACACCAAGAAAAAGGAA<br>AGC |
| WI-6608  | 46 C    | --- | --- | CTAATCACAGTAGCACTGAACATGGCTCTAGTAGTGAGTGGCCCTCAGT[C/-<br>JAGTTACGGCAGCTAAAGGGAGGGGATTCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG<br>GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG<br>GTAAACTGCAAAAAAGAAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACACCAAGAAAAAGGAA<br>AGC |
| WI-6666  | 68 C A  | --- | --- | GTTAGACAGTATCCAGCAAAAAAGGTTATTTTATACCTCTACTTTTCCAAAACGAGGAAACCTCCCC<br>A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATCTGTCTACTCTGTGGTTTCATGTAA<br>ATGTTGGGGTGACTCATTCGGCTCTCTCTTCTCAAGTCCAGGCTCTTGGGTAGACCAAAAACCTA<br>ATACAAATGTTAGGCACACAAGAGA                                   |
| WI-6670b | 120 A G | --- | --- | AGATTAACATAATTATCTAGGGCCATTGTAGGGTNGGAGGAGTGTCTTCTATCTGCAGCCAAA<br>CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA<br>GCATTGCCATTGAGGCGGAGTCAGGGTTGTGGGCCAGAACTTAGACAATTTGGGGAATTTCTGA<br>AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT            |
| WI-6670  | 120 A G | --- | --- | AGATTAACATAATTATCTAGGGCCATTGTAGGGTNGGAGGAGTGTCTTCTATCTGCAGCCAAA<br>CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA<br>GCATTGCCATTGAGGCGGAGTCAGGGTTGTGGGCCAGAACTTAGACAATTTGGGGAATTTCTGA<br>AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT            |
| WI-6704c | 33 T C  | --- | --- | TTTGAAAAATAAATTCATGCACCAATGTTTAACT[C]CACATATATCATACAGTGCAGGATTTATGA<br>ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTCATGACACACGGNCA<br>CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTGTTCTTCCACATGGTTATTT<br>CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG          |
| WI-6704b | 33 T C  | --- | --- | TTTGAAAAATAAATTCATGCACCAATGTTTAACT[C]CACATATATCATACAGTGCAGGATTTATGA<br>ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTCATGACACACGGNCA<br>CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTGTTCTTCCACATGGTTATTT<br>CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG          |
| WI-6704  | 28 T C  | --- | --- | TTTGAAAAATAAATTCATGCACCAATGTTTAACT[C]TAACCTCACATATATCATACAGTGCAGGATTTATGA<br>ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTCATGACACACGGNCA<br>CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTGTTCTTCCACATGGTTATTT<br>CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG    |

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| WI-6710  | 106 G A --- | --- | --- | CCATGGACAGTTTAAITAGGAAGCTTCGACTTGTAGATAACAGAGGAAGTCCAGTTATCTACCT<br>ATTCCCTTAAACACATTTTGTAGGCTGGAATGATCCCG[G/A]TAGTAAACCTCAACATCCACACCT<br>GCATAACATCGCTCCCAAGTGACTATTTACTGAGTCGACACAGGATGTCACCAAGTGAGCCTC<br>ATCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC      |
| WI-6766b | 148 G C --- | --- | --- | AAACAAATGGTGCAATGCATAATTTGTGGTCACAGTATAAACAATACAAATTAGTTCATATAAC<br>ATTGGATATGGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT<br>GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA<br>GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCAGTTCCTCTTC       |
| WI-6766  | 148 G C --- | --- | --- | AAACAAATGGTGCAATGCATAATTTGTGGTCACAGTATAAACAATACAAATTAGTTCATATAAC<br>ATTGGATATGGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT<br>GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA<br>GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCAGTTCCTCTTC       |
| WI-6787b | 97 A G ---  | --- | --- | ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA<br>ATACCTTGTGCAGCAATGTTCAAATTTTAC/GJTTTTACTGCAAGATATCTTCATGTACAACTGT<br>ATGCTTTGTCTCTTGGAGGACGCGTTAAAGACCTATGATAACACACATCCACATGACAAAGGA<br>GAGTGCAATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT        |
| WI-6793  | 105 C G --- | --- | --- | GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA<br>TCAACAAGGCGGCTTCAAATCAATCAGTCAACCCCG[G/G]AGTTAGAAAGTAGAGTCATGAGGAA<br>GAGCTGCTTGGCTGAGGAAGTAGGGTTAATGCCCTCTAATCCCGAAAGGGGAGACTGAAGCCA<br>GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAAAGGCAAC     |
| WI-6810b | 37 T C ---  | --- | --- | CACAATAATAAATCACTCCCTACCTGAAACCTTTAT/CJAGAAGCATTTTAAITTTACAACACA<br>AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA<br>AATTAAACCTTTAAATGTCTATGNACAAGTACAATTTCTTTTGTCTGCAGAGCAATGACC<br>ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT          |
| WI-6810  | 37 T C ---  | --- | --- | CACAATAATAAATCACTCCCTACCTGAAACCTTTAT/CJAGAAGCATTTTAAITTTACAACACA<br>AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA<br>AATTAAACCTTTAAATGTCTATGNACAAGTACAATTTCTTTTGTCTGCAGAGCAATGACC<br>ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT          |
| WI-6817b | 145 C A --- | --- | --- | GCATGATTAAACAGTGCAGAAAAATACCAAGTACATTTGGGTGAACGATGAGCTAGCTGTTCTAGTA<br>TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAACTCAACAATGTAGCT<br>GCAGGGTAAC[C/A]TTGTGGATACCTGTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGATCA<br>AAGATGTTGGACACCTTGTGTTCAAATCTTGTTTCAGGTGCGGCTGTGCAG |

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| WI-6817  | 145 C A --- | --- | GCATGATTAAACCAGTGCAGAAATAACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAAATCATCACTCACTCAACAATGTAGCTGCAGGGTAAC[C/A]TGTGGATACCTGTGTGCTCTACTNGCCTCCAAAGGCAATTCAGGGGATCATCA AAGATGTTGGACACCTGTGTCAAACTTGGTTCAGGTGCGGCTGIGCAG  |
| WI-6819b | 221 C ---   | --- | GATGGAAGGCCATTTATTTTCTCTAAATTTAAATAGAAAGACTTTAATGGAAACATTTTAGTACCATATGTCACCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAAGCCTAGTAAAGGCCCGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/C]ATATACAAAATTTCTGCTATTTTGCTTAGCAACACGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCAG     |
| WI-6819a | 175 G T --- | --- | GATGGAAGGCCATTTATTTTCTCTAAATTTAAATAGAAAGACTTTAATGGAAACATTTTAGTACCATATGTCACCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAAGCCTAGTAAAGGCCCGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/C]ATATACAAAATTTCTGCTATTTTGCTTTAGCAACACGCAATAACTTTTGTGTTCTCTATATGACACCTAATAT        |
| WI-6826b | 154 A G --- | --- | GCAAAAGCTTTATTGGCTCCAACAAATATCCCTTTTAAACCTCTCTCTCTCTGCTCAGTGGAACACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATACATGCAAAACCTTGACAT[G/C]GAGCTTAAATAATCAAAATGCAAAATATAGATTGGGTGCACIGTTAAGCTGAATTGCAAAATTATGGCAACACACACTGGACTGGGGTATACGTTG            |
| WI-6826  | 154 A G --- | --- | GCAAAAGCTTTATTGGCTCCAACAAATATCCCTTTTAAACCTCTCTCTCTCTGCTCAGTGGAACACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATACATGCAAAACCTTGACAT[G/C]GAGCTTAAATAATCAAAATGCAAAATATAGATTGGGTGCACIGTTAAGCTGAATTGCAAAATTATGGCAACACACACTGGACTGGGGTATACGTTG            |
| WI-6857a | 122 T C --- | --- | AGTGCAAACTATTTTGAACAAAAGTAAACTATGATCAGCATTCAGCAAGACATCAGACACGGAAGAGTGAACAATATTCACCTAAGTAAATACAGCAGATGAGATGCTCTCACATGAT[C/J]ATTTAATTATTCATGCTTTTCAATAGTCTCTAGTCAACTTTTCCAACTATATCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAAATGGCAAAAGTTTGGCAACTGTTTGGGCTAATT |
| WI-6865  | 153 G A --- | --- | TTATAGAATACTTATGGGGCATACGNGTAAATGAACTGTCAACCTTAAATCTAAACAAACAGCTTGTTTGTTGGTTCTGCTGAAATCTCCCTGCTCACAACAAACAGCAGCTACTNGGTTTCTAAAGACGTAATTTTGCAAGGCAAACTT[C/G/A]TAGAGCCATTTCTGTGCAAGGAAGGGAAGGAGCTGTTTGTTTACCTGTAGTAGAAGATATCTTTGCGCTGTTAGAACTGAGCTCATTAA      |
| WI-6909  | 73 C T ---  | --- | ATTGAAAAGCTGTTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAAATGAGAGAAGAATGCAGACTT[C/J]AAGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTGAATCAGATTTTATGATACGGAAAAAAATTTCCCTTTTGGCAACAGGATATTTCGAAATAATAAATCGCCAGTGCCCAATCAGAAACACCATTTCCACAATAATTGTCATGCCCTAGTTGCCCTATTTTATACATATC   |



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| WI-6910b | 163 G T --- | --- | --- | CACTCAAAACCTTTATTCAATTGATTACAAACTGTACAATATTTACAAAGTTTAGGCATTAATCCCA<br>TATTGACATGAATGCTGTGGAGAGTCTAAAAATAATATGTGGCACATAGCTTAATATACACATCAT<br>GGCTCTTTACACTTAAGCCATTACCAATA[G/TT]GAGATGAATGGAGAAATTTAATGTGGTAGAAAA<br>GTCAGAGTGGCTGACCAGTCCCGGAOCTTCCATGTGAATGACTCTTCCTTGGC<br>GCTGTTTTTTTTTTGTTTTTTTAAAGTGACACCTTGGCCCTGTGGGCATTCTTCACATTATCTTACCC<br>AAAGTGCCCTTTGGGCCAGCCACTGACTGATTTAAACCCAGAAATGTGGTTTTTAAACAATGTGGT<br>CGTGGTGAAATTCAGGTGATTTTNNATTTCTATTGGTAGTATTTTCAGATTTCCACAAAGAACATG<br>TATTGCTTTGTAAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT |
| WI-6915  | 144 A ---   | --- | --- | CAATCAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAGCCAGGTCTCTGACTTGCACCTGTGCAC<br>ACTGGATTTNCCTCTGATCCAGCTGCAGCCTCCCATAGAAGTTCACCTTAATTTTCATGTCCCATG<br>CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGTT[C]AAGTCTCTATAAGGATGGGTAGG<br>TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA  |
| WI-6928b | 175 T C --- | --- | --- | CAATCAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAGCCAGGTCTCTGACTTGCACCTGTGCAC<br>ACTGGATTTNCCTCTGATCCAGCTGCAGCCTCCCATAGAAGTTCACCTTAATTTTCATGTCCCATG<br>CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGTT[C]AAGTCTCTATAAGGATGGGTAGG<br>TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA  |
| WI-6928  | 175 T C --- | --- | --- | TTTTATGAACATTTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA<br>CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTCAATCCTAGGTAGATATCAAGTTACAAANTAC<br>AAGTCCCGNTAATTAACATATAGGTAGTATTAANCAAAAATGNGTTTTTNGCAATTTATGTGAAAT<br>AAGGCTTTAACCAAAGC  |
| WI-6955b | 79 G A ---  | --- | --- | TTTTATGAACATTTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA<br>CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTCAATCCTAGGTAGATATCAAGTTACAAANTAC<br>AAGTCCCGNTAATTAACATATAGGTAGTATTAANCAAAAATGNGTTTTTNGCAATTTATGTGAAAT<br>AAGGCTTTAACCAAAGC  |
| WI-6955  | 79 G A ---  | --- | --- | AAACTAAAAACCCCTTATTGTCTCCAAGTGTGGGCAAAAATAGAAAAAT[C/G]TTTCAATTACATTAGG<br>AAATCGGGTGGATAACGGAGTATAGTTATTCACATTAAGAAGCATTCCAGTCAAAATAATCACAATA<br>ACAAATTCAGATTGCTTGGATCTGGTCATTTATGGCTTGAAGAAGTGGATTTGAAAAACCACTTTAGG<br>CTAAATAAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAAATCATGC  |
| WI-6957  | 47 C G ---  | --- | --- | ACTTCTAGTGCCTCTGTTACCACCACTCTAATGCCCTGTGGTCCCGCACTTCTGATGTCGGTAGGCCT<br>TAAATCTGCCTGGCGTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGAGAGCGCGCAGTTCCCTG<br>CAGGAGAGAGGAGGGGCTGTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCCCTGTCTGACT<br>CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCTTCG[G/TT]GTCGGATC  |
| WI-6996c | 242 G T --- | --- | --- |   |

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| WI-6996b | 242 | G T | --- |  | ACTTTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTGGCGCACTTCTGATGTCCGTAGGCCT<br>TAAATCTGCCTGGGTCCCTCCCTCTGCTTTCAGACCCAGAGGAGGAGAGCCGGCAGTTCCTTG<br>CAGGAGAGAGGAGGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTCCTGACT<br>CTCTCCTGATGGTGGGCCCTCTGCTCTCTCTCTCCGCTGCTGGGATC     |
| WI-6996  | 228 | T G | --- |  | ACTTTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTGGCGCACTTCTGATGTCCGTAGGCCT<br>TAAATCTGCCTGGGTCCCTCCCTCTGCTTTCAGACCCAGAGGAGGAGAGCCGGCAGTTCCTTG<br>CAGGAGAGAGGAGGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTCCTGACT<br>CTCTCCTGATGGTGGGCCCTCTGCTGCTCTCTCTCCGCTGGATC        |
| WI-7021b | 112 | G A | --- |  | TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAGGTTCTCCAGAGTCATCTACCTGAGTC<br>CTGAAGCTCCCTGCTCTGAAAGCCACAGACAATATGTTCCCAATG/AJCCCGACTGCACCTTCTGTG<br>CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCAATCCAATTAATCAAACC<br>ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA |
| WI-7021  | 108 | A G | --- |  | TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAGGTTCTCCAGAGTCATCTACCTGAGTC<br>CTGAAGCTCCCTGCTCTGAAAGCCACAGACAATATGTTCCCAATG/AJCCCGACTGCACCTTCTGTG<br>CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCAATCCAATTAATCAAACC<br>ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA |
| WI-7056c | 118 | C T | --- |  | GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG<br>CCCTGCAGCCTCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA/C/TGGTTGGGAGCCTCT<br>GGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACACAGAAAGTCATTCCTCTCTTTTAA<br>ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTGCCATTGATA     |
| WI-7056b | 118 | C T | --- |  | GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG<br>CCCTGCAGCCTCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA/C/TGGTTGGGAGCCTCT<br>GGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACACAGAAAGTCATTCCTCTCTTTTAA<br>ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTGCCATTGATA     |
| WI-7091b | 153 | A C | --- |  | AATTCGCTGAAAAGGAACCTACCTATCCCTACATTTACCTACTAATGTCCTTCTAACATCTTAGAG<br>GTCCATGGAGAAGGCATATGGAGAACATGTTTATAGTCTCTATAAATAGTATTCCTCAATCACTGTG<br>CTTAATTTAAATAGCATT/AJCTCTTATCATTTATCAGCCTTTTATGATTTTCCAAAGTAAATATTA<br>ACATATTATTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT   |
| WI-7091  | 153 | A C | --- |  | AATTCGCTGAAAAGGAACCTACCTATCCCTACATTTACCTACTAATGTCCTTCTAACATCTTAGAG<br>GTCCATGGAGAAGGCATATGGAGAACATGTTTATAGTCTCTATAAATAGTATTCCTCAATCACTGTG<br>CTTAATTTAAATAGCATT/AJCTCTTATCATTTATCAGCCTTTTATGATTTTCCAAAGTAAATATTA<br>ACATATTATTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT   |



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| WI-7175  | 194 | CT ---  |  |  | CTCCTAGACTAGTGCTTACCTTTATTAACTGTGACAGGAAGCCCAAGGAGTGTCTCCTACCA<br>ATAACTTCAGAGAAAGTCAGTTGGAGAAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC<br>AGTTACTGGTTTCAGTTGACAAAATATAATGGTTTACTGCTGTCATTTGCCATGCCTA/C/TJAGAT<br>AATTTATTTGTAATTTTGAATAAAACATTTGTACATTCCTGATACTGGG        |
| WI-7178b | 273 | GA ---  |  |  | TGATCAGGTCAGGGACTTGGACAGGAGTCAGTGTGGCTTTTCTCTGAGCCAGCTGCCTGGAG<br>AGGGTCTCGCTGTCAGTGGCTCCTAGGGGAACAGACCAGTGACCCAGAGAAAGCATAACACCA<br>ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTTGCACCTAATGAATCTCGTTCCCAAGAACTACCC<br>CCTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGA         |
| WI-7178  | 273 | GA ---  |  |  | TGATCAGGTCAGGGACTTGGACAGGAGTCAGTGTGGCTTTTCTCTGAGCCAGCTGCCTGGAG<br>AGGGTCTCGCTGTCAGTGGCTCCTAGGGGAACAGACCAGTGACCCAGAGAAAGCATAACACCA<br>ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTTGCACCTAATGAATCTCGTTCCCAAGAACTACCC<br>CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGA        |
| WI-7182b | 116 | A C --- |  |  | GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG<br>AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCTA/C/TCTCTCCTCTATTT<br>TACTTGAGGCTGCCAATTACCAGCCCAAGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG<br>CCACTTGGTAGCAAGATGGCAGCTATTCTCGAAGCCTAGTACCCCAATT |
| WI-7182  | 106 | C A --- |  |  | GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG<br>AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCCA/C/TCTGAGCCTATCTCTCCTCTATTT<br>TACTTGAGGCTGCCAATTACCAGCCCAAGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG<br>CCACTTGGTAGCAAGATGGCAGCTATTCTCGAAGCCTAGTACCCCAATT |
| WI-7191b | 273 | T A --- |  |  | ATAATTGCTGTTTCTAGCCTGGCAAGATATTTTCAATAAAGAGGGATAACAATGCTGATTACTAC<br>CTTTTAAATAATTTAGATAAATGCACAGCACACAGACCCACATCTAAGCATTAGTGATGGTAGC<br>TGATGTCAGCTTCATGTGGATTTTAAAGCACCTAGAAACAATGAAGCTTCTTGGCATATTTAAGGAG<br>CTCCCAAAATGTGTACCTATTAAATTGTAACCTCAGCAAGTAGAAGACCATT  |
| WI-7199c | 112 | T C --- |  |  | CCCAGTGGTGAACAGAACCTCCCAAAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC<br>GCTTTGAGGTACCCACCGTCTGTGAGCTCCTGACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGT<br>TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGGTCTGCTGAATTCCTCTTATTAT<br>AGTCTATAGTTTACTCCTCAGTTCCTCACCATCATCATCTGTCTAA          |
| WI-7199b | 112 | T C --- |  |  | CCCAGTGGTGAACAGAACCTCCCAAAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC<br>GCTTTGAGGTACCCACCGTCTGTGAGCTCCTGACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGT<br>TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGGTCTGCTGAATTCCTCTTATTAT<br>AGTCTATAGTTTACTCCTCAGTTCCTCACCATCATCATCTGTCTAA          |

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| WI-7216c | 237 | T C --- |  |  |  | TGACACTAACACTCTTAATTCAGCGAATGTTGGAAACCATGACCTCCTCTGTGTGCTCTTCTCCCC<br>AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATCCCTCCAGAAAAATACGTATGT<br>TTAAAAACCCCTTCTGCTATACATAGGAAAAAGACACACATCCACCTAAATTTGACTGACTGTTTAA<br>CTGTCAATTCTCCTGAGGCTAAACACAGTTGTTTTT/CJCTTGTAATCACTT   |
| WI-7216b | 237 | T C --- |  |  |  | TGACACTAACACTCTTAATTCAGCGAATGTTGGAAACCATGACCTCCTCTGTGTGCTCTTCTCCCC<br>AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATCCCTCCAGAAAAATACGTATGT<br>TTAAAAACCCCTTCTGCTATACATAGGAAAAAGACACACATCCACCTAAATTTGACTGACTGTTTAA<br>CTGTCAATTCTCCTGAGGCTAAACACAGTTGTTTTT/CJCTTGTAATCACTT   |
| WI-7220b | 147 | A T --- |  |  |  | AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTTATTTGCTCTTTAAGCTGGCAAACCCA<br>TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA<br>GTGGCACTAGAA/AT/TAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA<br>AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTTT |
| WI-7220  | 140 | A T --- |  |  |  | AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTTATTTGCTCTTTAAGCTGGCAAACCCA<br>TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA<br>GTGGC/ATCTAGAAAAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA<br>AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTTT   |
| WI-7226  | 232 | C ---   |  |  |  | GATCGAATTTTTCAGATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATGTATA<br>TACATATCACCTCCTATTCCTTAATTTTGTAAATGTTAACTGGCAGTAACTTTTGTGATCATTT<br>CCCTTTTCCATATAGGAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAAAAATAA<br>TTACCCACAATGCCACCAGTAACCTTAACGATTCCTTCTTGGGGTTT         |
| WI-7228b | 254 | G A --- |  |  |  | ATAGCTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATCATAA<br>TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTGTCTTTGTATCTATTTAGTTGATTTAATTA<br>CTTCTGAATAACGGAAGGATCAGAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAATCCACA<br>CATATTGTTTTAAATAAGAAATGTTATCCAATATTAAGATATCTCAATGTT       |
| WI-7228a | 163 | G A --- |  |  |  | ATAGCTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATCATAA<br>TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTGTCTTTGTATCTATTTAGTTGATTTAATTA<br>CTTCTGAATAACGGAAGGATCAGAA/G/ATATATCTTTTGTGCTAGATTGCAAAATCTCCAATCC<br>ACACATATTGTTTTAAATAAGAAATGTTATCCAATATTAAGATATCTCAA       |
| WI-7233c | 213 | C T --- |  |  |  | CGATCGTACTGCCAGTAGCATTTGCTGTCTGCCGGCTTTGTTGTACATTCATTTTCAATTTGTACA<br>GATGTGAACCTTTATTCCTGTCACTAATATATTTAAATTTATTTCTAGGAAGTCAAAAAATATAA<br>TAAAGGTTGAGCCCTCTACTTTCTTCTTCCACCTTTTGTGGCAATATTAAGTGAACGTGCTAATA<br>GTGTAAGTATC/TGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCTG      |



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| WI-7252a | 520 T C --- |  |  | CCACGAGATCCAGGCCAAGCGGCCCTCCGCCCTTCCACTCGCAGCAGCCGCGGACAGAG<br>GCCTGCCGCGCGCGCAGCCCGGCCCTGGCTCGAGGCTGCCCGGCCCTCTGTCTCTGTCCG<br>GACACTCTAGAGAACGCGAGCCCTAGAGCTGCCCTGGAGCTTCTAGCAAGTGAGAGATGGGAG<br>CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCCA          |
| WI-7265m | 252 T A --- |  |  | AACTTGGTTATGTCAGTTCCTGTGTGACACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT<br>TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT<br>TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATATGTAATAATAACGATCTCTT<br>AAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCTTT/ |
| WI-7265l | 231 T A --- |  |  | AACTTGGTTATGTCAGTTCCTGTGTGACACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT<br>TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT<br>TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCTCTT<br>AAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT      |
| WI-7265k | 121 T G --- |  |  | AACTTGGTTATGTCAGTTCCTGTGTGACACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT<br>TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTA<br>GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCT<br>CTTAAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT  |
| WI-7265j | 174 T A --- |  |  | AACTTGGTTATGTCAGTTCCTGTGTGACACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT<br>TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT<br>TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCT<br>CTTAAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT      |
| WI-7265i | 227 T C --- |  |  | AACTTGGTTATGTCAGTTCCTGTGTGACACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT<br>TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT<br>TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCTCTT<br>AAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT      |
| WI-7265h | 80 T A ---  |  |  | AACTTGGTTATGTCAGTTCCTGTGTGACACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT<br>TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTA<br>GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCT<br>CTTAAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT  |
| WI-7265g | 170 T G --- |  |  | AACTTGGTTATGTCAGTTCCTGTGTGACACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT<br>TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT<br>TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCT<br>CTTAAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGGCT      |

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| WI-7265f | 231 | T A --- | --- | AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCGATGCTATGTGTACGTGTTT<br>TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT<br>TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATATAACCGATCTCTT<br>AAAAATACCACAGTTTGATTTTCTTTT/AJ/AAGGAGTAAGATTTGCCT       |
| WI-7265e | 227 | T C --- | --- | AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCGATGCTATGTGTACGTGTTT<br>TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT<br>TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATATAACCGATCTCTT<br>AAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAGATTTGCCT          |
| WI-7265d | 174 | T A --- | --- | AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCGATGCTATGTGTACGTGTTT<br>TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT<br>TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTT/AJ/TATATTATGTAAATATAACCGATCT<br>CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAGATTTGCCT     |
| WI-7265c | 170 | T G --- | --- | AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCGATGCTATGTGTACGTGTTT<br>TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT<br>TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATATAACCGATCT<br>CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAGATTTGCCT          |
| WI-7265b | 121 | T G --- | --- | AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCGATGCTATGTGTACGTGTTT<br>TTTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT<br>GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATATAACCGATCT<br>CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAGATTTGCCT      |
| WI-7265a | 80  | T A --- | --- | AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCGATGCTATGTGTACGTGTTT<br>TTTCCAGTATGTTT/AJ/TATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT<br>GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATATAACCGATCT<br>CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAGATTTGCCT |
| WI-7281b | 183 | C ---   | --- | GATCACCCCAGCCACAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGGCCAAGC<br>ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCTGGCCCTGCAGGTCTCCCATGAAGGCCA<br>CCCCATGGTCTGATGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCCGAGGCCGCGAG<br>GTGTTGTGAAGACCACTGCTTCTGTGGTTGGGGTCTGCAAGAAGGCCTCCTC        |
| WI-7281  | 171 | C A --- | --- | GATCACCCCAGCCACAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGGCCAAGC<br>ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCTGGCCCTGCAGGTCTCCCATGAAGGCCA<br>CCCCATGGTCTGATGGCATGAAGCATCTCAGACTC/AJ/TTGGCAAAAACGGAGTCCGAGGCCGCGG<br>CAGGTGTTGTGAAGACCACTGCTTCTGTGGTTGGGGTCTGCAAGAAGGCCT      |



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| WI-7282b | 159 | G C --- |  |  |  | TGTCACCTGGACATTCATTTCTCAGTTGAAGAAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA<br>GTTGCAACTTAAGTATATTTGGTAGGGTGAAGTGTTCCTCACTCAAAATATGTCAACTNNNNNNNT<br>AGGCCCTTTCATAAAACCAAACT[G/C]TAGCAAGATGCAAATGCATGGCAAATCTGTGGTCTCCA<br>GTTGGTATCTGAATAGTGTCAACCAATTCACCAAGACAGTGTGAGATTGG |
| WI-7292  | 92  | T C --- |  |  |  | CTTGATTACTTCCACTGAGGTGGGAGCATCTCCAGTGTCTCCCAATATATCTCCCCCACTCCACTAC<br>TCTCTCCCTCCACTTCATTTTC[C]/C]TTGTCTCTCTCTAATTCAGTGTTCGAGGCTGACTTG<br>GGGACAACGTATTATGATATTATGCTGTTTCTCTCTCCCAATAGAAATAAGTTCATGGAGCC<br>TGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA        |
| WI-7301f | 133 | A G --- |  |  |  | AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGACCGAGGATATGGAA<br>ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG[<br>A/G]CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCA<br>ATCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG        |
| WI-7301e | 94  | T G --- |  |  |  | AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGACCGAGGATATGGAA<br>ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA<br>TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCAA<br>TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG         |
| WI-7301d | 138 | A G --- |  |  |  | AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGACCGAGGATATGGAA<br>ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA<br>CGGT[A/G]TAACATATGGTGGTGGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCAA<br>TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG         |
| WI-7301c | 211 | A C --- |  |  |  | AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGACCGAGGATATGGAA<br>ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA<br>CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCAATCA<br>AATTATGGAC[A/C]CATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG         |
| WI-7301b | 182 | C T --- |  |  |  | AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGACCGAGGATATGGAA<br>ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA<br>CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAAT[A/C]TAGTGGACAACAGCAA<br>TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG        |
| WI-7301  | 88  | G T --- |  |  |  | AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGGACCGAGGATATGGAA<br>ACCAAGGTGGTGATATGGTGGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT<br>TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCAA<br>TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG                |

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| WI-7301  | 205 | A C --- | --- | --- | AACTATGGCAGTGGTCTGGTTATAGTAGTAGAGCGGGTATGGTGGTGAGCACCAGGATATGGAA<br>ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGAGGAAATTTTGA<br>CGGTAGTAACATATGGTGGTGGTGGAACTATAATGATTTTGGAAATACAGTGGACACAGCAATCA<br>AATTACITGGACACATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG        |
| WI-7314c | 49  | GA ---  | --- | --- | CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA/GAJTTGTTCTACCTCACTG<br>AGAGGAAACAGAAAGGATATTGCTTCTTTTCAGCAGGTATAAAGTCAATTAAAAACCTCCCGAGG<br>ATTTCTTTGGACCCAGGAAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCACAGGA<br>CAGAAATGTGTAGTCTACCTTTATTTTTTATTAAACAAAACCTTGTTTTT  |
| WI-7314b | 49  | GA ---  | --- | --- | CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA/GAJTTGTTCTACCTCACTG<br>AGAGGAAACAGAAAGGATATTGCTTCTTTTCAGCAGGTATAAAGTCAATTAAAAACCTCCCGAGG<br>ATTTCTTTGGACCCAGGAAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCACAGGA<br>CAGAAATGTGTAGTCTACCTTTATTTTTTATTAAACAAAACCTTGTTTTT  |
| WI-7314  | 36  | A G --- | --- | --- | CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAA/GJTTGGGAGGTCA/GAJTTGTTCTACCTCACTG<br>AGAGGAAACAGAAAGGATATTGCTTCTTTTCAGCAGGTATAAAGTCAATTAAAAACCTCCCGAGG<br>ATTTCTTTGGACCCAGGAAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCACAGGA<br>CAGAAATGTGTAGTCTACCTTTATTTTTTATTAAACAAAACCTTGTTTTT |
| WI-7321b | 199 | CT ---  | --- | --- | ACTCAGGAAAGGATGCCCCATTAAAGTGACAAAGGGTGGGTGGGCACCATGGCATGAGGAAG<br>AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCTCCA<br>GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAAAGNNNNNNNAGGGTGGCACACCCATC[C<br>T]GTTGCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA     |
| WI-7321  | 199 | CT ---  | --- | --- | ACTCAGGAAAGGATGCCCCATTAAAGTGACAAAGGGTGGGTGGGCACCATGGCATGAGGAAG<br>AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCTCCA<br>GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAAAGNNNNNNNAGGGTGGCACACCCATC[C<br>T]GTTGCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA     |
| WI-7336b | 248 | A C --- | --- | --- | AGACATTCCTGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGACCCACGAAACTGCCCTGGC<br>TCCAGTAAACTTGGGCACATGCTCAGGCTACTATAGTCCAGAAGTCTTATGTTAAGCCCTGGCAG<br>GCAGGTGTTTATTAAAAATCTGAATTTTGGGATTTTCAAAGATAATAATTATACATACACTGTATGT<br>TATAGAACTTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA/A/CJA  |
| WI-7336c | 221 | A G --- | --- | --- | CTCTTCTCAGCACATTGATGGGCACTAGAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA<br>AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTCTTACCTTGAGC<br>CATATTGTGTGAGAGAACAAAGAAACAGAATCAATATATAAATTCAAAGACTATCTGCAGCTA<br>GTGTGTTCTCTTTACACAC/A/GJATACACACAGACATCAGAAATTCGTGT      |

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| WI-7338b | 125 A C --- | --- | CTCTTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA<br>AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTA/C/CCTTG<br>AGCCATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG<br>CTAGTGTTCTCTTTACACACATATACACACAGACATCAGAAAATTCGTGT |
| WI-7338  | 125 A C --- | --- | CTCTTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA<br>AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTACCTTGAGC<br>CATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA<br>GTGTGTTCTCTTTACACACATATACACACAGACATCAGAAAATTCGTGT  |
| WI-7338  | 221 A G --- | --- | CTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTTAAATAATAAATTCACCATAG<br>CAATACAGAATAACTTTAAATACCATTAATACATTTGTTATTTTCATTGTGAACAGGTATTTCTTCA<br>CAGATCTCATTTT/A/JAAATACTTAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA<br>TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA     |
| WI-7384c | 146 T A --- | --- | CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTTAAATAATAAATTCACCATAG<br>CAATACAGAATAACTTTAAATACCATTAATACATTTGTTATTTTCATTGTGAACAGGTATTTCTTCA<br>CAGATCTCATTTT/A/JAAATACTTAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA<br>TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA    |
| WI-7384b | 146 T A --- | --- | CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTTAAATAATAAATTCACCATAG<br>CAATACAGAATAACTTTAAATACCATTAATACATTTGTTATTTTCATTGTGAACAGGTATTTCTTCA<br>CAGATCTCATTTT/A/JAAATACTTAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA<br>TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA    |
| WI-7384  | 145 T A --- | --- | TGAAATCCTGGGTCTCTGGCCTGTCTGTAGCTGGTTATTTTACTTTGCCCTCCCTCCCTTTT<br>TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTA/JTAAAGGTTTGAATTCAGATTTAAAA<br>ACCAACTTATAAGCATTGCAACAAGGTACCTCTATTTGCCACAGCGTCTCGGGATTGTGTTGA<br>CTTGCTGTCTGCCAAGAACTTTCCCTCAAGATGTGTATAGTTATGG               |
| WI-7388c | 106 A T --- | --- | TGAAATCCTGGGTCTCTGGCCTGTCTGTAGCTGGTTATTTTACTTTGCCCTCCCTCCCTTTT<br>TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTA/JTAAAGGTTTGAATTCAGATTTAAAA<br>ACCAACTTATAAGCATTGCAACAAGGTACCTCTATTTGCCACAGCGTCTCGGGATTGTGTTGA<br>CTTGCTGTCTGCCAAGAACTTTCCCTCAAGATGTGTATAGTTATGG               |
| WI-7388b | 106 A T --- | --- | CTTGCTGTCTGCCAAGAACTTTCCCTCAAGATGTGTATAGTTATGG   |

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| WI-7388  | 94 T A ---  | --- |  | TGAAATCCTGGGCTCTTGGCCTGCTGCTAGCTGGTTATTTTACTTTTGGCCCCCTCCCACTTTT<br>TGAGATCCATCCCTTTATCAAGAAGT/AJCTGAAGCGACTATAAAGGTTTTGAATTCAGATTTAAAA<br>ACCAACTTATAAGCATTGCAACAAGTTACCTCTATTTGCCACAAGCGTCTCGGATTTGTTTGA<br>CTTGCTGCTGCTCCAGAACCTTTCCCCCAAGATGTGTATAGTTATGG          |
| WI-7438  | 64 A G ---  | --- |  | TTAGATTTTAATTGGCAACCAGCAACTCACTGCCACCATCCACTGCAGATCTNCTATTCCTGG/A/GJ<br>GTTGATATGACAAGGAAACCCATTGGAACCAAGTCTTCAGATTGNCATGTGCAGACAGGCTCCT<br>TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTACTGTAACATAGTTTGNCCTGGTATTTGTTA<br>TTGGAATGAATATCGCTCCACTGACTTTTACCA                   |
| WI-7454b | 152 T C --- | --- |  | CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC<br>CAGTACAACTGAGAAATGAGAGAACCTGATAGCACTGTCTGAATTCAGGAGCCTCCAAGGCTAA<br>TCCTACCCCTGGATTTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA<br>CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTTGACA |
| WI-7454  | 152 T C --- | --- |  | CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC<br>CAGTACAACTGAGAAATGAGAGAACCTGATAGCACTGTCTGAATTCAGGAGCCTCCAAGGCTAA<br>TCCTACCCCTGGATTTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA<br>CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTTGACA |
| WI-7464c | 177 G C --- | --- |  | AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT<br>CCATTTTCACTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTCTATGTA<br>CAACAGAGCCACAGCACAAGAGGGTGGGCATAAGCAGTTGCCA/GCJCCAGAAGAGCTTTCACATCAT<br>GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCCACCAACAATTAT    |
| WI-7464b | 168 C A --- | --- |  | AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT<br>CCATTTTCACTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTCTATGTA<br>CAACAGAGCCACAGCACAAGAGGGTGGGCATAAGC/AJAGTTGCCAGCCAGAAGAGCTTTCACATCAT<br>GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCCACCAACAATTAT    |
| WI-7464a | 103 C A --- | --- |  | AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT<br>CCATTTTCACTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTCTATGTA<br>GTACAACAGAGCCACAGCACAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAAGAGCTTTCACATCAT<br>GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCCACCAACAATTAT    |
| WI-7499b | 134 T G --- | --- |  | CAATTTCAATCCAACTAGTCTGTGTCCTAAACCATCCAGACAAACTCCACTTCGAAGGTTTTTA<br>AATGCATAAGTCAGATAGCAATCCTCAGTTGCCAGAGGACATCAGCTTCTTTGAATGCTTCAT<br>/GJTATAGTCTCTTCAATTTAGCAATCAGTGAGGGAATACACTGGCATCATGCCCTTTTTTTAGGA<br>ACTCTGTACAAAAATCCCTTTGAAAAATATAAATTTGGAAATGAGTGATGA       |

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| WI-7499a | 33 A C ---  | --- | --- | CAATTCTCAATCCAACTAGTCTGTNTGCCTAAJAGJCCATTCCAGACAAACTCCCACTTCGAAGGTTTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCGAGGACATACAGTCTTTTGAATGCTTCATTATAGTCTCTTCATTTAGCAATCAGTGAAGCAATACACTGGCATCATGATCCCTTTTTTTTAGGAACTCTGTACAAAATCCCTTTGAAAATATAAATTTGGAAATGAGTGATGA        |
| WI-7506b | 118 A C --- | --- | --- | TGGAATAGTAAGAGAGAAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAATGCATCCAGCAGCAGACCACTTNAAGAGTAGTCTCTGGTGTGATGGCTAGCJACJGGAGAGTTGAGTGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTAAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT |
| WI-7506  | 118 A C --- | --- | --- | TGGAATAGTAAGAGAGAAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAATGCATCCAGCAGCAGACCACTTNAAGAGTAGTCTCTGGTGTGATGGCTAGCJACJGGAGAGTTGAGTGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTAAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT |
| WI-7534b | 143 C T --- | --- | --- | TGTGAATCTTAGCTCTGGAAGGTGTTTATGCCCTTCGCGGTTCTTGATGTGTCGCAGTGTCAACCCAAGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAACACATTCOCGGTGATAGAATTGCTAAATTTGTCJTGTAAGATAGGTAGAAATTTTCTTTAAATATAGTTTCTTATTCGTGAAAAATTCGGAGAGTGTCTGCTAAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT      |
| WI-7534  | 135 T C --- | --- | --- | TGTGAATCTTAGCTCTGGAAGGTGTTTATGCCCTTCGCGGTTCTTGATGTGTCGCAGTGTCAACCCAAGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAACACATTCOCGGTGATAGAATTGCTCJAAATTTGCTGTGAATAGGTAGAAATTTTCTTTAAATATAGTTTCTTATTCGTGAAAAATTCGGAGAGTGTCTGCTAAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT       |
| WI-7543b | 162 G A --- | --- | --- | GGGAAAGAATAAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACCAAGTCTGTTTCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCCTCTTGTCTTTGJAGJGGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTTCTCTCGGCTCCTTGGATGTAGTCAGTTA     |
| WI-7543  | 162 G A --- | --- | --- | GGGAAAGAATAAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACCAAGTCTGTTTCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCCTCTTGTCTTTGJAGJGGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTTCTCTCGGCTCCTTGGATGTAGTCAGTTA     |
| WI-7555c | 60 T C ---  | --- | --- | GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTTCJTCATAAAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCATTCTGTTAAAGCCACTTGGGTCATAAAGAGGGAAAGTAAAAAATGAAGTCTGACTAGAAAATCTATTGCAGAGGCCCAAGTACATTTAGTATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCAATTTGAAATTCAG |

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| WI-7555b | 60 T C ---  |  | GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATTCCOCTCAAATTTGTAGAGGTC/TCTTA<br>AAAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTCGCATTCCTGTTAAAGCCACTTGGGTC<br>ATAAGAAGGGGAAGTAAAAATGAAGTCGACTAGAAATTCATTGCAGAGGCCAAGTACATTTAGT<br>ATGGCATTGAGTTGTGATATAGTTTTCAITTGATGTGCATTTTGAATTTGAG    |
| WI-7555  | 60 T C ---  |  | GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATTCCOCTCAAATTTGTAGAGGTC/TCTTA<br>AAAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTCGCATTCCTGTTAAAGCCACTTGGGTC<br>ATAAGAAGGGGAAGTAAAAATGAAGTCGACTAGAAATTCATTGCAGAGGCCAAGTACATTTAGT<br>ATGGCATTGAGTTGTGATATAGTTTTCAITTGATGTGCATTTTGAATTTGAG    |
| WI-7567b | 290 G T --- |  | TGAGCCATCACTAGAAAGAAAGCCATTTTCAACTGCTTTGAAACTGCCTGGGGCTGAGCATGAT<br>GGGAATAGGGAGACAGGGTAGGAAAGGGCGCTACTCTTCAGGGTCTAAAGATCAAGTGGGCTTGG<br>ATCGCTAAGCTGGCTCTGTTTGTATGCTATTTATGCAAGTTAGGTCATGATTTAGGATGCGCCTAC<br>TCTTCAGGGTCTAAAGATCAAGTGGGCTTGGATCGCTAAGCTGGCTCTGTTT        |
| WI-7569b | 63 T C ---  |  | AATGTATCCCCCTTCGGTCCAACAACAGGAAACCTGACTGGGCGAGTGAAGGAAGGATGGCATTC/CJ<br>AGCGTTATGTGTAAAAAACAAAGTATCTGTATGACAACCCGGGATCGTTTGCAAGTAACTGAATCCAT<br>TGCGACATTGTGAAGGCTTAAATGAGTTTAGATGGGAAATAGCGTTGTTATCGCCTTGGGTTTAAATT<br>ATTGTGAGTTCCACTTGTATCATGGCCCTACCCGAGGAGAGAGGAGTTTG |
| WI-7574c | 216 A G --- |  | GCCACAGCAGAAATGGAGCGGTGTAGGAAGGTCCCCTTTTCTCTGTTTGTGTTTGCAGAGCCAAAAC<br>TCCCACCTCTGCCCCCTTTAATCCCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTG<br>TACCACCTACATTTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG<br>ATAGCCAGGGC/A/GTCTGCTGGGCTGACCACTACTCATCCCGTTA      |
| WI-7574b | 216 A G --- |  | GCCACAGCAGAAATGGAGCGGTGTAGGAAGGTCCCCTTTTCTCTGTTTGTGTTTGCAGAGCCAAAAC<br>TCCCACCTCTGCCCCCTTTAATCCCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTG<br>TACCACCTACATTTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG<br>ATAGCCAGGGC/A/GTCTGCTGGGCTGACCACTACTCATCCCGTTA      |
| WI-7574  | 216 A G --- |  | GCCACAGCAGAAATGGAGCGGTGTAGGAAGGTCCCCTTTTCTCTGTTTGTGTTTGCAGAGCCAAAAC<br>TCCCACCTCTGCCCCCTTTAATCCCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTG<br>TACCACCTACATTTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG<br>ATAGCCAGGGC/A/GTCTGCTGGGCTGACCACTACTCATCCCGTTA      |
| WI-7576c | 168 A T --- |  | AATGATGATGATAATGATGATGACGACGACAAACGATGCTTGTAAACAAGAAAACATAAGAGAGC<br>CTTGGTTTCATCAGTGTAAAAATTTTGAAGGCGGTACTAGTTTCAGACACTTTGGAAAGTTTGTGT<br>TCTGTTTGTAAAACTGGCATCTGACACAAAAAAAJVTGTTGAAGGCTTATTTCTACATTTTCACTAC<br>TTTGTAAAGTGAGAGACAAAGAAAGCAANNNNNNNNNNAAGAAAAAATAAAC     |

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| WI-7576b | 168 A T --- | --- | --- | AATGATGATGATAATGATGATGACGACGACAAACGATGCTTGTAACAAGAAAACATAAGAGAGC<br>CTTGGTTCATCAGTGTTAAAAATTTTGAAGGCGGTACTAGTTCAGACACTTTGGAAGTTTGTGT<br>TCTGTTTGTAAACTGGCATCTGACACAAAAAAT/GTGTGAAGGCCCTTATCTACATTTCCACCTAC<br>TTTGTAAGTGAGAGAGACAAAGAAAGCAANNNNNNNNNNAAGAAAAATAAAC        |
| WI-7577g | 77 T C ---  | --- | --- | AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCTTAA<br>AAATATGCA/T/CJCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT<br>TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC |
| WI-7577p | 50 GC ---   | --- | --- | AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTT<br>TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT<br>TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC   |
| WI-7577o | 157 GA ---  | --- | --- | AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTTAA<br>AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA<br>AGAAGTTCAATTTGGTTTACAC/GAT/AGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT<br>ATTGATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC   |
| WI-7577n | 48 A G ---  | --- | --- | AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTT<br>TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT<br>TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC   |
| WI-7577m | 84 GA ---   | --- | --- | AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTTAA<br>AAATATGCATCAAAATC/GAT/CTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT<br>TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC |
| WI-7577l | 93 T C ---  | --- | --- | AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTTAA<br>AAATATGCATCAAAATCGTCTCTCATT/CJACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT<br>TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC |
| WI-7577k | 154 CA ---  | --- | --- | AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTTGCCTTCCCTTAA<br>AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA<br>AGAAGTTCAATTTGGTTTAC/JACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT<br>ATTGATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC         |

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| WI-7577j | 117 A G --- | --- | AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA<br>AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT<br>TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC  |
| WI-7577l | 77 T C ---  | --- | AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA<br>AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT<br>TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC   |
| WI-7577h | 50 G C ---  | --- | AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA<br>TAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT<br>TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC  |
| WI-7577g | 157 G A --- | --- | AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA<br>AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT<br>AGAAAGTTCAATTTGGTTTACAC/GAJTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACT<br>ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC  |
| WI-7577f | 48 A G ---  | --- | AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA<br>TAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT<br>TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC  |
| WI-7577e | 84 G A ---  | --- | AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA<br>AAATATGCATCAAAATCGAJTCTCTCATTACTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT<br>TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC |
| WI-7577d | 93 T C ---  | --- | AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA<br>AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT<br>TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC        |
| WI-7577c | 154 C A --- | --- | AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA<br>AAATATGCATCAAAATCGTCTCTCATTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT<br>AGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACT<br>ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC          |



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| WI-7577b | 117 A G --- | --- | AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA<br>AAATATGCATCAATCGTCTCTATTACTTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAGTGGAGATATGTTAACTAT<br>TGATAATGTGGCCTGTATACATGACACTCTTCTGAATTGACTGATTTTC        |
| WI-7577  | 107 G A --- | --- | AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA<br>AAATATGCATCAATCGTCTCTATTACTTTCTCTGAG/GJAGTGTAGTAAACAGTAGGAGTTAAT<br>AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAGTGGAGATATGTTAACTAT<br>TGATAATGTGGCCTGTATACATGACACTCTTCTGAATTGACTGATTTTC       |
| WI-7619q | 106 C G --- | --- | ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC<br>AGAGAAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACT/GJCTGTGCTGGGGTGCTAATTAC<br>ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCT<br>CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC  |
| WI-7619p | 150 T C --- | --- | ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC<br>AGAGAAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG<br>CAGGAAGAATGGGGCT/CJCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC<br>TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC |
| WI-7619o | 228 A G --- | --- | ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC<br>AGAGAAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG<br>CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT<br>CGCTTTCTTCTTACACAGAAACAT/A/GJACATACCGAGAAACCTATTTC |
| WI-7619n | 237 G C --- | --- | ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC<br>AGAGAAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG<br>CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT<br>CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC    |
| WI-7619m | 99 C T ---  | --- | ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC<br>AGAGAAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG<br>TGCCAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC<br>TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC |
| WI-7619l | 189 T A --- | --- | ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC<br>AGAGAAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG<br>CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCCTC<br>TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC    |

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| WI-7619k | 90 C G ---  |  |  | ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC<br>AGAGAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC<br>ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCT<br>CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC |
| WI-7619j | 206 T G --- |  |  | ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC<br>AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG<br>CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT<br>CGCT/GTTCCTTTACACAGAAACATACACATACCGAGAAACCTATTTC      |
| WI-7619i | 106 C G --- |  |  | ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC<br>AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC<br>ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCT<br>CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC        |
| WI-7619h | 150 T C --- |  |  | ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC<br>AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG<br>CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCT<br>TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC       |
| WI-7619g | 228 A G --- |  |  | ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC<br>AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG<br>CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT<br>CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC        |
| WI-7619f | 237 G C --- |  |  | ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC<br>AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG<br>CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT<br>CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC        |
| WI-7619e | 99 C T ---  |  |  | ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC<br>AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG<br>TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCT<br>TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC    |
| WI-7619d | 189 T A --- |  |  | ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC<br>AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG<br>CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT<br>TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC     |

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| WI-7619c | 90 C  | --- | --- | ACAAGGCGACTTGAAGAGGACGCGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC<br>AGAGAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC<br>ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTCCATCTTTTCCCT<br>CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC        |
| WI-7619b | 206 T | G   | --- | ACAAGGCGACTTGAAGAGGACGCGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC<br>AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG<br>CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT<br>CGCT[G]TCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC            |
| WI-7619  | 189 T | A   | --- | ACAAGGCGACTTGAAGAGGACGCGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC<br>AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG<br>CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTCCAT[ A ]CTTTTCCCTC<br>TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC         |
| WI-7626d | 105 A | G   | --- | CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA<br>TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGC[A/G]TTAAACCCACATCATGGACCAATGTG<br>CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT<br>CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTCA |
| WI-7626c | 155 C | T   | --- | CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA<br>TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAATGTGCCA<br>TACTAATGATGAGCAATTTAG[C/T]ACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT<br>CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTCA    |
| WI-7626b | 28 T  | A   | --- | CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAG<br>TAATCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAATGTG<br>CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT<br>CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTCA       |
| WI-7626  | 144 T | C   | --- | CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA<br>TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAATGTGCCA<br>TACTAATGAT[C/G]GAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT<br>CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTCA  |
| WI-7689c | 134 A | G   | --- | TCCATAACCGCTGATTCTCAGGGTCTCTGTGCGCCCAACCCAGATGGGGAAAGCACAGGTGGGC<br>TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGACGCCACCCAGCAAAAGGTTGTTCTCTAA[A]<br>[G]TAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT<br>GATAATATTGTGGTGCCCAAAATAAATGGATTATTATAGAAATTCATATGAC         |

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| WI-7689b | 134 | A G --- | --- |  | TCCATAACCGCTGATTCACAGGCTCTGCTGCCGCCACCCACCCAGATGGGGAAGACAGGTGGGC<br>TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGCTCTAAJA<br>/GTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT<br>GATAATATTGGTGGCCACAAATAAAATGGATTATTAGAAATTCATATGAC   |
| WI-7689  | 121 | G A --- | --- |  | TCCATAACCGCTGATTCACAGGCTCTGCTGCCGCCACCCAGATGGGGAAGACAGGTGGGC<br>TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGCTCTAA<br>AATAAGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT<br>GATAATATTGGTGGCCACAAATAAAATGGATTATTAGAAATTCATATGAC          |
| WI-7690  | 45  | G A --- | --- |  | TGGAGAACATTCATCTTCCGTCACATTTTCATCAATGAAGATTAG/ACTGAGATCCAGAGAGG<br>CTGGATGACTTGTCTCAAGTTACACGACATGGTAGTGGCAAGAGAGTCCAGAGTCTGGCCCTTGAT<br>GCCAGCTCAGTGCACAAAGCTCAGTAGGAGGATGTTCCAGTGATGAGGCCACCCAGGAAGCAC<br>AGGTCCAAAGGCTGGTCCACACTTATCAGCAGCAACACTGTCAAGTTCATCC |
| WI-7703b | 164 | T C --- | --- |  | ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC<br>AGTGATCAAGTTATTTTAAATTTGTTTTCACATTTGGAACAAGTCAGTCAATTCAGATATGATCAAA<br>TGCTATAAACCAAACTGATGAAGTAAATTC/CGGTCTCTCACTGTTTTTAACTCTAAATTC<br>TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATGTT   |
| WI-7703  | 156 | T C --- | --- |  | ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC<br>AGTGATCAAGTTATTTTAAATTTGTTTTCACATTTGGAACAAGTCAGTCAATTCAGATATGATCAAA<br>TGCTATAAACCAAACTGATGTT/CAAGTAAATGGTCTCTCACTGTTTTTAACTCTAAATTC<br>TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATGTT   |
| WI-7743e | 106 | C A --- | --- |  | TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGGCCTTGGAGCCAAAGG<br>GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT<br>GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCAGGAGGTCAGGA<br>GAGGGCAGAACAGCCGCTCTGTCTGOCAGCCAGCAGCCAGCTCTCAGCC     |
| WI-7743d | 275 | C T --- | --- |  | TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGGCCTTGGAGCCAAAGG<br>GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT<br>TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCAGGAGGTCAGGAGAG<br>GGGCAAGACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG   |
| WI-7743e | 106 | C A --- | --- |  | TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGGCCTTGGAGCCAAAGG<br>GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACT<br>GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCAGGAGGTCAGGA<br>GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC     |

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| WI-7743d | 275 | C T --- | --- | TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG<br>GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAAATAAGTACTGTG<br>TACAGAAATTCGTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG<br>GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCTCTCAGCCAAACG  |
| WI-7743e | 106 | C A --- | --- | TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG<br>GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAAATAAGTACTGTG<br>GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAAATAAGTACT<br>GTGTACAGAAATTCGTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA<br>GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCTCTCAGCC |
| WI-7743d | 275 | C T --- | --- | TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG<br>GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAAATAAGTACTGTG<br>TACAGAAATTCGTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG<br>GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCTCTCAGCCAAACG  |
| WI-7743c | 106 | C A --- | --- | TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG<br>GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAAATAAGTACT<br>GTGTACAGAAATTCGTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA<br>GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCTCTCAGCC  |
| WI-7743b | 275 | C T --- | --- | TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG<br>GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAAATAAGTACTGTG<br>TACAGAAATTCGTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG<br>GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCTCTCAGCCAAACG  |
| WI-7743  | 106 | C A --- | --- | TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG<br>GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAAATAAGTACT<br>GTGTACAGAAATTCGTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA<br>GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCTCTCAGCC  |
| WI-7743  | 275 | C T --- | --- | TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG<br>GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAAATAAGTACTGTG<br>TACAGAAATTCGTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG<br>GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCTCTCAGCCAAACG  |
| WI-7758  | 144 | A G --- | --- | TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATTTAAAGAGGTATCTGTTTAAACATTTCC<br>TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG<br>GAGAGAAATC[A/G]TAGTTTAAACTGCATTATAAAATTTTAAACAGAAATTAAGTAGATTTTAAAAA<br>GATAAAATGTGTAAATTTTGTATTATTTCCCATTTGGACTGTAACTGACTGCC   |

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| WI-7765b | 126 | G C --- | --- | ACAGGGGCTTTGGCAGGTGCAGCCCCCACTGCGCTTTGACCTGCGCTCCCTTCATGCATGGAATTCCTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAGGGTGCAGTATGG[G/C]TAGGGGAAACATTCCTCCTTGAGTCAAAAATCTCAATTCCTCCCTATCTTGGCCACCCTCATGCTGTGTGACTCAAAACCAATCACTGAACCTTTGCTGAGCCTGTAAAATAAAAGGTGGGA |
| WI-7773b | 237 | C G --- | --- | TTAATTTACTGATTCAGCAAGACCAATCATTTGTATCAGATTATTTTAAAGTTTTATCCGTAGTTTTGATAAAGATTTTCTATTCCTTGGTCTGTGCAGAGAACCTAATAAGTCTACTTTTGCCATTAAAGGCA GACTAGGGTTCATGCTTTTACCCCTTNNNNNNNNNTGTAAAAGTCTAGTTACCTACTTTTCTTTGATTTTCGACGTTTACTAGCCATCTCAAGCAA[C/G]TTTCGACGTTTGA      |
| WI-7774b | 170 | T C --- | --- | TGCAACCTCTTTTCGTGATGGGAGCCTGCTGTGTCAGACTCCAGTAGCGAGACGGACCCAGAAATCAGATCCAGCTTCGGCAITTTGATCAGACCAACAGTGTCTTCCCGGGAGGAAACACTTTTTTTAA TTACCTTTTGCAGGCACCACTTAACTGTCTTT[C]ATACCTTGTCTTATTAAATGAGCGACTTAAA ATGATTGAAAATAATGCTGTCTTTAGTAGCAAGTAAAATGTGCTGTGCT        |
| WI-7785c | 165 | G ---   | --- | GCAGAGACCTTCCAAGGACATATTGCAGGATTCGTATAAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCAATGGAAATAAACTGTCTCCCACTTGTCTATGAAACTGCG ACATTGGTCAITTTGTAATANNNNNNNNNGCCAGGCTAATCCAATTATTATATCACAATTTACCA TAAATTTATTGTGCTCAITTTGATGATTTATTGTAATGTATCTTGGTGTGCTG    |
| WI-7785b | 165 | G ---   | --- | GCAGAGACCTTCCAAGGACATATTGCAGGATTCGTATAAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCAATGGAAATAAACTGTCTCCCACTTGTCTATGAAACTGCG ACATTGGTCAITTTGTAATANNNNNNNNNGCCAGGCTAATCCAATTATTATATCACAATTTACCA TAAATTTATTGTGCTCAITTTGATGATTTATTGTAATGTATCTTGGTGTGCTG    |
| WI-7785  | 156 | T ---   | --- | GCAGAGACCTTCCAAGGACATATTGCAGGATTCGTATAAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCAATGGAAATAAACTGTCTCCCACTTGTCTATGAAACTGCG ACATTGGTCAITTTGTAATANNI-<br>/TJNNNNNNNGCCAGGCTAATCCAATTATTATATCACAATTTACCATAATTTATTTTGTCCATTGA TGTATTTATTTGTAATGTATCTTGGTG |
| WI-7789c | 84  | G A --- | --- | TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCGCTCTGCTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT |
| WI-7789b | 84  | G A --- | --- | TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCGCTCTGCTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT |



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| WI-7830d | 150 | C T | --- |  |  | GCAGGAAATAGTCACTCATCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA<br>TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTATCATCATTTCTATGCCAAACAGGAACG<br>ATCCATAACTTTAGT[C/TTTAAATGTACACATTGCATTTTGATAAAATAAATTTGTTGTTCCCTTTG<br>AGGTTGATCGTTGTTGTTGTTGCTGCACITTTTACTTTTTTTCGGTGTGGA |
| WI-7830c | 54  | G A | --- |  |  | GCAGGAAATAGTCACTCATCCACTCCACATAAGGGTTTAGTAAGAGAAGTCT[G/AT]CTGTCTGA<br>TGATGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTATCATCATTTCTATGCCAAACAGGA<br>ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATAAATTTGTTGTTCCCTTTG<br>AGGTTGATCGTTGTTGTTGTTGCTGCACITTTTACTTTTTTTCGGTGTGGA  |
| WI-7830b | 134 | G A | --- |  |  | GCAGGAAATAGTCACTCATCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA<br>TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTATCATCATTTCTATGCCAAACAGGAAC[<br>G/AT]TCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATAAATTTGTTGTTCCCTTTG<br>AGGTTGATCGTTGTTGTTGTTGCTGCACITTTTACTTTTTTTCGGTGTGGA |
| WI-7830  | 44  | A G | --- |  |  | GCAGGAAATAGTCACTCATCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGA<br>TGATGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTATCATCATTTCTATGCCAAACAGGA<br>ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATAAATTTGTTGTTCCCTTTG<br>AGGTTGATCGTTGTTGTTGTTGCTGCACITTTTACTTTTTTTCGGTGTGGA      |
| WI-7865e | 25  | C T | --- |  |  | CCACTTCTATCTGATTTTCCAG[C/TTAAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA<br>GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG<br>GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC<br>CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA    |
| WI-7865d | 191 | C T | --- |  |  | CCACTTCTATCTGATTTTCCAG[C/TTAAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA<br>ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGGG<br>ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC<br>CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA         |
| WI-7865c | 25  | C T | --- |  |  | CCACTTCTATCTGATTTTCCAG[C/TTAAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA<br>GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG<br>GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC<br>CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA    |
| WI-7865b | 191 | C T | --- |  |  | CCACTTCTATCTGATTTTCCAG[C/TTAAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA<br>ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGGG<br>ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC<br>CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA         |



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| WI-7865  | 25  | C T | --- |  |  | CCACCTCCTATCTGATTTTCCAG[C]TAAATGAGGCGAGGCAATCTAGCTTCCACAAAACATCTA<br>GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG<br>GGTATGCTACTCATAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC<br>CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA       |
| WI-7865  | 191 | C T | --- |  |  | CCACTTCTATCTGATTTTCCAGCAATGAGGCGAGGCAATCTAGCTTCCACAAAACATCTAGCC<br>ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGGT<br>ATGCTACTCATAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGT[C]TJGAAAAAC<br>CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA         |
| WI-7867c | 92  | A C | --- |  |  | TTCAAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCC<br>CTAACAATTACCTGTCAAGAG[C]GAGTGCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC<br>CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTTCTTGTCTATAAATCTATGT<br>CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG      |
| WI-7867b | 92  | A C | --- |  |  | TTCAAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCC<br>CTAACAATTACCTGTCAAGAG[C]GAGTGCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC<br>CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTTCTTGTCTATAAATCTATGT<br>CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG      |
| WI-7868c | 173 | C T | --- |  |  | TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT<br>CACCAACCTGTCTCCCTGTGATCCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACACAAT<br>CATTTAATTTCCCTGTCTTACCCCTATTCAAGCA[C]TJTAGAGGCCAGAAAAATGGGCAAAATTAT<br>CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT     |
| WI-7868b | 173 | C T | --- |  |  | TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT<br>CACCAACCTGTCTCCCTGTGATCCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACACAAT<br>CATTTAATTTCCCTGTCTTACCCCTATTCAAGCA[C]TJTAGAGGCCAGAAAAATGGGCAAAATTAT<br>CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT     |
| WI-7868  | 66  | T C | --- |  |  | TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT<br>/CJTCACCCAACTGCTCCCTGTGATCCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACAC<br>AATCATTTAATTTCCCTGTCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAAATGGGCAAAATTAT<br>CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT     |
| WI-7870b | 85  | T C | --- |  |  | ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG<br>GTGGGGTGGCGGGAATCCJTCJATTTATCAGACTCTGTAATTTGAATATAAATGTTTACTCAGAGGA<br>GCTGCAAAATGCTGCAAAATGAAATCCCAATGAGCACTAGAAATTTTAAACATCATTTACTGCCAT<br>CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG |

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| WI-7870  | 76 C T ---  | --- | --- | ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAGGG<br>GTGGGGTGGC/TGGGAATCCTATTATCAGACTCTGTAATGGAATATAAATGTTTTACTCAGAGGAG<br>CTGCAAAATTGCTGCAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATTAATGCCCATC<br>TTTATCATGAAGCACATCAATTACAAGCTGTAGACACCTAATATCAATTG   |
| WI-7889c | 54 C ---    | --- | --- | TTAGGTCATGCCACTCCCGCAGGAGCAGCTGGCACTGACAGCTGGGGGGGGGGCTCTCCOCTG<br>CAGCCGTGAGGACTTAGCTCATGAGTGGAAGTCACTACAGGACTGGCCGGGGGGGGGGCTCT<br>GGCTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAAATGGGGGGCTGGACACC<br>TACAGCAGCAGCATGTCCCTCCAAAGGCTGTCTCTCCAGAGCACAAGAAAG            |
| WI-7889b | 54 C ---    | --- | --- | TTAGGTCATGCCACTCCCGCAGGAGCAGCTGGCACTGACAGCTGGGGGGGGGGCTCTCCOCTG<br>CAGCCGTGAGGACTTAGCTCATGAGTGGAAGTCACTACAGGACTGGCCGGGGGGGGGGCTCT<br>GGCTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAAATGGGGGGCTGGACACC<br>TACAGCAGCAGCATGTCCCTCCAAAGGCTGTCTCTCCAGAGCACAAGAAAG            |
| WI-7894c | 142 A G --- | --- | --- | AGCCACCCCAATATACTGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT<br>TTTACTATATACATACATCAATTAACCTATGCTCTATGTTTGTGAATTTATTTGCGTATAC<br>ATTATC/A/GJTATGTAATAATTTGCAITTTTATTTGAAATTTATGTTCTTGAGATTTATCCACATTG<br>AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA               |
| WI-7894b | 142 A G --- | --- | --- | AGCCACCCCAATATACTGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT<br>TTTACTATATACATACATCAATTAACCTATGCTCTATGTTTGTGAATTTATTTGCGTATAC<br>ATTATC/A/GJTATGTAATAATTTGCAITTTTATTTGAAATTTATGTTCTTGAGATTTATCCACATTG<br>AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA               |
| WI-7900e | 84 C T ---  | --- | --- | GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT<br>GCCACAACCTGGCCATG/C/TGCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGA/C/TJACA<br>AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAGTACATCTCTCAGATTTGAACCCAGTGAAA<br>TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC |
| WI-7900d | 128 C T --- | --- | --- | GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT<br>GCCACAACCTGGCCATG/C/TGCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGA/C/TJACA<br>AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAGTACATCTCTCAGATTTGAACCCAGTGAAA<br>TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC |
| WI-7900e | 84 C T ---  | --- | --- | GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT<br>GCCACAACCTGGCCATG/C/TGCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGA/C/TJACA<br>AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAGTACATCTCTCAGATTTGAACCCAGTGAAA<br>TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC |







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| WI-8021b | 57 C T ---  |  |  | ACAACTCTCAGAAGGACTGTGCAAGTCAATGAGTCGGCTGTGAATTCATCTGGAAC[C/T]GATCCC<br>ACGTCCTTAGAACCTTCACCACAAGGAGTTTCTGTAGTATTCTCAAAGTCTTGGTAGGCATTCGA<br>ACTGGTCTTTCACCTTTGAGATCTTTCTTTTGGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG<br>GATTTACGTTTGGGCTTGTAGGSGTGATTCGAATTCGGTGAATGGCA          |
| WI-8021  | 57 C T ---  |  |  | ACAACTCTCAGAAGGACTGTGCAAGTCAATGAGTCGGCTGTGAATTCATCTGGAAC[C/T]GATCCC<br>ACGTCCTTAGAACCTTCACCACAAGGAGTTTCTGTAGTATTCTCAAAGTCTTGGTAGGCATTCGA<br>ACTGGTCTTTCACCTTTGAGATCTTTCTTTTGGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG<br>GATTTACGTTTGGGCTTGTAGGSGTGATTCGAATTCGGTGAATGGCA          |
| WI-8024c | 206 A G --- |  |  | CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA<br>GCTTGATTTACAGGAGGACAGGGCAGAGGATCCCAAGTGGCACTTCCCATGGGAAGACAGAAGAGT<br>GGCCCCAGAGATGGAAGGACCCAGTGTCTATCACCACAACCACTTTCAAGCCGCTCTAGCCTCTAA<br>TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCGTGCTAGTACACAAGGAAGAGC |
| WI-8024b | 206 A G --- |  |  | CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA<br>GCTTGATTTACAGGAGGACAGGGCAGAGGATCCCAAGTGGCACTTCCCATGGGAAGACAGAAGAGT<br>GGCCCCAGAGATGGAAGGACCCAGTGTCTATCACCACAACCACTTTCAAGCCGCTCTAGCCTCTAA<br>TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCGTGCTAGTACACAAGGAAGAGC |
| WI-8077  | 167 A G --- |  |  | GAATGAGCCTTCTAGCGCGAGGACCTGCTGCTGTGTTGGCCTGCACATGCTATGGAATGC<br>TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAACTCCTTTCT<br>AAGGAGTCTGGGTGTCTATGCCCTACAACCC[A/G]TAAATTCATCAGATGGATTTTATTAAACGTT<br>GTGATTGTGACTTACTTTCCAACTGACTCTGGCATAACAAGGGAATAA                |
| WI-8118f | 114 G C --- |  |  | TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTCTAAGGAAGCTAT<br>GTACTTCATGCTGTGGAACTGGCAATACAGATGTAGCTGTGTTG[C/T]TTCTTAGCCTTGAAGA<br>TGACCAGGTAGAGACAGAGTGAGACCAAGTTTTCGTGATTTCCCTGCTCCTCTATTCCTTCCT<br>AAAAATCAGACTCAATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA          |
| WI-8118e | 40 A G ---  |  |  | TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTCTAAGGAAGCTAT<br>GTACTTCATGCTGTGGAACTGGCAATACAGATGTAGCTGTGTTGTTTCTTAGCCTTGAAGA<br>TGACCAGGTAGAGACAGAGTGAGACCAAGTTTTCGTGATTTCCCTGCTCCTCTATTCCTTCCT<br>AAAAATCAGACTCAATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA              |
| WI-8118d | 118 T G --- |  |  | TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTCTAAGGAAGCTAT<br>GTACTTCATGCTGTGGAACTGGCAATACAGATGTAGCTGTGTTGTTG[C/T]TTAGCCTTGAAGA<br>TGACCAGGTAGAGACAGAGTGAGACCAAGTTTTCGTGATTTCCCTGCTCCTCTATTCCTTCCT<br>AAAAATCAGACTCAATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA          |

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| WI-8118c | 44 C T ---  |  |  | TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGATGA/C/TCACTCCCTTCTAAGGAAGC<br>TATGTACTTTCATGCTGTGGAACTGGCAATACAGAAATGAGCTTGTGTTTCTTAGCCCTTGAAGA<br>TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTCCCTGCTCCTCTATTCCTTCTCT<br>AAAAATCAGACTCATTTGACCACTAGTCTTGAGGACTCAAGCTGAATGA            |
| WI-8118b | 88 T C ---  |  |  | TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGTAAAGGAAGCTAT<br>GTACTTCATGCTGTGGAAAC/T/CJGGCAAAATACAGAAATGAGCTTGTGTTTCTTAGCCCTTGAAGA<br>TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTCCCTGCTCCTCTATTCCTTCTCT<br>AAAAATCAGACTCATTTGACCACTAGTCTTGAGGACTCAAGCTGAATGA        |
| WI-8171d | 299 C T --- |  |  | TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCTCGGGAAG<br>AGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGAGACCCCTCTTGGCACACA<br>TTTATGGAGGTTGTCCCTGAAGAGAGGCGAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAAGGC<br>ACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCACGGCA             |
| WI-8171c | 46 A G ---  |  |  | TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGTGGCAGCAGGCTCGGG<br>AAGAGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGAGACCCCTCTTGGCAC<br>ACATTTATGGAGGTTGTCCCTGAAGAGAGGCGAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAA<br>GGCACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCAC              |
| WI-8171a | 46 A G ---  |  |  | TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGTGGCAGCAGGCTCGGG<br>AAGAGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGAGACCCCTCTTGGCAC<br>ACATTTATGGAGGTTGTCCCTGAAGAGAGGCGAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAA<br>GGCACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCAC              |
| WI-8171b | 298 T C --- |  |  | TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGCTCGGGAAG<br>AGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAAGAGACCCCTCTTGGCACACA<br>TTTATGGAGGTTGTCCCTGAAGAGAGGCGAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAAGGC<br>ACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCACGGCA            |
| WI-8314b | 85 G C ---  |  |  | GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT<br>TTCTCTATCTCTAAGGG/G/C/AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT<br>GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAAGCTTTC<br>TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT |
| WI-8314  | 78 C G ---  |  |  | GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT<br>TTCTCTATCTCTAAGGG/G/C/AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT<br>GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAAGCTTTC<br>TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT |

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| WI-8321  | 178 | G A | --- |  |  | TTTTAAATATGCCCCGTTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG<br>TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTATACTAGTCTCTGAGAAG<br>TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA<br>TTTTGCTATGGTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC |
| WI-8321  | 178 | G A | --- |  |  | TTTTAAATATGCCCCGTTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG<br>TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTATACTAGTCTCTGAGAAG<br>TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA<br>TTTTGCTATGGTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC |
| WI-832b  | 123 | A C | --- |  |  | TATGTACTCACTTTTCAGTTACCCCGTGCCTCCAGAAATGCGATGTTGCTCCACCTGGGGGGGATATA<br>AATTACCTCTAGATTGTCAAAGCCAGTCTTTCCCTTCCCTGTGCAGCCTTAGA/CJACTAAGTAG<br>CAGTACTGTTGGTGTGTTTCTTCTCCAGCAATGCTACTGCAGCTACTTAGTAACAACCTAG<br>AGGTGGAGGNTTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA      |
| WI-8332  | 114 | A C | --- |  |  | TATGTACTCACTTTTCAGTTACCCCGTGCCTCCAGAAATGCGATGTTGCTCCACCTGGGGGGGATATA<br>AATTACCTCTAGATTGTCAAAGCCAGTCTTTCCCTTCCCTGTGCAGCCTTAGA/CJACTAAGTAG<br>CAGTACTGTTGGTGTGTTTCTTCTCCAGCAATGCTACTGCAGCTACTTAGTAACAACCTAG<br>AGGTGGAGGNTTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA      |
| WI-8378b | 311 | T C | --- |  |  | TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATATGGCAGAAGCGAAGG<br>GGAAGCAAGGACCTTCTCACATGGCAGCAGGAGAAAGAGAAAGGAGAGAGTCTACACACTTTT<br>AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCAGTGGGGGATGGCACTAAACCATTAGA<br>AACTGCCCCATGATCCAATCACTNTCACCAGGCCCTCCTCCAACACGTTGGG   |
| WI-8378  | 308 | T C | --- |  |  | TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATATGGCAGAAGCGAAGG<br>GGAAGCAAGGACCTTCTCACATGGCAGCAGGAGAAAGAGAAAGGAGAGAGTCTACACACTTTT<br>AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCAGTGGGGGATGGCACTAAACCATTAGA<br>AACTGCCCCATGATCCAATCACTNTCACCAGGCCCTCCTCCAACACGTTGGG   |
| WI-8426  | 184 | T G | --- |  |  | TTTAGCACATATTTAGCATTAGCCTCAACGATACAGCAATATGTTACATTCTCTGTGAAAACAG<br>TTGTTGTAGACTGTTAANNNNNNNAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNNTAA<br>GAGGNTTCTTTGCTGTGGANGGGTGGCTTGTGCTGAACCTCCATCTGT/GJGCCCTGTAGCTGGTG<br>AGGCTGGAGTATGGANGGNCNCCGGGGCCCTTGGCNATGNATCAGTGAG    |
| WI-8450h | 61  | C A | --- |  |  | TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCCTCTACATACACTC/AJCA<br>TCITCTATCTTAGTTCCAAGTTTATGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA<br>AAAAACCTTCCAGTTATTGTGAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAACTAC<br>AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCTAT  |



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| WI-8450g | 55 T C ---  |  |  | TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCCAT<br>CTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA<br>AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC<br>AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT  |
| WI-8450f | 108 T A --- |  |  | TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT<br>CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTC/TTTTAAAGA<br>AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC<br>AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT |
| WI-8450e | 125 T C --- |  |  | TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT<br>CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTC/TTTTAAAGA<br>AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC<br>AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT |
| WI-8450d | 125 T C --- |  |  | TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT<br>CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTC/TTTTAAAGA<br>AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC<br>AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT |
| WI-8450c | 108 T A --- |  |  | TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT<br>CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATTCACCAATTCCATTGTTATTTTAAAGA<br>AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC<br>AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT   |
| WI-8450b | 61 C A ---  |  |  | TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTTCACACTC<br>TCTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA<br>AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC<br>AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT |
| WI-8450a | 55 T C ---  |  |  | TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT<br>CTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA<br>AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC<br>AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT   |
| WI-8458b | 60 A G ---  |  |  | CAAGGAAAGCTGTCAGTCTTCATAAACTTCAAGAGTTACAAAATACGTTATTTTAAAGCTA<br>CAATTCAAGATTAGCATCCAAACCTACAAACATGATGATACATTGTCACACACCATACAACTTCAG<br>ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATACCTTGTAAGAACTTTATTGTGCACAGT<br>GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTTCTCA       |

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| WI-8461c | 105 A T --- | --- | --- | CTTCCTCCTCCAAAATCTACATGAATACCTGAAGACAAATTAACACCACTTACAAATGCCAATTA<br>GACAAAGAGANTAAATGATATAATATAATCAATTTTATJNNNNNNNNCCCTTGCTTATTACAT<br>TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA<br>AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG       |
| WI-8461b | 38 T C ---  | --- | --- | CTTCCTCCTCCAAAATCTACATGAATACCTGAAGACAAATJGATAACTACAACCTTACAAATGCCAA<br>TTAGACAAAGAGANTAAATGATATAATATAATCAATTTTNNNNNNNNCCCTTGCTTATTACAT<br>TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA<br>AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG     |
| WI-8461  | 38 T C ---  | --- | --- | CTTCCTCCTCCAAAATCTACATGAATACCTGAAGACAAATJGATAACTACAACCTTACAAATGCCAA<br>TTAGACAAAGAGANTAAATGATATAATATAATCAATTTTNNNNNNNNCCCTTGCTTATTACAT<br>TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA<br>AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG     |
| WI-8461  | 105 A T --- | --- | --- | CTTCCTCCTCCAAAATCTACATGAATACCTGAAGACAAATTAACATACTACAACCTTACAAATGCCAATTA<br>GACAAAGAGANTAAATGATATAATATAATCAATTTTATJNNNNNNNNCCCTTGCTTATTACAT<br>TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA<br>AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG |
| WI-9438  | 77 A G ---  | --- | --- | AATAACATGTTATGAACAAGCTGGTTACAAGTAGTAGGTAGTAACTTAAATTTTGATAAAAAAAT<br>TAAAAAGCATJAGAACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTACTTC<br>TGCTCAGTAATTAATATTCTCCCTTTGTTTGTCTTTTAAAAAACATTATTCTGAAAAAATAA<br>ATCAGAAAAACATGATCGTGGAGAAATTATTA                            |
| WI-9439b | 101 C T --- | --- | --- | ACAGAAAATTGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA<br>CAGAAAAATCCCAGTCTGCAGTCACTACCTGTGJTGTCACACTGTACCATCTCAGTCCCCTCT<br>GCCTGTAACCTTAGAAAAACAGCCCTACCCCGAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA<br>CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGACCTGTAAAAACAAG  |
| WI-9439a | 76 C T ---  | --- | --- | ACAGAAAATTGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA<br>CAGAAAAATJCCAGTCTGCAGTCACTACCTGTGTCGCACACTGTACCATCTCAGTCCCCTCT<br>GCCTGTAACCTTAGAAAAACAGCCCTACCCCGAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA<br>CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGACCTGTAAAAACAAG   |
| WI-9446b | 75 T C ---  | --- | --- | GAAAGCTTGATTAGGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA<br>TAAAAAAATJCCCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAGCAAAACCTTTTAAAT<br>TACTCATCTTTCATATGTGTGTTGTNCCCTACTNTTATCACTGTGCTCTGCTCTTTGCTACCTA<br>TGNGAACTGCACACTATCTGTGGCAATATTGT                        |

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| WI-9446  | 75  | T C ---  | --- |  | GAAGCCTTGATTAAAGGAGGNNTTATTGTGATGNAACCTACCATTCCATAGACTATAAAGANCAITTA<br>TAAAAAAAT/CJCCTCTAAAGNGACACATGCCCAAATGACCCANGNCATGAAGCAAACCTTTTAAAT<br>TACTCATCTTTTCATATGTGTGTTGTCNCCCTACTNTTATCACTGTGTCTCTGTCTTTGTCTACCTA<br>TGNGAACTGCACACTATCTGTGGCAATATTGT                          |
| WI-9497b | 185 | A -- --- | --- |  | ATTAAATGTCAAGGTTTCATGTTACATTTTCTTATATCAAGTACAATGGTATATATACITTTTTTT<br>GAGATAATTATCTAGATCCAGGCTTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA<br>TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAGTATGTTAATGTCACTT<br>GGAATTCACATGGAAGGCCAACAAAATAACTAAAACITGACTAATGAAG            |
| WI-9497  | 185 | A -- --- | --- |  | ATTAAATGTCAAGGTTTCATGTTACATTTTCTTATATCAAGTACAATGGTATATATACITTTTTTT<br>GAGATAATTATCTAGATCCAGGCTTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA<br>TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAGTATGTTAATGTCACTT<br>GGAATTCACATGGAAGGCCAACAAAATAACTAAAACITGACTAATGAAG            |
| WI-9523b | 193 | C A ---  | --- |  | GTGAAAAAGTTTCTATTCTATCCATCATACAATAGATTGTGCTAAGGATCATTTTGGAGAATGTG<br>CAGCATTGAGAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCACA<br>GACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGGTATTTCCACACATTGTAC/AJAGTG<br>AAAGCTCTTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT          |
| WI-9523a | 47  | G A ---  | --- |  | GTGAAAAAGTTTCTATTCTATCCATCATACAATAGATTGTGCTAAGGATCATTTTGGAGAAT<br>GTGCAGCATTGAGAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCA<br>CAGACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGGTATTTCCACACATTGTACAGTGA<br>AAGCTCTTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT             |
| WI-9554  | 202 | T C ---  | --- |  | AAAAACACAAGTTTTCATACATCACAAAAAGCTTCCATTATAACACAGAAGTGATTATTACCAGAC<br>AAGCATCAGTGATGTATCTACTGCCCTTNTAGTTGTTATTGTACAATGCTGTAGATAATGCGCCCATG<br>CAATACACCCAAAGAACACTAGAGTCTCTACACCCCAAGTACAATAATGATAAAGCAGCCCTCTGCAAGTG<br>GTT/CJGCTGGATACCACTAAGAACTCTACTGCAGCCATGTTGGTTATGATTTT |
| WI-9555  | 97  | G A ---  | --- |  | CCAAAAGCCAAACCATTCATATGTATGGATTTCATAAACAATTTATGATCCTTTTTTGAGGTAAGTAT<br>AAATACCTTTTACATGGCTAACCTTCTAAC[G/A]CTTGAAAAATCAATTTCAAGGGACTCTTTAATCA<br>GTTAAATATCTGCTTTAGAAGGCCAACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTCAG<br>GGNTAAATGGTACAAAAAGGCTGTAACCTCTTTTNCITTCACATTGATCACA    |
| WI-9625b | 172 | A T ---  | --- |  | TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT<br>TAAACAATAGCTACCATATATTTGTATCTNCTCCTGGGAAAAAATCTTGAAAAAACAACACGCACA<br>TAAGTATCAATAACTGAGGGTTGTGGACAAGTTACTTCTTA/TGTTTACCAATTTTATATTGACATAA<br>AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACTGACAAATCTTTTC       |

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| WI-9625  | 172 A T --- | --- | TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT<br>TAAACAATAGGTACCATATATTTGTATCTNCTCCTTGGAAAAACCTTGGAAAAACACGCACA<br>TAAGTATCATAACTGAGGTTGTGGACAAGTTACTTCTTA/TGTTTACCAATTTTATATTGACATAA<br>AGTAGCACAGACTAGTTATTTCAATTAATAAAAAACACACTGACAAATCTTTTC     |
| WI-9647  | 144 C T --- | --- | TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTATGCTACTATACCTTTTTCATCCTTTCA<br>ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAGCT<br>TACAACTC/TGTCCTTTACCTGATACATTTATCCATTTACTTTCAATTTGGATTTTAAAAATGTTA<br>ACTTAATACGTCTCTTCAGATGTCCTGCTTTTGTAGTTAATGTTT            |
| WI-9676n | 114 A G --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA<br>GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA/AG/GATGTGGCTTTCCTGCC<br>CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCTGTCATGAAATAACTTGA<br>GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT |
| WI-9676m | 184 G T --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA<br>GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC<br>ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCTGTCATGAAATAACTTGA<br>GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT       |
| WI-9676l | 84 A C ---  | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA<br>GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC<br>CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA<br>GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT      |
| WI-9676k | 202 C T --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA<br>GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC<br>ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA<br>C/T/CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT        |
| WI-9676j | 92 C T ---  | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA<br>GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC<br>CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA<br>GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT      |
| WI-9676i | 173 T C --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA<br>GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC<br>ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTTCCTCTGTGCGCATGAAATAACTTGA<br>GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT         |

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| WI-9676h | 134 | C A --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA<br>GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGGCCCC<br>C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA<br>AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT |
| WI-9676g | 202 | C T --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA<br>GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGGCCCC<br>ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA<br>C/TJAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT     |
| WI-9676f | 184 | G T --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA<br>GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGGCCCC<br>ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA<br>GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT     |
| WI-9676e | 173 | T C --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA<br>GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGGCCCC<br>ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTT/CJCCCTCTGTGGCATGAAATAACTTGA<br>GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT |
| WI-9676d | 134 | C A --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA<br>GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGGCCCC<br>C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA<br>AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT |
| WI-9676c | 114 | A G --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA<br>GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGGCCCC<br>CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA<br>GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT   |
| WI-9676b | 92  | C T --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA<br>GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGGCCCC<br>CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA<br>GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT   |
| WI-9676a | 84  | A C --- | --- | GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA<br>GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGGCCCC<br>CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA<br>GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT   |

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| WI-9738b | 40 C A ---  | --- | --- | TGGACCAACACAGACAGATGATTCTCGTGGTGCCTGTGTAC/AJATTACAACCTCAATTGATCACATGC<br>AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTTCCCTTT<br>GAGTCAACAAAAGACTCTGCTTGTACCTTGCCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA<br>TCTTTTATTCTGTCCCTTATGTTGGTGGGCACATGCTGTATTGCTGCC         |
| WI-9738  | 40 C A ---  | --- | --- | TGGACCAACACAGACAGATGATTCTCGTGGTGCCTGTGTAC/AJATTACAACCTCAATTGATCACATGC<br>AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTTCCCTTT<br>GAGTCAACAAAAGACTCTGCTTGTACCTTGCCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA<br>TCTTTTATTCTGTCCCTTATGTTGGTGGGCACATGCTGTATTGCTGCC         |
| WI-9756  | 47 A ---    | --- | --- | ACTGAAATGTAATGGCCAAAGGCCACCCAGGACCTTAAATCATAGAAGTTAATCTGTGGGAAAA<br>GAGTAACACAAAAGATCTAAACAGAGCAGGATGTGATGTAATGTGCCCTTATCACCTTTAGTC<br>AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTTCCACAAACACACAGAAATATACACTTTTGGGAA<br>ATTCCACTTAACCACTTGATTCTTCACTTTTATGATTTAAACTCTCCGTGG            |
| WI-9758  | 135 A G --- | --- | --- | GATGGTCCCTTAAGGATTGCAATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT<br>TAGGAACTGGGAGAAATCAATTCAAGAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA<br>A/GJTAATAAATAACTCTGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTTCTAAAT<br>ATTACG   |
| WI-9778  | 127 G A --- | --- | --- | ATTTAATCCAGGCAGCGGGGAAAAATGGATACITTTTCATATGCTCTGTACCCAACTATAAACTTTTG<br>GTTCTCATGCACCATTTTCATTTTGCCTTCTCCTCACTCCAGTACCCTGATTTTACCAATT[G/A]CTCTC<br>ATAATTGACTTTGCTACTCTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATACACACTTTGCCCTCA<br>AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC |
| WI-9832  | 116 C A --- | --- | --- | TCTCCCTTTGCTCCTCATGCCCCACTCCCTCAGCCTGCACAGAGCGTTTCTOCAGTGTAGTCTCTGGT<br>CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAATGCAGTTT[C/A]JTGATCCACCCAGGA<br>CTCAAAAACCTAGGAATTGGGAGAAAGAGGACCTGGAATCGGTGTGCTAGCAAGCCCCCAGGTGG<br>TTTGTAAAGTGACTAAAGTTTGAGGACCAGACATGGAAAGTTGGCTTTGGC         |
| WI-9841  | 101 A G --- | --- | --- | TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAATGGCATGA<br>TATGAAATTCATTTTGAATGAATAAATAATAC/AJGTGTGTATGATATATATACTATTAAACACTT<br>AGGATTATATACACACAATAAAACGCTGTGTAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA<br>TTGAAAAGAGGGGATGTTACTTGTATGATGCTGTG                        |
| WI-9880c | 222 G A --- | --- | --- | GAACTAACACCTTTCTGCATGGATTTTCTTGATTATGGCAGTTAAACAATAAAATGTTATTAGATC<br>ACTGGTCTTCTGTGTGGGTTGAGTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA<br>GTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATTTATATTTATATAAGCACATGAA<br>AATGGAATGAAATAATGA[G/A]JTGACATAGGAATTACCTACATATTTTG              |

|          |     |         |     |   |
|----------|-----|---------|-----|---|
| WI-9880b | 157 | C A --- | --- | GAAC TAACACCTTCTTG CATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC<br>ACTGGTCTTCTGTGGGGTGGATTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTGTGA<br>GTTGTTTCTACATCCTTGAAGC/AJATATATAAGATCCTCTTTTAAAAATTATATTTTATAAGCACAT<br>GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATAATTTTG |
| WI-9880a | 108 | C T --- | --- | GAAC TAACACCTTCTTG CATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC<br>ACTGGTCTTCTGTGGGGTGGATTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTG<br>TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAAAATTATATTTTATAAGCACAT<br>GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATAATTTTG      |
| WI-10183 | 127 | C T --- | --- | ACACTGGAGGCACTCCAAATCCTNACAGACATATGCACTCGGAATCAACTCAGGCATGCACAGCAT<br>CCCTGTGCTGGAGTTTATTTTAAAAACAACGCCCCAGTTATCACAGTTCTNTTTTGTCTJACCC<br>ATTTCCATAACAAAAGAGCTACACAAAATTNCGGGGAGANACTCTCTTTGGAGACTGACACATT<br>TGCAGAGGGGTCATGAATAATGATTCCTAAA                       |
| FB25G10b | 109 | A G --- | --- | TCCCTCAATGACAGATGAACATAAATTTCTCTTGGGTAAAGAAATACITTTATGTCCATTGTGATAAA<br>AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAAG/GJTGATTTTATGATCCTCCCCCAG<br>TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC<br>CGGAC                                      |
| FB25G10  | 109 | A G --- | --- | TCCCTCAATGACAGATGAACATAAATTTCTCTTGGGTAAAGAAATACITTTATGTCCATTGTGATAAA<br>AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAAG/GJTGATTTTATGATCCTCCCCCAG<br>TGACAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC<br>CGGAC                                      |
| IB3071   | 102 | C A --- | --- | ACAAAGCTGAACCTCCATAACAGTCAATGGTACAGTCAAAACATCAGATGTACAGAACACACAAATTTA<br>GATGAACCTGAAATTTAAGNTAAATAAAATAAAATC/AJCAATTTAGNAAACAAAATCAAAAC<br>ATTAAGGNTCCCTGNNATATCTTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA<br>GGCATTCACAATATGACCCTATTAAACCAGTCTAGGGATTCTG      |
| NIB551   | 161 | C T --- | --- | CGTCCCTTCCCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAAATGGGTTGTCCC<br>TACTGAGCTTGGGGCCAGGTGTACTTAGGAACCAATCCACCAGAGAGACTCATCTATGTTA<br>ACACTAAGGATGCCCTGGAGGAGGTGCTGTTGACCACATACATCGGGCATTGGTTGATTCAGCTTT<br>GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTC                   |
| S72904   | 51  | G T --- | --- | AGCATAGAAAGTGATTTATATTTTAAATGGTTTCAAGTGAAGTCCCTTTGTTAATTTGTGAGTTT<br>ATTCCTGGAAAATCTTTTGAGTTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA<br>GAGAAATGCCTCAACACCAAGTGCTGAACCTCCCTCTTCTGTCAATTTGGTTGTTCTTTAAATA<br>TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTCTTTCAGTGTCTGTA  |

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| UTR-00481 | 115 | C T | --- | --- | TATCTTTTATCTCTGGGCCACAGTTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAAACC<br>CATTCAGATAAATGGCAGTACTTTAGGACACACACAAACACAGAC/C/JACACCTTTTGATATGTA<br>AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC |
| ESTC1     | 33  | --- | --- | --- | CCCTGTAGCAGTCTTCAGCCTCCTCTACCTACNAGATCTGGAGCAACAGCTAGGAAA  |
| ESTC102   | 37  | --- | --- | --- | GCTACTACCACGGCTGCTTGGTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA   |
| ESTC103   | 21  | --- | --- | --- | GCCATCAAAATTTCCCTTACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC<br>ACTTGAA   |
| ESTC107   | 20  | --- | --- | --- | TGCTGGCTCACTTCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT   |
| ESTC109   | 35  | --- | --- | --- | AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGAOC  |
| ESTC110   | 23  | --- | --- | --- | AACTCTACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA   |
| ESTC113   | 37  | --- | --- | --- | AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANAACAGTTTTCCTTTAATTGTAAAGCGGG<br>CATCG   |
| ESTC117   | 24  | --- | --- | --- | AATTGGCTCTTCCACATGATACNTAAGTTCAAGGTCCAAGTTCCTATCACAAATTACAAAAAGC<br>CTCCA  |
| ESTC119   | 24  | --- | --- | --- | TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT  |
| ESTC122   | 34  | --- | --- | --- | GACAATAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG<br>AGAAAAATCTGAAA  |
| ESTC123   | 21  | --- | --- | --- | GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA   |
| ESTC128   | 42  | --- | --- | --- | GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCCAGGCCCATCATNTCCATGGGACCGGCTGGCTCAA<br>TGTTGGAACCTGG   |
| ESTC129   | 20  | --- | --- | --- | AGTCACCATGCCCCAGCCTAGNATGAGTTTAGTAAGATTGTTGTTGCTGGGAG  |
| ESTC13    | 46  | --- | --- | --- | GTGTATCTGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA<br>TCAGAAAA   |
| ESTC130   | 49  | --- | --- | --- | GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAACANGAGAGCTGAAACAAT<br>CTACACCTGAATG   |



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|---------|----|-----|-----|-----|-----|--|
| ESTC132 | 30 | --- | --- | --- | --- | GGTAAAGTCTAAATTACTGCCTTAGCAAACNCATGTTGICAGGTTTTCTGCTGCA  |
| ESTC137 | 21 | --- | --- | --- | --- | CCAGTTGGCTTCTGTCCTCANAGTCTCTCTCCATGTGGCAAACA   |
| ESTC139 | 45 | --- | --- | --- | --- | AGGAGCACAGCCTAAGGACATGAAGGTGAGAGTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG<br>GAGGAGG                             |
| ESTC14  | 20 | --- | --- | --- | --- | CCATTGTGGTACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTAGAAAGC<br>TTGCCCTGGTG                       |
| ESTC142 | 72 | --- | --- | --- | --- | CCTAGGCTCATAAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCAATTTAAATC<br>AAAGANACCATTCCATTTCTCTAACAAACA  |
| ESTC143 | 29 | --- | --- | --- | --- | GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCTCTTTTG   |
| ESTC144 | 26 | --- | --- | --- | --- | AAATCCATATTTCTTGACATGAGGNGCTTTTAGCAGCATTTCCGG  |
| ESTC146 | 20 | --- | --- | --- | --- | CATGTCAGGATAAGGAGCANACACCAGGATTATACACGGTGGCAGCG  |
| ESTC148 | 42 | --- | --- | --- | --- | TCTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGATGCGCGGCTGTGGAGGCCCTG<br>GGGTGGCTGGGCTGTGTCTCTGAG             |
| ESTC149 | 28 | --- | --- | --- | --- | TCAGTTCATTTATTTGCTTTAAGAGTTANATACCATGAGACACAGTTCTGCG   |
| ESTC15  | 28 | --- | --- | --- | --- | GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAAGTTTCTTCAGTGATCTT   |
| ESTC150 | 20 | --- | --- | --- | --- | CCAGGAAACAAGCAGACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATCAATATT<br>AAACCTGATGTTTAAAGAACCTAATGAGA     |
| ESTC151 | 49 | --- | --- | --- | --- | GAAGCTAAGGCCCATTTTTTTCTTTTAAATACAAATCTACTGGTGCNAAAACCTCAGAGCTTAGGA<br>AACACAGCC                        |
| ESTC155 | 37 | --- | --- | --- | --- | TTTTAATTGACAACCTCAATCTCTACATACATACAGTNTGCACGAATTATAAGTGGATCAACAATT<br>ATATTATTGATACAAACTCATGAGCATTTACA |
| ESTC156 | 32 | --- | --- | --- | --- | GCAGCATTTGTGACAGGAGAGCGCAAAACAAACCTGGCTGCCTCGGGATGGAGGGGGCGGCTCA<br>CCACCACTGCAT                       |
| ESTC158 | 35 | --- | --- | --- | --- | ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC<br>AA                             |
| ESTC159 | 31 | --- | --- | --- | --- | AGCTGGCAAGAGACTTCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGGTTCTGCA<br>GCTTTGAAAGG                     |

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|---------|----|-----|-----|-----|-----|---|
| ESTC16  | 23 | --- | --- | --- | --- | CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT                                       |
| ESTC160 | 38 | --- | --- | --- | --- | TTCTAGCATTGCTGGTGCAGTGGGGGCTGAGCTGGGNGCAGTCGGCAGTGTCACTGGGCCCGTTTG<br>GGACTGGGTGA                   |
| ESTC162 | 36 | --- | --- | --- | --- | CTCTTCGTCGGTTTGCAGTTGCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG  |
| ESTC164 | 31 | --- | --- | --- | --- | TCATTCTCCATAGAATATTGGTTTGTAAACANCGAATACAATCCAATATATAACATTAAACAATCC<br>GATACATACCA                   |
| ESTC169 | 22 | --- | --- | --- | --- | GTCTCTGGTGTGCAGGGAATCANITTTGCTGGATTAGAGGAAGGTGCCCGCTGTGTTTCCATGACTT                                 |
| ESTC176 | 23 | --- | --- | --- | --- | CACCTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA   |
| ESTC177 | 42 | --- | --- | --- | --- | TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAAATTTTNCCTTATTCTATTAAATACCTTTTAT<br>TCTCTTTATCCCATAAAAAGCAACCA |
| ESTC18  | 29 | --- | --- | --- | --- | TCAGACACTGCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCCTGCAGGGCGCCCTGGGAGAC<br>AACTGGACAAGA                  |
| ESTC181 | 21 | --- | --- | --- | --- | TAGGGATTCCAAGTTGCCTGGNTTAAATATAATACATATTACAAAAATTTACACAGCTCATGCATAC<br>CA                           |
| ESTC186 | 43 | --- | --- | --- | --- | GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCATTCAGCTTG<br>ATTTTTCACCTCA               |
| ESTC187 | 24 | --- | --- | --- | --- | ACCATGATTGCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG                                  |
| ESTC188 | 25 | --- | --- | --- | --- | TCTATTAAACAGGGTTATGTCACACCNITGTCAACCTCAAAACAGATGATCACTCATCTTGTCTTCCAT<br>CTTGC                      |
| ESTC189 | 27 | --- | --- | --- | --- | AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA  |
| ESTC196 | 42 | --- | --- | --- | --- | TCCTCAAATACCACCTTTCCCTTAACCTTATCAGTCTAGTAAGCNITTTCAAGGAGGAAAATGGGTTAC<br>CTTTCAGGGG                 |
| ESTC197 | 26 | --- | --- | --- | --- | ATCTCCAGTGTCTGCTGCTCCTCCCGCAAAGTCTCCCAAGCACA  |
| ESTC20  | 33 | --- | --- | --- | --- | AAGATTAGACAGACCGCGTATAGTAAGCTCTGNGGAACCTCAAGAATCTAGAGGGGGCTGTGGGAA<br>CGCTGCTTAGATC                 |
| ESTC200 | 44 | --- | --- | --- | --- | TTTGGTGAATAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAAACAGTACTTTAAAT<br>CAATTACTCCTTTTGGCCTGCAACAG  |

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| ESTC201 | 35 | --- | --- | --- | TCCTACTGGGTAGTTAGCAACATTTTTAAANCCACATCCAACAGATTGGTT                                    |
| ESTC202 | 22 | --- | --- | --- | CTGCTGGAGGGAGGACAGACGNCAGGGCGCTGGGTGGCGCCAGAAAGGCTGGCGTGATGTT<br>CGAGATGAGOC           |
| ESTC203 | 27 | --- | --- | --- | ACACTTAACAGGTTAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTATTGTGCTAC<br>AAGACACGTTGCA     |
| ESTC208 | 43 | --- | --- | --- | TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC<br>CTAAGAGTGAAAA    |
| ESTC210 | 29 | --- | --- | --- | GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAGTGAGTGACGGTGACCTGTG                                 |
| ESTC212 | 27 | --- | --- | --- | GGGTAACTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGGCTCTCAGAGCAGAGGGCTTGGT<br>TCAAGTC            |
| ESTC214 | 21 | --- | --- | --- | CTCCAGAGTCCCTCCTCTCANACCGGGGCGAGGGAGTTAGGGAAT  |
| ESTC216 | 49 | --- | --- | --- | TGGCAAGAAATTTATTACACTAACAAATTAATTTAATCACAGGTATTNTAGATTGGTCAGAAAA<br>CAAAAGACCA         |
| ESTC217 | 28 | --- | --- | --- | TTTTGTCAGTAATGAGCAATACACTGANTGGAATCTGCATGATTAATAACATTAAACAAGTTCAT<br>AAACACACCCCA      |
| ESTC219 | 32 | --- | --- | --- | GTACACATCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG<br>GCAAGGAAGC          |
| ESTC22  | 41 | --- | --- | --- | TCATTGAAGAAATATGGGTTTATTCTTATTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA<br>TAAGGCC            |
| ESTC223 | 27 | --- | --- | --- | CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTTCTTGATTTAAAAAACAGAAAGGGAGGAGGA                      |
| ESTC224 | 37 | --- | --- | --- | CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACACACA                           |
| ESTC225 | 20 | --- | --- | --- | TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAAGTGCTTCAGAAAGGA<br>ATGTGTAGGATCG |
| ESTC23  | 27 | --- | --- | --- | TTCTACTTTATTTCATATCCACCACNATAACGACTCCCTTTAATTTAAACTAAAAACCATACAGGGT<br>TCCTGAAGGG      |
| ESTC230 | 43 | --- | --- | --- | GCTTCCTCCAGCAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA                   |
| ESTC231 | 24 | --- | --- | --- | CAAAAGGGTTAGTCATATTCCCCCANCAACAGCATGATAAAATAATTCAAC                                    |

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| ESTC28 | 23 | --- | --- | --- | GAAGAGCTGGGCAGGCATCTGACNTTCTCTCTATTCCTATAAAAAATAAAGGAGCAGAAATCT<br>GC                |
| ESTC3  | 20 | --- | --- | --- | CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTTATCTTGAGCCGCTTGGTCAGGTTTGAT<br>TCGCACACTCC     |
| ESTC31 | 32 | --- | --- | --- | ACAGCCCCACAGAACTATTGTAACAATATNTCAGTCGGTGATCATTGTAATATACAAATACAAAG<br>CAATTTCTCTAGA   |
| ESTC33 | 25 | --- | --- | --- | AGCACTCCAGCTCCTTGACGTTGTNGGACAGGGAACCTCCGGAA   |
| ESTC39 | 26 | --- | --- | --- | AAGGAAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTA                               |
| ESTC4  | 23 | --- | --- | --- | CCACTGAATCACACAACATGGACNAATCTCAAAICATTATGCTGATGGAAGAAACCATTT                         |
| ESTC40 | 22 | --- | --- | --- | GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTAAAAATATTTTGACTTGTCCCTTCAC                       |
| ESTC45 | 37 | --- | --- | --- | TTTGGAGGTTTGTGTGGAGTTTGTCTTTGTACNCTCTCATCATCGAGGCTATATATTA                           |
| ESTC50 | 56 | --- | --- | --- | CTGTCCGTGTGAGCCCTGCCGCTGCCATGGCCAGGAGCCACTGTGCGGANCCTGGGCAGATG<br>TTTACCCCTGT        |
| ESTC56 | 45 | --- | --- | --- | GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTCGAGGAAGNAGTGGAGGAAAGGACACCA<br>AGT                 |
| ESTC57 | 20 | --- | --- | --- | AAGTGGCCCTCCAGTCCCTCTCTGGGCACAGATCCACCAGTCTGCTC                                      |
| ESTC59 | 38 | --- | --- | --- | GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGCCAGACTTCAGGAAAAATGATTTCC<br>ACATGGTAAGGCC     |
| ESTC6  | 27 | --- | --- | --- | TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATG<br>TGGACTGAACCG |
| ESTC61 | 57 | --- | --- | --- | AGTGATTTGGCTAGCGTGGTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCC<br>ACCCACTCAAG      |
| ESTC63 | 20 | --- | --- | --- | ACAGACACAGCATCACACCANAGGGCCACGGGAGGGTGGGGAGAGCAGACATTTTCCCTGGGAAA<br>GGCAGCTCTAATC   |
| ESTC69 | 20 | --- | --- | --- | GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTAAATCCCCACACTTACTTACTGCTCATCCGT<br>CACTTTCGCTAA      |
| ESTC7  | 45 | --- | --- | --- | AGTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCTGAGTTGCANGCAGATGGAGATTGGACACT<br>G                 |

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|---------|-----|-----|-----|-----|--|
| ESTC72  | 37  | --- | --- | --- | GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGGNTTGGCGTGACGCCCTAAAAAGTGTGACC<br>AACAAATTCACAGCTACAGGAAATCTAGAACAAAATCAAATATTATCACCNTTGGGTTGAAAAGTTG<br>GAAGA   |
| ESTC74  | 49  | --- | --- | --- | ATGACTTTCTGTCCCATCGGAACACAGAGTTTCCCCAGGNGAGCCCTTCTATCTGCGGTTA  |
| ESTC77  | 40  | --- | --- | --- | GGCTCAGCACAGGATAAGANCCCCACTCCCGCATGTCCCCAGAGGGCAGCACTCCAG<br>TTTCAGATGATGGGGTCTGAGATGNTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA<br>GAGCCTGACCCA   |
| ESTC81  | 20  | --- | --- | --- | CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC<br>TTTCACAAAACCT   |
| ESTC82  | 25  | --- | --- | --- | TTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGTGTTGGGGAGGCTACAGCCTGACCACATTC<br>TTTGC   |
| ESTC83  | 53  | --- | --- | --- | ATTGCAAAGGAAGTGGAACTGNTCAAACAGAAATGGTGACAATGA  |
| ESTC85  | 28  | --- | --- | --- | CTGGTCTCTTGCTTGGCATTCGTCTCCTCCTCNGGCCAGTGCTCCACCCAAAGTGCTCTCCCGATGAT   |
| ESTC89  | 22  | --- | --- | --- | CTCCCCCTCCTCAGTTACAGTGGAGACTANGGAGATTTCAGGGCAGGATCC  |
| ESTC90  | 33  | --- | --- | --- | GCACGTTCTTTGTTCTCCTCTCCAGAAGTTGNAGACGCTATTAGTTTGAATTCGTGCG   |
| ESTC93  | 29  | --- | --- | --- | AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCTCTAATTCA<br>GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGGAATGCTTCTGACTGTTCTCCA/C/TGCCAG<br>ATTCTTATCAATGATCTTTCACCTAAGAAACAGGAAAGATTCTGGCAAGCACACGATCTAGAGATAC<br>ATCTTATTGCGATTTTTCACAAAATCAAAGAAAGAAAGGCTTAGCTG |
| DWU-100 | 127 | C   | T   | --- | TTCCATCTAGATATCTACTCAAAAATAATTGAGACAAGTGTCAAACAGAAAAGACGCTTGTGCTGAA<br>TGTTTCATGGC/A/GJGCCCTATTACAGTAGCCAAACGATGAAAACAAACCCCAAGCTATATATACCA<br>GATGAAAGGATAAACAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAGGAAT<br>GAAGCAGTGAATCCCTACTACACTGTGGAT                  |
| DWU-177 | 77  | A   | G   | --- | CAAACTGAGCTATCAACCTGTTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC<br>ATTTTGAATTCACGGGTGCCACCCCAATCATGCCAGCTTCTGTATGAATGAGATATACATTT<br>ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG<br>TCAACAGGG/A/CTGGGAAACCCAGCCCTATCTGAGTCTTCGGCTCCCTCC      |
| DWU-286 | 213 | A   | C   | --- |  |

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|-------------|--------------|-----|--|
| DWU-252     | 94 A G ---   | --- | AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACTTCATGTAAAGTGT<br>CAGAAAGGAGCTACAAAACCTACCTCA/GJTGAGCATGGTACTTGGCCCTTGGAGGAACAATCGGC<br>TGCAATTGAAGATCCAGCTGCCTATTGATTTAAGCTTCTGTTGAATGACAAGATATGIGGTTTTGTA<br>AT   |
| DWU-330     | 85 C T ---   | --- | GAACATTCCTCTGCAGCACTTCACTACCAATGAGCATTAGCTACTTTTCAGAAATTGAAGGAGAAAA<br>TGCAATTATGTGGACTGAAGC/TJCGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTTCTCTTTGCAA<br>CAAGACAAAGCAAGCCACATTTTGCATTAGACAGATGACGGCTGCTCGAAGAACAATGTCAGAAA<br>CTCGATGAATGTGTGATTGAGAAATTTTACTGACAGAAATGCAATCTCCCT |
| DWU-370     | 231 A G ---  | --- | GAAAATGTTAATTGGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAGAG<br>AAGCATCATTTCCCAACAGGGCAACTGTAGAGGCCAGCTGAAGAGTAAGGAAAAGGTCTGAGG<br>ACTGAGCCTGTGGCTGGCTGGAAAAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAAGAAAGTC<br>ATTAGACGGTACCAATTCAGTGTCTGTTCCJ/A/GJGCATCTATTCTCTGTGC     |
| DWU-1537b   | 89 A G ---   | --- | CTCTTAACCTCAGTTCCTCATCTATAAGAAATAGGATTCAGTTGTGATCACATAGCTCAGGTAATC<br>CAGGACCAGAAAACCCAGGAGC/A/GJTGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT<br>ACAGCATTTTCTGAAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA  |
| DWU-1537a   | 52 C T ---   | --- | CTCTTAACCTCAGTTCCTCATCTATAAGAAATAGGATTCAGTTGTGATCAJ/TJTAGCTCAGGTA<br>ATCCAGGACCAGAAACCCAGGAGCATGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT<br>ACAGCATTTTCTGAAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA  |
| ESTD-ADAb   | 196 C G ---  | --- | ACCATCTTATACTATGCGAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGTC<br>CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCTCTCTCTCCCTGTGGGAAT<br>CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGCCCTCGGCACCTGAGCTG/C/GJAGA<br>CCCGCAGACCAACTCCTGAGCTTTCTGGGCTCTGAGTCTTGCTCTC       |
| ESTD-ADAA   | 184 G A ---  | --- | ACCATCTTATACTATGCGAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGTC<br>CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCTCTCTCTCTCCCTGTGGGAAT<br>CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGCCCTC/GJAGCACTGAGCTGCAGA<br>CCCGCAGACCAACTCCTGAGCTTTCTGGGCTCTGAGTCTTGCTCTC       |
| ESTD-ANT1   | 160 T C ---  | --- | TCCTCTGTCAATTCCTACTCCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAACCAAGTAATCA<br>TGGACTGCCCAACTCGAAACAAGAGGGCGCAGTGGAGCAGGATATTATGCTACGCGGTACCTT<br>TTTTATGGAGGACCGAACTGAGGCT/CJGAGCTCAGATGATCCTGT   |
| EST10398 2b | 168 A' G --- | --- | TGCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA<br>AGATGCTGCCACCTCTTATCTACTTGTATGATGTTCACATTTGGGGCTTGACTTTCCACACCGGAGAAG<br>CATGTGTTTCTTCGGGCCAAGAAGGTATCTACCA/GJATAGTGTCTATTAGGCATTG  |

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| EST10398<br>2a  | 147 C T --- |  |  | TGCTGGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA<br>AGATGCTGCCACCTCTTATCTACTTGATGATGTTTCACATTTGGGGCTTGACCTTCCACACGGAGAAAG<br>CATTTGTTTCTTTC/TGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG  |
| ESTD-C7         | 14 G C ---  |  |  | ATATCGTGGCCTTA/GCTTACCTAGAGCTGGACAATCCTGCTGGA   |
| ESTD-<br>D4S95  | 90 T C ---  |  |  | CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAATTTGAGAAGAGCAAAACAACCTTTCAAAGG<br>ATAATGGGGCAATCACTTCTTTT/CCTTCTTTAGAGTCTACCGG   |
| ESTD-<br>GPPK2L | 38 G A ---  |  |  | AGTCTCATCTGCGGTGCCAGGTAGATCCCTTTCACC/GA/CCGAGAACTGCTCGATATC   |
| ESTD-<br>HRASb  | 82 A G ---  |  |  | CTGGGCTGCGCCGACAGCTGCTGGCACCTGGACGGGGCGGCGCAGGCTCACCTCTATAGTGGGGTGG<br>TATTCGTCCACAAA/GTTCATCTGGATCAGCT   |
| ESTD-<br>HRASa  | 37 C T ---  |  |  | CTGGGCTGCGCCGACAGCTGCTGGCACCTGGACGGG/C/TGGCGCCAGGCTCACCTCTATAGTGGGG<br>TCGTATTCGTCCACAAAATGCATCTGGATCAGCT   |
| ESTD-<br>NRAMP  | 81 A G ---  |  |  | GGAGGCAGGAGGTGGGAGGGGGTCTGCTGCTCCAGGTCCACAGACAGAGAGGCGGCTCAGTG<br>TATCCACACCCCA/GTGTGGCGCTGGGAGATGAAGAGGATGATGCAGGT   |
| ESTD-OTC        | 18 A G ---  |  |  | GTGACCTTCTCCTTAA/GA/AACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC<br>AGATCTGAAATTTAGGATAAAACAGAAAGAGAGTATGTAACA  |
| EST36751<br>7   | 36 C T ---  |  |  | CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACT/C/TGATTACTTTTCTATTCAAATCTCTGTA<br>AAATTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG   |
| EST40562        | 109 A G --- |  |  | CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAATCTGTCCCAAACTTGTGGCTGAC<br>TTTATGGCTAAGAAAGTTTCACTGGATGCATTAATAACAAAT/G/TTTTTACCTTTTGAAAAATAA<br>ATGAAGGATTTGACCTGCTTCGCTCTGGAAGAGTATCCGTACCGTCCCTGACGTTTTGAAACAATACA<br>GATGCTTCCCTTGTAGCAGTTTTCAGCTCCTCTACCTA            |
| EST18288<br>3   | 121 C T --- |  |  | GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA<br>GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA/C/TGGGAGCCAGT<br>GTGGACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAAGGTAAAGCAACCTCTCTGCTGGCTC<br>TGGCCCTAGGACTTAGTATCC                           |
| ESTD-AK-<br>168 | 31 C T ---  |  |  | GGGAGTGACAGCTAGACACCAAGGGGGGCT/C/TTACAGCTGTGTTCTCATGGAGGACAGGCTTCT<br>GCTCAATCTGG   |
| ESTD-ALB        | 180 A G --- |  |  | AATCCCAGACCTTTAGGAGGCTGAGGCGGCATATCACAGAGGTGAGGATTTGAGACCAGTCTGA<br>CCAAACATGTTGAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGATGGTGGTGCATGCCTGT<br>AATCCCAGGAGGCTGAGGCGAGGAGATCGCTTGAACCTGGGAGCG/GA/GIAGGTTGTGGTGAGCCGA<br>GATGGCACCATTGCACTCCAGGCTGGGCAACAAGAGTAAACTCTGCTTC |

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| EST70523<br>3  | 182 | G T --- | --- | TTCCGGCAGCCCCCATCTTGCCACCTGGTCCCTCAGGGGCCACCCCGGGCACTCACCGCTCT<br>CGCTCTCGGTAAACATCCGGCGGGCGGCTCTTGAGACATAGCCTGGACCGTTTCCTGATAGGAGG<br>ACCGTGATGGCTTCTGTCCCGGGCTTGCCAGGGCCAGCCCTG/JCAGAGAGAGGGGTCCCTGT<br>GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGTTG                      |
| ESTD-<br>APOA2 | 101 | C T --- | --- | CCAGGTGTTGGCACGTGCCTGTAATCCAGCTACTCGGGAGACTGAGGCATGAGAACTCTTTGAAC<br>CGGGAGGCGGAGGTTGCAGTGAGCTGACATCG/JTJGCCACTGCACCTCCAGCCTAGGTGACAGAGC<br>AAGACTCC  |
| EST58707<br>7  | 112 | C T --- | --- | CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGTTACAGGAGGCTTT<br>AAGTTACAGCATCTTTGGCTCACATGAAGGCCAAATCCGAGAGAC/JCTAGAAAGATACACGAGAC<br>CGAATGTATCAAAATGGACATTCAGCAGGAACCTTCACGATACCTGTCTGTAGGCCAGGTTTATA<br>GCACACTTGTACCTACATTTCTGATTGGTGACTCTTGCTGCTAAGAACCTT   |
| EST74167<br>6  | 137 | C ---   | --- | AGACATGAAGGAGTTGAAGGCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG<br>AGACGGGGCAGGCTGTCCAGGAGCTGCAAGGCGCGCAGGCCCGGCTGGGCGCGGACATGGAGGA<br>CGTGGCGGGCGGCTGTGTGAGTACCGGGCGAGGTGACGGCCATGTCTGGCCAGAGCACCCGAGGAGC<br>TGCGGGTGGGCTCGCTCCACCTCCAGCTGCGCAAGCTGCGTAAGCGGCTCTC |
| EST43211<br>8  | 132 | C ---   | --- | CGCTGGTGCAGTACCGGGCGAGGTGCAGGCCATGTCTGGCCAGAGCACCCAGGAGCTGCGGGTGG<br>CCTCGCCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAAAGCGC<br>TGGAGTGTACAGCGCGGGCGCGAGGGCGCGAGCGGCTCAGCGCCATCCCGGAGCGCCTG<br>GGGCGCTGTGTGAACAGGGCGCGTGGCGGCGCCACTGTGGGCTC                |
| ESTD-<br>ARSB  | 126 | A ---   | --- | GGAAGAAATGGAGCTGTGGAGGAGGCGTCCGAGGGGTGGCTTTGTGGCAAGCCCTTGCTGA<br>AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTGACTGGCTGCCAACACTCATGAAGCT<br>GGCCAGGGGACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAAACCATCAGTGAA<br>GGAAGCCCATCCCCCAGAAATTGAGCTGCTGCATAATTTGACCCAAAC          |
| EST36770<br>4  | 144 | C ---   | --- | TGTAGCCAAAGTCACTGCATCATTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC<br>ATCGAAATGTAATTTTCAATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT<br>TCAACCTCCCGATAGGGCTGGCCTGACCAAAATATATACTGGTGTCTGTTTCTTCTGATCAT<br>TCTTACAAGTTATCTCTTATTGGAGGCCCTAAAGAGGCTTATG            |
| EST26021<br>1  | 137 | A ---   | --- | TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTGCAAACTGT<br>CCATAAAGTAATTTGTGAAGAGGAGCAAGAGAACATCTCTGCAGCATTCTACTACCAAAATGA<br>GCATTAGCTACTTTTTCAGAAATTGAAGGAGAAATGCATTATGTGACTGAACCGACTTTTCTAAAGC<br>TCTGAACAAAAGCTTTCTTCTCTTTTGAACAAGACAAAGCAAGGCC         |
| ESTD-<br>BA511 | 29  | A G --- | --- | GGGCAACATAGTGAAACCCCATCTCTACAJ/GIAAAATACAAAATTAGCCAGGTGTGGTAGCAAG<br>TGCCTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG<br>CAGTGAGCCAAAGATGGTGCCACTGCA  |



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|------------------|-------------|-----|-----|--|
| ESTD-<br>BCL2    | 116 A G --- | --- | --- | AGCTGGATTATAACTCTCTTCTTCTGCGGCGCTGGGGTGGAGCTGGGGCGAGAGGTGCCGTT<br>GGCCCCGTTGCTTTCTCTGGGAAGGATGGCGACGCTGGGAGAAC[A/G]GGGTACGACAAACCGGG<br>AGATAGTATGAAGTACATCCATTATAAGCTGTCGACAGAGGGCTACGAGTGGGATGCGGGAGATGT<br>GGCGCCGCGCCCGCGGGCGCCCGCCGACCGGGCATCTCTCTCCCA        |
| ESTD-BCR         | 69 C T ---  | --- | --- | CAGTGGCTGAGTGGACGATGACATTAGAAACCCATAGAGCCCCGAGACTCATCTGCGCAAGA<br>GA[C/T]CAAGAGGTCAGCTTCTGTGTCGCGGAAAGGGAGGACGGTGACAAAGCTAACTCTGCTTC<br>AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCCTGGCACA  |
| ESTD-<br>BRCA1aa | 119 C T --- | --- | --- | AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA<br>GTGGAGAAAGGTTTTCAAACTGAAAGATCTGTAGAGTAGCAGTATTTC[A/C]TTGGTACCTGG<br>TACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACCTCTAGGAAAGGCAAAAACA<br>GAACCAATAAAT                                       |
| ESTD-<br>BRCA1bb | 139 A G --- | --- | --- | ACTAAATGTAAGAAAAATCTGCTAGAGGAAACCTTTGAGGAAACATTCAATGTCACCTGAAAGAGAA<br>ATGGGAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAAATACATTAGAGAAAAATGTT<br>TTTAAAG[A/G]AGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA<br>GTATTAATGAAA                                 |
| ESTD-<br>BRCA1cc | 126 A G --- | --- | --- | ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGTTGTAATAAAGGAAGATAC<br>TAGTTTCTGCTGAAATGACATTAGGAAAGTTCTGCTGTTTATAGCAAAAGCGTCCAGA[A/G]AGGA<br>GAGCTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTGGCTCAGGTTACCGAAGAGGGGCCA<br>AGAAATTAGAGTCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC |
| EST51212<br>0    | 122 A C --- | --- | --- | ATCCTGAGCTCGCCAAATAGCTTCTTGTTCTACTTCTCTCTCCACAGCCCCAATTTCACTTCTCA<br>GAGGAATCCCAAGCTTAGAGCCCTGGAGCCCTTGTGCTCCCACTCAATACA[A/C]AAAGGCCCT<br>CTCTACATCT   |
| ESTD-C1R         | 40 A G ---  | --- | --- | ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCT[A/G]ATTTGCTCCGGGAAGCACATTCTAT<br>CAA   |
| ESTD-C1R         | 40 A G ---  | --- | --- | ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCT[A/G]ATTTGCTCCGGGAAGCACATTCTAT<br>CAA   |
| ESTD-C6          | 31 A C ---  | --- | --- | CCAGTCAGTTTGGGGACAGCCATGCACCTG[A/C]GCCTCTGGTAGCCCTTCAACCATGCATTCCATC<br>TAAGCTCTGCAAAAT  |
| EST20118<br>2    | 119 C ---   | --- | --- | GTCCGAATCCTCCTCTGAAAGTGCCGGTTTAACTGCTCATGACGCTGCGGCTGTGTCCAGCT<br>GAGGTGAGGGGCCCTTGAAGCTGGAGTGGGTTTAGGACGCGGGTCTCTGCGTGCATCTAAGCTCT<br>GAGAGCAAAACCTCCCTTGAAGCTGGAGTGGGGTTTAGGACGCGGGTCTCTGCGTGATCCTAAGCT<br>CTGAGA  |
| EST53018<br>6    | 67 A G ---  | --- | --- | ACAAATCCAGGTACACATTCAGAAAGAGGAGGGTGGTCAAGTGGGTTAGGTTCCAGTAATCCA<br>[A/G]GGATTGAGGAAGGAGGCCACAGGATCGAAGTTAGTGAAGTC  |

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| ESTD-<br>CB22     | 119 C T | --- | --- | GGCAAGTTTTATTGATAGAGAGAAATCAAATATGGCAATGAGGAGACATCACCTGGAATGTTAG<br>GCAGTGCCTAACTGGGGGATGGACAGACAATGGGAGTGCCAAACCCATAGGCTGAGATACAAAAG<br>ACAGGCAAGGAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCT<br>AGTAACATAATTGTGCTTCAATTATGGTCTTTCCCGGCTCTCTCTCACACAC |
| ESTD-<br>CB23     | 136 C   | --- | --- | TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGACCTAGTAACATAATTGTGC<br>TTCATTATGGTCTTTCCGGCTTCTCTCACACATACAGAGCCCCCTACAGGACACAGACGCT<br>CTCAGAGCAACCCCTAGCCCATACCTCTTCCCTTCCAGAGGACCTGAAAAACGTGTTCCCAACCCGA<br>GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA       |
| ESTD-<br>CB24     | 145 A   | --- | --- | ACAGGACACAGACAGCTCTCAGAGCAACCCCTAGCCCATACCTCTTCCCTTCCAGAGGACCTGAA<br>AAACGTGTTCCACCCGAGGTGGTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAAG<br>GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACACAGTGGAGCTGGTGGTGAATGG<br>GAAGGAGGTGCACAGTGGGGTCAGCACAGACCCGACGCCCTCAAGGAG        |
| ESTD-<br>CB25     | 146 A G | --- | --- | GTTTTCTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTCTCTCTATCTTTCGCCGTC<br>TCGTCTCGAACCCAGGGCATGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG<br>TGACAGGTGAGCTCTGCTCTGTTCTGTCAACAGAGTCTTACCAGCAAGGGGTCTGTCTGCC<br>ACCATCTCTATGAGATCTTGTAGGGAAGGCCACCTGTATGCCGTG          |
| ESTD-<br>CB27     | 125 C T | --- | --- | TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT<br>TGTTGTTGGGCTGTGTCATTTAGGAGTGTCTGTGGAGTCTGCTCATCACTGACGCTTATCTTC<br>TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAAATGCT<br>GCTTCTCTGTTTCATCTGATGGAAGTCTCAACACCATTTCCATACC     |
| ESTD-<br>D4S338   | 59 A T  | --- | --- | TTTTCTGTTTACCTTGTTCAGATCTTCAGAGGAATCCCTATATATGGCAGGTATATGATATGTA<br>TTTTTAACAATAAATTTGAAAGTCCAAATTTACTCCTTGATCCATGGACTGCAGAAATAATGTTA<br>TTTTAGCTGTCAGAAAAACAATACTAATCTTGATATGTTTCATCAGAGCCCTTGGGTGACCCAGGTGA<br>TTGCCAATAAGCAGTAATTTTGGAGGAATCTGTTTCAATGCAGTAG  |
| ESTD-<br>CYP2D6   | 61 A G  | --- | --- | CAGGCCAGCGTGGTCGAGGTGGTCACCATCCCGGAGAGAACAGGTACGCCACCACTATGCAGJCA<br>GGTTCATCATTTGAAGCTGCTCTCAGGGTCCCTTGGCTGAGCAGGGCCGAGAGCATACTCGG  |
| ESTD-<br>D11S1873 | 40 A C  | --- | --- | AAAAAACATTTAACACCTTTTCAATCATATACACCATAGJCAJTTTCCATTTTTCACATAAGTCA<br>GTTTGAAGTGAATTTTCCAAATTTGCAATCTAAATGTCACTAACTGATTAATGCAAGTTCAACAG<br>ACAACCTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCA<br>TATCTGCATGTC                                     |
| ESTD-<br>D17S33b  | 169 C T | --- | --- | CATCCCCAAGCCCATCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT<br>CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCGGTG<br>GGGTTGTGGCTATGGTGGTCTGTGTAGAGCTTGGGGGCTTTGGTTTCAGTTGCATATTGCGTT<br>ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCTC                  |

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| ESTD-<br>D17S33a | 75 C T ---  | --- | CATCCCAAGCCCATCTCTAGCCACTGGCATTCTTTGCCGCTCTGACAGATACACTCAGGGCCGT<br>CATGCTGCTACACATCCAGGGGCGCCCTACCCCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCG<br>GTGGGTTGTGGCTATGTGGTCTTGTTAGACGGGGCTTTGGTTTCAGTTGCACACTATTGCGTT<br>ATTGCAGATTGCTTTTCCACCTGAGCGAGCCTC                            |
| ESTD-<br>D18S8   | 133 A G --- | --- | TTTGAGACCACCCTGGCCAAACATGGCGAAATCACAATCTCTACCAAAATACAAAATTAGCTGGTGT<br>GGTGTACATGCCTATCGTAATCCAGCTACATCGGAGGCTGAGCGAGGAATTGCTTGAACCCJA<br>/GJGGAGGCAGAGCTTGACGTGAGCCAAAGATCACACCCTGCACTTACAGCCTGGGTGACACAGTGA<br>GACTCTGTCTCAA  |
| ESTD-<br>D3S11   | 44 G ---    | --- | AACTGATTAGAACCTGAAATACATATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG<br>AATTTTGCATCAATTAATAATCCAAATAAGTACACTGTAAATAAGAAATTTAACAGAAATATCATTTG<br>TTATTCAAACTATTATCACTTATTTATTGTTAAGCCATACATAAATCTAAAGCATGTTCTGAAAG<br>TTTA   |
| ESTD-<br>D3S12   | 37 A G ---  | --- | AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCGJGJGGAGCCTTGATGTCATCTGTATCTCCT<br>CAGGTATCCCACCTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTTATTAAATCAAGGT<br>TGAACATAAAGTA  |
| ESTD-<br>D3S2b   | 247 C T --- | --- | GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC<br>TGAGTCTTATTCAAAACTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC<br>AGAAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATCTGATGTTCTGTTCCGGTCTTACCGATGG<br>CAGGTATGAAATATAATACTGCTCTTATTGGAAGGATGCTGCTGGT     |
| ESTD-<br>D3S2a   | 248 G ---   | --- | GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC<br>TGAGTCTTATTCAAAACTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC<br>AGAAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATCTGATGTTCTGTTCCGGTCTTACCGATGG<br>CAGGTATGAAATATAATACTGCTCTTATTGGAAGGATGCTGCTGGTATGT |
| ESTD-<br>D7S399  | 83 A G ---  | --- | TGAATCTTAATTGCTATCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT<br>AACTGCTAGAGACCCJGJGJGCTCTCATCATCTCTTTCACAAACATTTTCATCCATGGACTCCATAC<br>TAGAATATTTGAAGAAACAAACATGACAAACATTTTC  |
| ESTD-DMb         | 146 A C --- | --- | GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACGTGTGGCTCAAGCAGCTGCTGGGCTCCACT<br>TCCATGGGTGGGGCTGGGACCTCACTGCTCCCTGGGAGAGAGAGGGAGTGGGAGGGAGACA<br>GAATGCTGATTJACJCTGTGTGAGAACCAAGAACTCTGCGCTGTGGTAGGGCAGCTGCTTCCAAG<br>ACCTCTGATTGAGGAAGGGGAGCAGAGCGAAGAGAACAGAGT                      |
| ESTD-DMa         | 66 C G ---  | --- | GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACGTGTGGCTCAAGCAGCTGCTGGGCTCCACJ<br>GJTCCATGGGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGAGAGGGAGTGGGAGGGAGAGA<br>CAGAATGCTGATTATCTGGTGAGAACCAAGAACTCTGCGCTGTGGTAGGGCAGCTGCTTCCAAGA<br>CCTCCTGATTGAGGAAGGGGAGCAGAGCGAAGAGAACAGAGT                     |

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| ESTD-<br>DRD1  | 154 C T --- | --- | --- | TCCCCAGCCCTATCGGTCTATTTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACTCATCAC<br>ACAAAACGGTCAGCACCCCAACCTGAACCTGCAGATGAATCTGOCACACATGCTCATCCCAAAAGCT<br>AGAGGAGATTGCTCTGGGIC/TTCGCTATTAAAGAACTAAGGTAC   |
| ESTD-<br>DRD2  | 144 C ---   | --- | --- | TCTGCCCTTGGTGCAGGAGCTGCCGGGAGCCAGGAGCTGGAGATGGATGCTCTCCAGCACCA<br>GCCACCCGAGAGAACCCGGTACAGCCCCATCCACCCAGCCACCCAGCTGACTCTCCCGGACCCG<br>TCCCACACGGTCTCCACAGCACTCCGACAGCCCGCCCAACACAGAGAATGGGATGCCAAAG<br>ACCACCCCAAGATTGCCAAGATCTTGAGATCCAGACCATGCCCAATG       |
| ESTD-<br>DRD3  | 109 C T --- | --- | --- | AAGACGATGGCCAGGATAGGCGGCAGTAGGAGAGGCGATAGTAGGATGTGGCGGGCCTGGCTGG<br>CACCTGTGGAGTTCTGCCCCACAGGTGTAGTTCAAGTGGC/C/TACTCAGCTGGCTCAGAGATGCC<br>ATAGCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTCTGTGAGGAGA  |
| ESTD-<br>ERBB2 | 93 C T ---  | --- | --- | TCTTCAGGATCCGCATCTGCCCTGGTTGGGCATCGCTCCGCTAGGTGTGACGGGCTCCACAGCTGG<br>GGTAGGGGGTGGTGGGTGAGTGC/C/TGGGGGCCGCTGCAGACCCACGCGGCTGGGAGGACTTCA<br>CCCCGCCTCACTCCGTTCTCGCAGCAGTCTCCGCATCGTGTACT  |
| ESTD-<br>ETS2  | 43 A G ---  | --- | --- | ACTCACAGTGCTTTTAAGTGAATGTGCGAGAAAGAGGCACCI/AGGAAAGCCGCTCTGGCGCCTG<br>GCAGTCGTGGGACGGGATGTTCTGGCTGTTGAGATCTCAAAGGAGCGAGCATGCTGTGGACACA<br>CACAGACTATTTTGAATTTCTTTGCCCTTTTGCAACAGGACGCAATGCAAAAACCTCTTTGAG<br>AGGTAGGAGGGTGGGAGGAACAAACCATGTCTTCAGAAAGTTAGTTTG |
| ESTD-F9        | 111 A G --- | --- | --- | AGATCCTGATGATTTTCTCTATTTTCTCTAAATGTTTACAGTTTGAAGTTTATAGATTTATGCCCA<br>TGCTCCATTTGAGTTAATATTGTGTAAAGTATGATGTTT/AGTGTCAAACTCATTTTTTTTTTCC<br>ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC   |
| EST68787<br>5  | 144 A ---   | --- | --- | CTTCTATGGGATTTGACTTTATTTTCTCCATGCTTACCTTTTACAGGTGTTAATATAGTGAAAAG<br>GAAGCTTGACGCTCATGACAAATTTGAAGCTGACAAATACACAAGAGGAAATAAATTCACAGTCAA<br>AGAATCAAGCACCTTTTCGAAACATTGAAGTTGTTTTGAACCTGGTGTCACTTTAATTACAACCTAG<br>CAGACGGAACTGAACCTCAGGGTAAGAAT              |
| ESTD-<br>GODH  | 200 C G --- | --- | --- | CGCAGACGGTCAGTGTGGGTGGGAGTGTGGAGGAGGAGGAGGAACTGGGGGTTTAGGGACT<br>TTCCGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAGGGGGAGAACACAGAGCCAACTGGCTAA<br>GTGTAAAGGACCTCTGTGTCGACCGTGTGTTCTGTCTGCCCTGTTTCACTGTCTGTCTGCCGAGT/C<br>GIGACTCTGTCCCGAAATCCGAGAGCT                     |
| ESTD-GCK       | 88 A G ---  | --- | --- | GTTTTATGCATGGCAGCTTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGGTCACCATGAC<br>AACCACAGGCCCTCTCAGGA/AG/CACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC<br>TGGAGCAGGAAATGCCGAGCGCGCCTGAGCCCCCAGGAGGAGGCTAGGATGTGAGAGACACAGTC<br>ACCTGCAGCCCTAATTACTCAAAGCTGTCCCGAGGTACAG  |

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| EST34088<br>2    | 62 A T ---  | --- | GTGGGGCAACAGTGGAGAGAAAGGGCCAGGGTATAAAAGGGCCACAAGAGACCGGCTC[AT]<br>AGGATCCCAAGGCCCAACTCCCGAACCACTCAGGGTCTGTGGACAGCTCACTGCTGCAATGGCT<br>ACAGGTAAG  |
| ESTD-<br>GNAT2   | 56 A G ---  | --- | GACCCTGAGTAOCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGTCACAAACCAC[AG]GGCATCA<br>TTGAAACCAAGTTTCCGTCAAGAGACTTGAATTCAGGTAAGTCATGGTTCCTTAGG  |
| ESTD-HT2         | 154 G ---   | --- | GGGCTAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTGACTTGACAGGATGCTAGAGATAGG<br>CAGGGAGAGGAAGATGTGTACAGTTTGTACAGAGAGATAAAAGGATAACCTGGGTTTTCTGTGC<br>TTTGCTTCTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA<br>AAGCGCAGTCGTGAAGTTTCAACAAGACACACCTT   |
| ESTD-HT5         | 149 C ---   | --- | AACACAAAGCCCCAGCGAGAAITGAACTCGCAGCCCCCTGTTTACAAGACCAAGTCTCTAACCCCT<br>GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTTCTCTTCATCTTATAGATTGATGTTATGCTCCTA<br>GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCCTACAAAATGAAA<br>ACATTTGCTGCTGTGAATCCCTCGAAAAGGTTCT  |
| EST37382<br>5    | 124 A G --- | --- | CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCTCCCTTGGA<br>CTTTGAGTCAAAATTTGGCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAGG[AG]GCCCCAGA<br>AATCACAGGTGGGCACGTCGCTACCGCCATCTCCCTCTCACGGGAATTTTCAGGGTAAACT<br>ACCCAGTGGAGCCCGCTCATTCACCGTCTTGGCAGGAGTG[C]TCTGGGAGAAGAAGGAAGATG<br>TTCCAGGGCACACATAGCTTAGTGGAGACTC |
| ESTD-<br>IGHV4-6 | 120 C ---   | --- | TTTACTATTTCAATGGATACAGAATTTGGGAGTCACTATATCTATGAACAAAAATTCAGATTT<br>CAGGTTAAGTAATTTGCCCTACATTTGTGAGTGACGGGCAGTGGTGGATCCGAGAGTGTGGTGG<br>TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT<br>ATGTAATACCTCACAAATACTAATAACGGAGTTGAATATAAACCCCA  |
| ESTD-IL1A        | 110 A G --- | --- | CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTTATTTATTTATTTATTTTGTG<br>AGATGGAGTCTGGCTCTGTACCCAGGCTGGAGTGCAGTGGG[AG]GCAATCTCGGCTCACTGCAAGCT<br>CTGCTCTGGTTCATGCCATTCTCTGCTCAGCTCCGAGTAGTGGGAATACAGGCAACCCGCC<br>ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT   |
| ESTD-IL1B        | 99 A G ---  | --- | CCACTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT<br>GGGTCTCTACCTTGGGTGCTGTTCTCTGCCCTC[AG]GGAGCTCTCTGTCAAITGCAAGG   |
| EST74082         | 134 A T --- | --- | TCCAGGGTGGCTGGACCCACGGCCCCAGCTCTGCAGCAGGGAGGACGTGGCTGGCTCGTGAAGCATG<br>TGGGGTGAGCCACAGGGCCCCAAGGCAGGGCACCTGGCTTCAGCTCCTCAGCCCTGCCTGCTGCTG<br>TCCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGCGCTCTCTGCCCTGCTGGCGCTGCTGGCC<br>CTCTGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGGG   |

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| EST45311<br>0           | 151 C T --- | --- | GGCCCTCCTCTCTCCAAATCTGTCCCTATAGTTTCCCTCTATTAAAGTGAACATACATGCATCTTTTAGT<br>GGATAGATGCACACAAACACAGCCCATATATGGGAAGGATCCACGTGTGGCCCATATTGTAACA<br>CATTTTCTGCAAT[C/T]ACCTCTTTCAITTAACAGCCCTTATCAATGGCCTTTTCTTTTTCAGTA<br>GTACATACACATCTGTGTCATTGTTGAAT                  |
| EST65258<br>8           | 80 A G ---  | --- | TGCCCATCACGCGCGGAGACATGGCTTGCCACAGCTTTGAGGATGTCACCAATTAACCAGAAAT<br>CCAGTTATTTCC[A/G]CCCTCAAATGACAGCCATGCGCGCGGGTCTTCTGGGGGCTCGTCGGG<br>GGGACAGTCCACTCTGACTGGCACAGCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT<br>GAGTTAGGTGCGTGTCTCTGTGCAAGTCAGGACATCAGCTGATTAAA         |
| EST38216<br>3           | 26 A T ---  | --- | ATGCAGGATGAAGGTGGACAGGGAGG[A/T]GAGGGCCAACTGTATCCAGGGCCTGCAGATGTCG<br>CTGGACTATGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG   |
| EST62782<br>149 G T --- | ---         | --- | ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTTAGCATTTGTTTAGCATTAACCTAA<br>TTTTTTCTGCTCCATGCAGACTGTAGCTTTTACCTTAATGCTTATTTTAAATGACAGTGAAG<br>TTTTTTTCTCTG/T]AAGTGCCAGTATCCAGAGTTTGGTTTTGAACTAGCAATGCCTGTGAA<br>AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGGTGCAATGCA         |
| ESTD-<br>KRT10b         | 183 C T --- | --- | CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT<br>AAAGGAAGAAATGCAATTTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACATATTACTTCTAAG<br>AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAG[C/T]TGCTTTTAAATAGT<br>CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA  |
| ESTD-<br>KRT10a         | 133 A G --- | --- | CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT<br>AAAGGAAGAAATGCAATTTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACATATTACTTCTA[A/<br>G]GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGT<br>TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA   |
| ESTD-<br>KRT8b          | 231 C T --- | --- | ACCCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG<br>ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT<br>TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG<br>GCTGCCTATCTCTCCGCTCAGGTTTACCA[C/T]GTCAACATTGACACA |
| ESTD-<br>KRT8a          | 21 C T ---  | --- | ACCCTCACCCCTCCCTTAGCC[C/T]GTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC<br>GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG<br>TTTGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT<br>GGCTGCCTATCTCTCCGCTCAGGTTTACCACGTCAACATTGACACA |
| EST75099<br>6           | 82 C T ---  | --- | CACCTGTGTGTCTAGATCTCCTCAGTGGCCGCTCTACTGGGTGACTCCAACTTCACTCCATCTCA<br>AGCATCGATGTCAA[C/T]GGGGGCAACCGGAAGACCATCTTGGAGGATGAAAGAGGCTGGCCCCACC<br>CCTCTCCTTGGCCGCTTTGAGGTGG   |

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| ESTD-<br>LF79  | 142 A G --- | --- | GGGTGATTTGAGGCTCAGTTAATATTTCAAATTTAAACCGTAGCAAACTGCATTGGTATTTAGA<br>AAAAATAAAAAATTTCCAATATGTAGTGTGTATATACCTGCCTCTGCCATGCAGCATCATAGCCTGT<br>GGGAACC[A/G]GGAGGGCTTCCTTACCACCCAGA   |
| EST35879<br>9  | 142 A C --- | --- | GAGATCGGTGTGTGAGTTATTAGGCATGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG<br>GAACTGCCGGCAATCTGACACGTGTGCACCCAGGCTACCCAAATTAGGTGAACATGGCTTCGAG<br>AGAGTTG[A/C]ACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCTGGATGA<br>A   |
| ESTD-<br>LMP2  | 35 C G ---  | --- | TACACACTTTCCTTACCCATTCACTGAAAACGACT[C/G]GCAAACTGGAGCCTTGTAGGAATGGAGT<br>TGACCTTCCCCAAAAGCCACTATGATAAGCTATTGGTG   |
| ESTD-LPL       | 113 C T --- | --- | TGTCAGTGTCCCCTAGGGGCACCTCACACATCCAGCTTCTCAGCTGTGCTGTGCTGCTGCTGCTGCA<br>AGGGTTTGTCTTAATCTCAATTCATGCTCTCTTCATCTTTTAG[C/T]AGCTGTGGGTTTGTGTTG<br>TTCTTCTGTTTTTGTCTAGTATCTGACTACTTTTAAATTATAAAAGAGATGATCTAAACAAAAATAG<br>AGATTGTTATCAGAAGTTCAACAACATTTATTAAAAATTTTTCACCTG   |
| ESTD-MCC       | 45 C T ---  | --- | TTGTCAGGAGTGTGCTGATGCTGCCTCCCGAGCTCTGTCCCTAGC[C/T]GAACTTCAGGACAAACGTGC<br>AG   |
| ESTD-<br>METH  | 118 C T --- | --- | CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA<br>TCTCAGGAAGTCTCTGCTTTCCAAAGGTTTGGTCTAAGTTGCTGATTACC[C/T]GGATTTTCTGACG<br>ATCTTCAACTGCTAGAGCATCTGGTCTCTGTTTAGCATGG  |
| ESTD-NF1       | 25 A G ---  | --- | ATTATCCAGATGAATTTACAAAAC[T/A]GTTACCAGATCCACAGACTGATATGGCTGGT<br>AACATGGACTTGTATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAAAA<br>AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCT[A/G]GCCCCAAACGCTTATTGTGGT<br>AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATCT<br>GAGAAAACTTCTTTTAAACCTCACCTTTGTGGGTTTGTGGAGAAAGTTATCA |
| ESTD-<br>NFKB1 | 107 A G --- | --- | TGTCCTTAGGGCCAGCCCTGCTTGTCTCCTCCCTGGCTGTTATCTTC[A/G]GTACTGCAAGAGAACACA<br>GACAT  |
| ESTD-<br>NPPA  | 45 A G ---  | --- | GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT<br>GGGTTTCTTTTATGTAGGGTGATATTGGATACTTTTGTGTTGATTATATATAGCAATTTGAGGG<br>ACAAACCATAGAGCAGAAATGGGCTTGAATAGTAGTCTTATTTAACCTTGGCAATAGCATTTG<br>CTTATCCCTGTGGTTTTTAATAAAAT  |
| ESTD-<br>NFKB1 | 202 C T --- | --- | GCCACCACACCCACCCAGCACACCTCAACCTCAGCCAGACAGAGTTGTTGACACAAGAGAGCCC<br>TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG[A/G]GTCAGCCGTGTATCATCGAGGCGGCCGG<br>CACATGGCAGGATGAGGGAAGACCAAGAGTCTCTGTGTTGGGCCCAAGTCTCTAGACAGACAAAAAC<br>TAGACAAATCACGTGGCTGGCT  |
| ESTD-PA11      | 100 A G --- | --- |  |

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| ESTD-PAR         | 120 A | ---  | --- | CTCTTCAGGAACCAACAGCTCTTCTACCAAAACACGACCTATTGCTGTCCGAGAGGTACAACCCGTAGA<br>ACTTCTTCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT<br>AATCGACTGGCTTTCATTAGCTCTGTAGTGTTTCTTTCACCTTTTCTGTGTTCTAGAACGTTTCTTAG<br>GACTGGCAGTTTAAGCTTTCACITTAGGCTTCTGTATACCCATGCCC |
| ESTD-<br>Per/RDS | 74 A  | G    | --- | ACCTACAGACGTCGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCAGGGCTGGCTG<br>CTGGAGAGGAGCGGTGCCGGAGACCTGGAAGGCTT   |
| EST68308         | 5     | 29 C | T   | GGAAAGAGATTAAAGAACTTGATTGGAGTC/TAATCTGGTCTTTGAGTGTGGAAGAGTTTATGTC<br>TCTGGCTGAGTTACAAACAGAACTCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT<br>GGAGAAGTAGACTTTAAGGTAAGAAAGTAGTTATTTTTTA  |
| EST54045         | 6     | 39 A | G   | GGAAATATTAAAAATATTTTAAATACCTCCATTTTGCTT/AGTTCCTTTTAGTGAAGATGATACCTGC<br>AAAAGACATGGCTAAAGTTATGATTGTCTATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA<br>TCTGTTAAGTAAGTACTGTTTGGCTTGGAAITGGATTTTAAATGTTGACTTTATCAT   |
| ESTD-<br>PXMP1   | 88 A  | G    | --- | ATGAAACATGGTCTTTAATTTATGATATGTTTGTATAGCTATCTTAAAAGGGCTTCTTTTTTTTA<br>ATGCAGAAAGAGGGGAAATA/AGAGCGAGCTGTGGTGGACAAGGTGTTTTCTCAAGGCTCATAC<br>AGATTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATATATACTT  |
| ESTD-RDS         | 127 A | ---  | --- | CCCGAGAACTCTGAGAGCAGCGAGGCTGGCTGTGGAGAGAGCGTGCCCGAGACCTGGAAGG<br>CCTTCTGGAGAGTGTGAAGAGCTGGGCAAGGGCAACCAAGTGAAGCCGAGGGCGCAGACGCGAGG<br>CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC<br>CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA                 |
| ESTD-<br>s14544  | 94 G  | T    | --- | TTGGGAAGTTAGAGCCTATATTAAATACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA<br>TATCCCAAAAGTTGAAATGCTCAGTTG/CTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTA<br>ACCTCT  |
| EST52908         | 0     | 45 A | C   | ATCACAGGCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/CTGTGGTGTCTGCAAGCCCTT<br>TGGCAATGTGAGATTGATG   |
| EST19590         | 55 C  | T    | --- | AGGAGAAAGCTGAGGAGGGGAAAGAGAGACAAAGAAATGACATTGATGAGTGAAGATGT/CTGGCTCAG<br>GATGCCGGGAAATGAC  |
| EST76136         | 39 C  | T    | --- | TGAAGCTTCTGCCAGCTTGCAATTGTTCTAGGAGAACCT/CTGGCTCATACCTTTATCTATAGCCTT<br>CCCCTAGGCTCT  |
| ESTD-<br>SPTB    | 176 C | T    | --- | TGAACACCCCTGTGTCCGGAGCCAGGTGTGTTCTCTCTGGAGCCTGAGGAGTTTGTGTCTGTGTG<br>CAGTCCCCCGGCCACCTGCTGTGTTGAGCCTGGACATACACCTTCACTCTTGGCCCGGAGAGAC<br>ATTACCCACCTGGCCATGCCCTGGCTGTGTGTCAC/CTTCTCTGTGAAGACCCCAACCCCTGC<br>CTCCCCACCAAGCCAGTTTCTAGCAAGGGCAGGAC                        |



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| ESTD-TAT       | 224 C   | --- | --- | AAATGGTCAGGACCCTGATCCACAAGAGTGGTACCATTTTCATAGGGCCATCAGTTTCATTAGCTC<br>CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGGACAGGATCA<br>ATTTCCTCTCACCTAGAACGTTTGTTTACAACTTTTCTCCAGTATGGATGGGATTATGATGGGGG<br>GAGAAGCAAAATTTTAAATAGGACCCATGAGACACATCA   |
| ESTD-<br>THFB  | 125 A C | --- | --- | TGGGGCTTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTGATTTCCAGAGAAAGAGTCCCAAG<br>CACAGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATC/A/CJCTTCAT<br>CCACACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG<br>TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGATTCTTGTCCACCCGCAACAAGAGTCTATGC<br>CAAGGCAGAAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCA/G/TJATCCCCAA<br>GCAGTGCATCCATTGACACATAAATATGCATCCAGACAAGAGGTCAATAATATTGATGTCGTAA<br>CATGGGTGTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA |
| ESTD-TYR       | 122 G T | --- | --- | AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA<br>AACTCCAGAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTTATGCATTAGTATCACAA<br>AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTTCACCTTTATTACCTTCTTCT<br>AATACAAGCATATGTTAG/A/CJATTAAGTTCTAGGCATCTT   |
| ESTD-<br>TYRP1 | 222 A C | --- | --- | AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA<br>AACTCCAGAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTTATGCATTAGTATCACAA<br>AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTTCACCTTTATTACCTTCTTCT<br>AATACAAGCATATGTTAG/A/CJATTAAGTTCTAGGCATCTT   |
| ESTD-<br>TYRP1 | 222 A C | --- | --- | TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA<br>GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG<br>ACTCTGAGATGTCA/C/TJGAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC<br>ATGGGCTGAGGCTGATCCATTACTCATAT  |
| ESTD-<br>VB12  | 148 C T | --- | --- | TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA<br>GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG<br>ACTCTGAGATGTCA/C/TJGAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC<br>ATGGGCTGAGGCTGATCCATTACTCATAT  |
| ESTD-<br>VB12b | 148 C T | --- | --- | TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA<br>GGACAC/A/GJTGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCA<br>GTGACTCTGAGATGTCAACAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC<br>ATGGGCTGAGGCTGATCCATTACTCATAT   |
| ESTD-<br>VB12a | 74 A G  | --- | --- | ATGGGCTGAGGCTGATCCATTACTCATAT   |

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|----------------|-------------|-----|--|
| EST58607<br>0  | 105 A G --- | --- | CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC<br>CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCACAGTGGCGGGATGGCCGGCGGAGTTC<br>TGGTTGCGGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGT<br>TTCCTGGCCAAAGGAGGGGGGGTGCATGCTGAGATGTAGATGGGGCC    |
| ESTD-VWF       | 36 G ---    | --- | AGGTAGGAAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTTTGG<br>TCCCCTAGAGTCTG   |
| EST71770<br>6  | 189 C G --- | --- | AGCACCACTCTCAGCTCAAGCCTCAGCACAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA<br>CATCTCTCCATGAAGAGCAGACAGAGTTATTTTCTCTGAAGTCCGGATCTATGACTCAGGGACAT<br>ATAATGTACTGTGATTGTGAACAACAAGAGAAAACCACTGCAGAGTACCAG[C/G]TGTGGTGGA<br>AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG   |
| ESTD-<br>TNFAB | 152 A G --- | --- | TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG<br>CAATAGGTTTGGGGGCATGAGGACGGGTTGAGCCTCCAGGGTCTACACACAAATCAGTCAGTG<br>GCCCAGAAGACCCCTC[A/G]GAATCGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGATG<br>CTGTGTGTCCTCCCACTTCCAAATCCCCGCCCGCGGATGG              |
| ESTD-<br>TNFAa | 88 A ---    | --- | TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG<br>CAATAGGTTTGGGGGCATGAGGACGGGTTGAGCCTCCAGGGTCTACACACAAATCAGTCAGTG<br>GCCCAGAAGACCCCTCAGAAATCGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT<br>GTGTGTCCTCCCACTTCCAAATCCCCGCCCGCGGATGG                 |
| EST52418<br>6  | 113 A G --- | --- | CAATTACAGGGTCAACTGCTATGATGTGTTGGAGCCCACTGACCCCTTTGGTGCTACAAGATGTG<br>GGGAGTGGCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACT[A/G]AAGTGAAACCTGTGAGTG<br>TGG   |
| EST13586<br>3  | 89 A G ---  | --- | CCCCTCTATTGCCCCAGCCCCAGGGACAGAGTATCCTTGAACCTCTTAAGTTCCACATTGCCAGGA<br>CCAGTGAGCAGCAACAGGGCC[A/G]GGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA<br>CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC<br>CCGGTCACTC                                      |
| EST51976<br>7  | 123 A T --- | --- | AGGCAGAAACTGGGCCCCATCGGGGGACGTGGAAGGCCACTTGAGCTTCTGAGAGAGGACCTGA<br>GGGACAAGGTCAACTCTCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG[A/T]CTCTCTC<br>CTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGCAGGAGTGCAGATGCTG<br>GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC                     |
| EST11458<br>6  | 140 A G --- | --- | CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTTCTCGAGTTTT<br>CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT<br>CCC[A/G]TTAAAACATTCTATGAGCCAGGAGAGATACGTATTCCTGCAAGCCGGGCTATGTG<br>TCCCAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC |

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| ESTD-<br>AT3aa    | 60  | CT ---  | --- | AGACCTCAGTTTCTCTGTAAAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGCCTJAGCA<br>CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACACAGTGGAGGAAATTTGAAAGGGCA<br>TTGGAATTCAGAGCAAGAGACAGATATTAAAGAGCTGGGAAATGTGG  |
| EST39852<br>8     | 106 | C G --- | --- | CGGCTTCCTTCCAGGTATTGTCAGAAAGCCGAGATGACCTCTATGTCAGATGCATTCATAAG<br>GCATTTCTTGAGGTGAGTACACCTTCCCACTCTTTCAGGCTACAGAAAGGAGATGCATGAACA<br>GCAGGAACACGCTGGAAGGCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGCTAT<br>AATACAGCCCT   |
| EST62448<br>0     | 112 | A G --- | --- | ACCTGGTGTGCTGGTGTGGTGAACCTGGTCTCTTGGCATTGGCGCCCTCTGGGGCCCGTGG<br>TCCTCCTGGTGTGGTAGTCTGGAGTCAACGGTGTCTTAAAGTGAAGCTGGTGTGATGGCA<br>ACCCTGGGAACGATGTCCTCCAGTCCGATGGTCAACCCGGACACAAGGGAGAGCGCGGTTACCC<br>TGGCAATAT  |
| EST36027<br>2     | 120 | A C --- | --- | AGTGACTTCCAAGGAATGGCTACCAACCTGCTTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA<br>ACATCACCTACCACTGCAAGAACAGCATTCATACATGGATGAGGAGACTGGAC/AC/AACTGAAAA<br>AGGCTGTCACTTACAGGGCTCTAATGATGTTGAACTTGTGCTGAGGGCAACAGCAGGTTCACTTAC<br>ACTGTTCTGTAGATGGTCTCTAAAAAGACAAATGAATGGGGAAAGACAA |
| ESTD-<br>COL2A1cc | 112 | A G --- | --- | AGAAATATATAGTCTCAAACTGGCCATCTCCATTTTACGTCCAAAAGTTATACAGCTAGACAACA<br>GTGGTACATACGTTGCTATTTATGCTCTCTTCTCTGTCACCTTCAG/AGGGGTGTTCAAGGTGAAAA<br>GGTGAACAGGGTCCCGTGGTCTCCAGGCTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCT<br>TTGGTCAGCCTATTGAGCTGTAATCACCATACCGTACCT            |
| ESTD-<br>COL2A1dd | 97  | CT ---  | --- | TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC<br>AATAGACTGAGTTGCTGGACCTGGAACA/CTTGGACTTCTTCTACTGCAGCAGACAAGACTTA<br>CCCAAGAGAGATTAAATGGCAAGATATACAATAACAATTTTATTTGACCAAACTATCATGGAACA<br>GCATT   |
| ESTD-<br>CPT2     | 150 | A G --- | --- | GCCGCAATGCCCGGAGTTTCTCAATGTGTGGAGAAGCCCTTAGAAGACATGTTTGTGCTTAGAA<br>GGCAAAATCCATCAAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCATCATGAAAC<br>TGGGAGGCCCGGCAT/AG/GTGCTCATGCCTGTAATCCAGCATTTTGAGAGGCTGAGCGGGTGGAT<br>CACTTGAGGTGAGGAGTTTGAGACCAACCTGGCCAACT             |
| EST12274<br>0     | 135 | A G --- | --- | CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTGCTCCAAATAGAGGCTTACCAAAGTGAT<br>TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAATAATCTTCCCTCTTAGGATGAGGTG<br>AVGTAGTAAATGACCGATGGGTGAGAACTGTTCTGTCACTGAGGAGTACTATAACTGTGAAGA<br>TAAATTCAGCCACAGAGCTTGCCAGATC                               |
| EST76807          | 91  | G ---   | --- | ATGCTAAGGGGATCGGACATGAAAGACCCCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCATC<br>CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCAACCACTGCCCCCT<br>GCTGCCATGTGACTGGTGCAGTTGAGGACTTCTTG  |

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| ESTD-SSA1                | 111 C T ---             | --- | TTTGGCTTTGGGATGTTCTTTGCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAAG<br>TTTGGCTTTGGCTGCTGTGCTGTGGGATATTTGAAAGAGATGCTTTTGGCCAGTCCAAATGTCTCTAGA<br>GAGTTTCCCAATGTTTCTTTGTAATAGTTTCATAGTTTGGGCCCTTAGATTTAAGTCTTTAATCCATT<br>TTGATTTGATTTCTGTA   |
| ESTD-RVR1                | 109 A G ---             | --- | CTTCGTGACGGGAGGTACAGTCTCCGCTCTTCATGGACATATGGATGAGTGTCTGAACATTTCCC<br>CTGCTGACAGTATGACACGCGAGACTTGTCTACTATAGAG/GJGGGAGCTGTGTGCACTCATGCC<br>CGCTCCCTCTGGAGGCTGGAGCCACTGAGATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCC<br>ACTCCGAGTCCGGCATGTCACTACCGGCGAGTACCTAGCGCTCACCGAGG  |
| ESTD-WT1                 | 70 A G ---              | --- | AAGACCTACGTGAATGTTACATGTGCTTAAAGCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG<br>CG/GJGCTGTGCTGGAGTAGCCCGGACTCTTTGTACGGTGGCATCTGAGACCAGTGAGAAACGCC<br>CTTCATGTGTGCTTACCCAGGCTGCAA  |
| ESTD-F2<br>EST44438<br>7 | 100 C ---<br>62 C T --- | --- | GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT<br>GCACCAATGGCTCCAAAGCCCGTAGGGAACTGGGGGATCTAGGGATGGGTGAGGAATGGCCC<br>AGCCAGTCCCGCGGTGCTGGGTCCCAACAGAGGAGGCGGTGGAGGAGACAGGAGATGGGC<br>TGGATGAG  |
| ESTD-PBDA                | 103 A G ---             | --- | GCAGCCAGGAGCCGCTGCACATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA/C/TG<br>TCCTGCTCGGACCTAAGCGAGCAGCTCAAGAGCCGAGCGAGGTGGG   |
| EST12839<br>3            | 122 A G ---             | --- | CCCTCTCATGCCAGATGGAATCCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAT<br>CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA/GJTCCTACCCGACGCTTGTCTCGCATACAG<br>ACGGACAGTGTGGTGCAACATTGAAAGCCTCGTACC  |
| ESTD-CTLA-4              | 48 A G ---              | --- | TGCAAAACACAAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT<br>CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAG/GJTCAGGTCCA<br>AGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAAGGGAACCTTGAATGTTATTCAAC<br>TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG   |
| ESTD-ACE                 | 96 C T ---              | --- | ATGGCTTGCTTGGATTTGAGCGGCACAGGCTCAGCTGAACCTGGCT/GJCCAGGACCTGGCCCTG<br>CACTCTCCTGTTTTCTCTCTTCATCCCTGTCTCTGCAAGCAATGCACGTGGCCAGCCCTGCTGT<br>GGTACTGGCCAGCAGCGGAGGATCGCCAGCTTTGTGTGAGTATGCACTCTCCAGGCAAGGCAC  |
| EST54419<br>8            | 88 A G ---              | --- | GATCAAGCAGTGCACACGGGTACAGTGGACAGCTCTCCAGTGCACCATGAGATGGGCCATATA<br>CAGTACTACCTGCAGTACAAGGATCTGCC/C/TGTCTCCCTGCGTGGGGGGCCAAACCCGGCTTCCA<br>TGAGGCCATTGGGACGTGTGGCGCTCTCGGTCTCCACTCCTGAACATCTGCACAAATCGGCCTGC<br>CTTCTGCCAATTTGAATGATATTGTTGCTGTGGGACCTGAGCCTTTTATGGCACAATGATCACTA<br>TTTTCTTGACCCCTACTTAC/GJATCCTGGGAGATGTAATTTGGGTTTAGCGTGGTGTGTTGTTCTA<br>CTATAGTCCAAGTGAA |

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| ESTD-PS-1     | 99 A G ---  | --- | GGGGAGTAAACTGGATTGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA<br>GCCAGTGGAGACTGGAAACACACCATAGCCTT/GJTTCGTAGCCATATTAATGGTTTGTGCCCTTAC<br>ATTATTACTCTTGCATTTTCAAGAAAGCATTGGCAGCTCTCCAATCCTCATCACCTTTGGGCTTGT<br>TTTCTACTTTGCCACAGATTATCTTGTA                              |
| ESTD-<br>B3AR | 104 C T --- | --- | GGCTGCCAGGGTTCCGTGGAGGCGGCCCTAGCCGGGGCCCTGCTGGCGTGGCGTGGTGGTGGCAOC<br>GTGGAGGCAACCTGCTGCTCATCTGGCCATCGCC/CJTGAGCTCCGAGACTCCAGACCATGACCAA<br>CGTGTGCTGACTTGGCTGGCCGACGCGACCTGGTGATGGGACTCTGGTGGTGGCGCGCGGGGCA<br>CCTGGGCGC  |
| WI-567b       | 48 A G ---  | --- | TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCCTTGGTTC/GJAGCCCTCATCTCTTTA<br>CAGGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGTCTCTCTCCAATCCATCTTCAAAAG<br>GCTGCCACTGTGATCTTCCCAAAGGTGATCTGATGCTACCATCTTGTCTCAAGCC   |
| WI-801c       | 58 G T ---  | --- | ATGGAAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/JAGATGG<br>TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC<br>ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA<br>CATTTCTGCCACCCCTC  |
| WI-801b       | 58 G T ---  | --- | ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/JAGATGG<br>TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC<br>ATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA<br>CATTTCTGCCACCCCTC   |
| WI-1099b      | 76 A G ---  | --- | GAAATTCACCTATACAAGAACTATTTCTCTAATTTATTTACATTAGTCTCATTTCTGAAATATTAT<br>TTTTACA/GJTACCCCTTGTATTATTTTGTATTCTTTGTAAACGAGAGATTACAATATCAGTAACGC<br>TGTTCAATTGATGTGCTATCACAATGTCTAAATACTTTTGGGTCAACATCAAAATTAGAAAGAAA<br>CTTACAAAGTTTATTTGCTTTATGGTTA                             |
| WI-2529       | 71 C T ---  | --- | AGGAAATGGCTGATACCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT<br>CAA[C/TTCTTAACCTGCTGCCCTCAGTCAGTGAAACATTTAATGAAGTCTACACAAATTAATTAGTGT<br>AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAGAGGAGAGACAACTGTGCTTT<br>TTAAGAAATAGAAGAGTCACTTTTCATTAGAAATGGCTTTGGGGATGACAAGTA |
| WI-10088      | 205 C G --- | --- | TAAGGCTGTCTTCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA<br>TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCCTATAGGTAACTGAGGATGAAGGA<br>GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC<br>AGG[C/GJAGCAGAAGCAGCAAGGAGAAAGGAAGT                        |

|          |     |                |                            |                                  |   |
|----------|-----|----------------|----------------------------|----------------------------------|---|
| WI-2625  | 98  | G A ---        | ---                        | ---                              | GGCAGTCTGGCTGTAGGTAGACAGCACTGAAGATGGAGGAAGAGAGAAACAGGCAGAA<br>GCACGTGTGGTAGTTAAAGGCTATTATAGGA[G/A]CAAATTGATGATACCTCGAGGACTCGCAG<br>AAATTACAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCA<br>GCCAGCAAAG                                      |
| WI-2924  | 54  | G A TAGG       | TGACCTTCCTA<br>GTCTTCTCTTA | GCCTAAGTGT<br>AATCACAGGG         | TCCTGTTGCATATTCCTCTTTGACTCTGACCTTCCTAGTCTTCTCTTATAGG[G/A]JACCCCTGTGATT<br>ACACTTAGGGCCCTACCTGGATTATTTAGAACAATC  |
| WI-2939  | 72  | G T GIGCCITT   | GGCTTGTCTCA                | CTTGTGAGGG<br>AAGGCTTG           | CCATTGTTGAGGTTGGTGGGTCACTTGTCTTCCCTCGCACTCAACAAAGTGGCTGTCTCAGTGC<br>CTTT[G/T]CAAGACCTTCCCTCAACAAGAATGTCTTCCATGCTCCCGTGTCTTTGAAAAATTCGACT<br>TTATCCTGAAAAACTCAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG   |
| WI-3203  | 99  | G A AGACGAG    | GGTTATGCCGC                | TCAAGTATTGC<br>CTTGTGGG          | CTTGCTACCATGCAATTCACAGCATACAACCCCTCAGTGAATGCCGTAAACCCCATTTATAAAACAT<br>CTTGCCATCGAAGGGTTATGCCGACAGCAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGA<br>GAATAAGATTGTGGATGGATGAAAGCAGAGAGGAGATGCTAAAAGTGA   |
| WI-3473  | 101 | A G GGCCTAGGGA | AAGCATTTTA<br>GGCCTAGGGA   | CCGTGATGCAC<br>CAACATTTTCT       | GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTTGGGAGATAGTTGGTGATAGGCCCTGTTTGA<br>GATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[G/T]AGAAAAATGTTGGTGACATCAGGGCT  |
| WI-1796b | 29  | A G ---        | ---                        | ---                              | ACACACTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGGCTCATTTCTGCACATGGTGATATTTAAG<br>CAGGAGAGCATGTCTTGGCTCCCC   |
| WI-1796  | 29  | A G ---        | ---                        | ---                              | ACACACTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGGCTCATTTCTGCACATGGTGATATTTAAG<br>CAGGAGAGCATGTCTTGGCTCCCC   |
| WI-4360  | 93  | C T AAATAA     | GTAGTCACATT<br>AGGTATTTTCC | GAGAGATATT<br>TTCAGAGGCAT<br>TTT | AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCTGCAGAGTAGGAAAGATGGGTGAGT<br>AGTCACATTAGGTATTTTCCAAATAA[C/T]JAAAATGCCTCTGAAAAATATCTCTCCCATGTCCCTGTC<br>TAAATATAACATTTTCCC   |
| WI-1959b | 87  | C T ---        | ---                        | ---                              | GCTGAGCTTTGTGGCAGAGCCAGGGACAATTCAGCTGCCGGATTTTAAATAGATTCTGCAGCACTGCAA<br>CAGGAACCAAAAATCAGTC[C/T]JGGGTAACCTGAGAGTGGTTTTCACACCCAAA   |
| WI-1973b | 28  | A G ---        | ---                        | ---                              | GTTGTCCCTGTAGCAGACACAGAAGGCA[G/J]AGAGGAAAAAGCCCTTTTGGTCCAGGGGCTTACAC<br>TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA<br>AAGGTATAGGGTTG  |
| WI-1980b | 140 | C T ---        | ---                        | ---                              | CTTGAGTATGCGTGGATTTTGGTATACACAGAAATGGGAGAGCTGGAACATAATCCOCCATATACCA<br>AGGGACAAATTGTATCTGTCTTCTACAAATTATACAGTAGGAGACATTATGTTCCATGACAATGGTAAT<br>TTTTAA[C/T]GACAGTTTTTAAITGAGTGAAATACCATAAAAAATAATAATAGTAGCAGCTAATATT<br>TACTGAGCTGTACTAGGTGCCTATAAATAGC |

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| WI-2015b | 190 A G --- |  |  | TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT<br>ATATATTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACACAAAGACTAT<br>GTGTGAATCGTCTATTAGGGTTTGTCTATAAACTCTACATGGTGCTTTTCCAACT[A/G]CATATACCTT<br>CTAATACCATAGAG |
| WI-754b  | 49 C T ---  |  |  | GAAGGCACAGGGAGAAGATGGCTGTCTATCCAGCCAGGGAGAGAAGC[C/T]ACATTTATTGGTAA<br>TCCTATAAAGTGCATCTTTAAAATTTGTATTACTTTAGA   |
| WI-754   | 22 T C ---  |  |  | GAAGGCACAGGGAGAAGATGGCT/CJGTCTATCTACCAGCCAGGGAGAGAAGCCACATTTATTGGTAA<br>TCCTATAAAGTGCATCTTTAAAATTTGTATTACTTTAGA   |
| WIR-1b   | 56 A G ---  |  |  | AGGCAATCAGACCTACAGAAGGAACCCCAATAAAAACCTCTGATGATCGTACATCC[A/G]TGCCTG<br>GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG  |
| WIR-1    | 56 A G ---  |  |  | AGGCAATCAGACCTACAGAAGGAACCCCAATAAAAACCTCTGATGATCGTACATCC[A/G]TGCCTG<br>GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG  |
| WIR-3b   | 72 A G ---  |  |  | TAATTTAAAATGGGGCCAAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA<br>GAAGT[A/G]TCTAAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGAAGTATAAACAAATAAGCA<br>AAGCTGGTGCTGAGATAAGA  |
| WIR-3a   | 69 A T ---  |  |  | TAATTTAAAATGGGGCCAAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA<br>GAATGTATCTAAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGAAGTATAAACAAATAAGCA<br>AAGCTGGTGCTGAGATAAGA   |
| WIR-4    | 47 T ---    |  |  | GAGCCTTTCTAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGCTCACACATGTGCA<br>AGGCAGCAGCAAAATTTGCCAGCTGCC   |
| WIR-5g   | 209 C ---   |  |  | CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG<br>TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCCTGGTCCCCTGTTAGG<br>TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGCTCTATGGAACACACAGG<br>TTTTACGTCCAG             |
| WIR-5f   | 196 C ---   |  |  | CGGGACAGAGAGACAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG<br>TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCCTGGTCCCCTGTTAGG<br>TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGCTCTATGGAACACACAGG<br>TTTTACGTCCAG               |
| WIR-5e   | 194 C ---   |  |  | CGGGACAGAGAGACAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG<br>TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCCTGGTCCCCTGTTAGG<br>TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGCTCTATGGAACACACAGG<br>TTTTACGTCCAG               |

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| WIR-5d   | 191 A | --- | --- | CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG<br>TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGAGCCAGAGCCTGTGTCCCACTGTTAGG<br>TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG<br>TTTACGTCCAG  |
| WIR-5c   | 177 C | --- | --- | CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG<br>TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGAGCCAGAGCCTGTGTCCCACTGTTAGG<br>TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG<br>TTTACGTCCAG  |
| WIR-5b   | 159 A | --- | --- | CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG<br>TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGAGCCAGAGCCTGTGTCCCACTGTTAGG<br>TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG<br>TTTACGTCCAG  |
| WIR-5a   | 37 A  | G   | --- | CGGGACAGAGACAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG<br>CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGTCCCACTGTT<br>AGGTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACAC<br>AGTTTACGTCCAG   |
| WIR-6    | 63 A  | C   | --- | TAACCTGAAACTTGTCTTCTCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C]<br>CCGAGTCTGGGGTGGGCAG  |
| WIR-7    | 12 C  | T   | --- | TTGTGACTATT[C]/AAGCATCTGTAGATATTGAATACATAGTCTTGAGATTGATC  |
| WIR-8    | 46 C  | T   | --- | GGCGTCTATGACTATCCTGGTCAATTGATTGACTAATGATTCTG[C]/TGGCCCTTG   |
| WIR-2    | 56 C  | G   | --- | AAACAGAAAAATAGAGGTTATAAGGATGGAACCTAAAGTTGTCAGAGAGGATGA[C]/GJCTGAAG<br>AAAGAAATTACTCTCTTTTGACCAATAAATACAATTGGGAACACTGGAAAAACCATGGCTTGATTACT<br>GACAAAC   |
| WI-7069  | 93 G  | A   | --- | TGTCTTGCTTATGCCTGCCTCTTTGGCTTGGCAGGATGATGCTGCTCATTAGTATTCACAAGAAGTA<br>GCTTCAGAGGGTAACCTAACAGAGT[G]/ATCAGATCTATCTTGTCAATCCCAACGTTTACATAAAA<br>TAAGAGATCCTTTAGTGACCCAGTGAAGTACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAAT<br>GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTCTCACTC |
| WI-18694 | 41 A  | T   | --- | GGTCAATTCTCTTTTATCTGTGAGGAGCCAGCTCTGACTT[A]/TCTCTCTGTTTCTGTCATCTCTCC<br>CCACATACCAACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA<br>AAATTAGACAGTGAAG  |
| WI-18612 | 37 A  | G   | TGC | CCTATATTCA<br>AGTTTGGAAA<br>TTGTATTGCTG<br>CTTGCAAT   |

CACACTGTTACACCTATATTCAAGTTGGAAATGC[A/G]AATTTGCAAGCAGCAATACAAAAGTA  
TTCATGAAGAATGCATAATCTCTGAAAATTAATGAAAACATCCCT



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|-----------|-----|-------|------------------------------------|----------------------------------|---|
| WI-18517  | 87  | C T   | CAGGAATCAG<br>CAGCCTGA             | TGTTTGACAA<br>GTGCAACA           | TTAAAAATCAACTAGGGCTACCCCTCAACACCCCTCCATTGTCAACCTCTACAGCCTGCATGCC<br>ACAGGAATCAGCAGCCTGA[C/T]GTGTGCACTTGTCCAAACACAACTGACTGC  |
| WI-18668  | 76  | C T   | GGCGAAAAAC<br>TAGGCAAAAA<br>CC     | GCTAAATTA<br>CTGCACCTTTT<br>CC   | CGATTGACAACCTTTATTTTCAACTTAGGTAAACAGTCCAAAATCAGTGTAGATTGGCGAAAAACT<br>AGGCAAAA[C/T]AGCAAAAAGTGCAGTTTAAATTTAGCAAAGGCTCAAGACAGTATGTGGAAGGAA<br>GGTGAGATTTCCTCTACT   |
| WI-18680  | 75  | T C A | AGCATCTGGA                         | CCTCTGAATA<br>TACAACGGAGC        | TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC<br>ATCTGGAAT[C/G]CTCCGTGTATATTCAGGAGGGA   |
| WI-18704  | 99  | A C   | GGTTCTCCGA<br>GGGGTAC              | TGAAGCCCTG<br>CTGG               | CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGCACACACCAAGGGCAGTTGGGCTTGAAGGAGCC<br>CTTGAGGAAACACGGGTTCTCCGAGGGGTAC[A/C]CCAGCAGGGCTTCAGCTTAAAGTCG  |
| WI-18673  | 29  | A G   | ---                                | ---                              | TGTGGGCAACCTTGTTTTAAATTGCAAC[A/G]ACCTTAAATTTACAGCACATTCATAATGAACCAAC<br>AGGAGAGTTGCTGACTTTGTACATATGAATATATAAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA<br>AAAAGCGCATACAAGGAAG  |
| WI-18640  | 121 | T C   | GTCGTGGGTG<br>GGGG                 | GCAATACCAC<br>TGAAGAGGAC<br>A    | ACCAGTCATGTTTTATTTGGAGGTTAATTCCTATTAGGATATGAAAGGATTTCAGCAACGATTGAGATT<br>GTGTTCTCACGGAGGGCTCGGGCCAAAGTCTGTTGGGGTGCAGAGT[C/G]GTGCTCTTC<br>AGTGGTATTGGGACC  |
| WI-18533b | 91  | T C   | ---                                | ---                              | GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCCTTTTATT<br>TATATTTTCATTTTCATCTTAAT[C/T]CTACTGAAGCCATTTCTTTGGTTAACTTTAGA  |
| WI-18533a | 59  | T G   | ---                                | ---                              | GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCCTTTGCTTTA<br>TTTTATTTTCATTTTCATCTTAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA  |
| D11734    | 83  | A C   | TCATCTGATAC<br>CTTGTTTCAGAT<br>TTT | AACCAGGATA<br>AGGCTACAAC<br>ATTT | GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA<br>CCTTGTTTCAGATTTC[A/C]AAATAGTTGTAGCCCTATCCTGGTTTACAGATGTGAAACTTT   |
| D49493    | 159 | A T   | CCTGAAGGAA<br>TCTGGGAATT           | ACTTTCAGGCC<br>AGGC              | CAGGACTTGTGGTGCAGCTGCAGACACAGACAGCAGCTCATGGGCAACATCACTGGGGCCAGAGAG<br>AGCTGTCGCCAGTGCATCATTAGGGGTCTTTTCATTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG<br>AGTACCTGAAGGAATCTGGGAAT[A/T]GGCCCTGGCCTGAAAGTGCCCATCATTCATACCCACTGTT<br>CT |
| EST10030  | 98  | T C   | CATTTTGTTC<br>TCTCAAGTCCC          | GCAGTGTGTT<br>ATGGATGA           | TATTTTCATAGAGGAGACCTAGGAGGAGTTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT<br>CCCTTAGCCATTTTGTCTCTCAAGTCCC[T/C]TCATCCATACCACCACTGCTGATTG   |
| EST10052  | 24  | G A   | GAGGCTG                            | TGTGGAACCTC<br>AATCTTAGACT<br>TC | TATTTGGCTCAGCTTCGGAGGCTG[A/G]GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC<br>CTGTTGAGTCAATAACCTGTTGGAAGTCATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA<br>A  |

|                        |                           |                                      |                                     |   |
|------------------------|---------------------------|--------------------------------------|-------------------------------------|---|
| EST10605<br>2          | 118 C G ---               |                                      |                                     | CTTGGTAATACAGTTCTGTATTATACAAAAAATTTGTTTTCTCTGACAAAATGTACACATAGA<br>AACAAATTTCCAAATGGACAGGAACCTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA<br>AAAAAGAAAAAGATCCC   |
| EST11048<br>0          | 61 T G TAATCT             | CTCTCAAGTAG<br>ATAAGAGGCA            | GCTAAATTTTC<br>AGAAAGAATT<br>TTGTTT | CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT[G/JAA<br>ACAAAATCTTTCTGAAAATTTAGCTTATGAACCTCATTACACTGCAACCCAGAGAGGAGCAC<br>TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTCTGAAAGAAATGAAGTGTCAACACAAAA<br>TTCTATATCCAGCTAAATATCATTTTAAAGATGAAG[G/T]GGAAATGAAGCAATATCAGATAAA<br>TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCCACCAAGTAGATTTCTTTGGACGAAGAAATCCT<br>TCTGTGATTGAGCTTTACCGCTTTTCCCTCATCTGCTGGTG[C/T]TCCCTCAGAGCTTTAATGTCCGT<br>CCTGCTCTCCGAGTCAG |
| EST11260<br>8          | 101 G T ---               |                                      | ---                                 | GAATCTGGGTATTAAATAGCGGTGCCACAGGACACATAGGAAGAGCATCCAACTACTTTGGAG<br>CCCT[AG/JAGGAGTTTTTAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA<br>AAGGGAGGAAGGAGTGGGAA  |
| EST11349<br>9          | 109 C T ---               |                                      | ---                                 | CCAGGAATAAAGAAAAAGAGTCAGAGGAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC<br>TTCCCTCA[AG/G]GACTATTTTCACTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA<br>CTTGCCATTTATTTTGTGCATGTTGTTCTTAAAGGCTTTGAAAGATAACTTGGAAATGTGGGAAAC<br>ACATAGATCCCAGA[G/A]TATTAAAGGGGCTGGAAAAGTAGCCTTAAAGAC   |
| WI-<br>16632a          | 71 A G TGGAGCOCT          | CCAACCTACTT<br>CTGAGCOCT             | TCCAGCTTTCT<br>CTAAAACTCC<br>T      | AGAGCAATGGTGGCATCTCAATAAGCAGCTCAATTTGATTAC[G/A]GGTATACATGAAGTAAAAATTC<br>ATGAAGTAAAAATTCATTATACAAAAAGCCTCCACAGAACTTTTCATGCACCCTGAGCTATGTGAAC<br>TGAAAAGTAACAGTGGGAT   |
| EST11772<br>6          | 74 A G ---                |                                      | ---                                 | GCCTAGTAATTCCAAAAGGAACATGTTTGTATAATAACACTCAGTACAAAAGTCTGT[AG/JATCCAGG<br>AAGTGACCAGCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC<br>GTGGAAAATTTTATCTGTACGTTCTTCC[T/C]ATTATATTTATCTTGTCTTGTGATTTTCAGCACCC<br>CACCCGATTTGCAGGCAGTCTTTCTAAACTGTGCCCTGTGAGCTGTTAAAAAGTCTTCT  |
| EST11795<br>3          | 82 G A ---                |                                      | ---                                 | CCCTAGCAAAATGACTTGGAGTTGTGCCAATACCAAGTTACATCTGTTGCCAAAATTAAGCTCTC<br>TTCCCCAGAGGCATTAACTGAGATTAT[AG/G]GGAAACGCCACAGCAAAAATTGACGATGCAGCTTTTA<br>CCTTTTTA   |
| WI-16644<br>42 G A TAC | CAATAAGCAG<br>CTCATTTTGAT | ACTTCATGAAT<br>TTTACTTCATG<br>TATACC |                                     | ATCTTGAGGTTCTGGCCTGTCAG[AG/JAAGTGACATCTTTTACTTACCAGGTCAGGAACCTAT<br>AAAGAACTGTGTAGAAAAGATATCAGGTCAGACTTTTTAAAGGGCTTCTTATCAGCTCAATAAA  |
| EST12005<br>9          | 56 A G CAAAGTCTGT         | TTGTATAATA<br>ACACTCAGTA             | GGCTGGTCACT<br>TCCTGGAT             |   |
| EST12055<br>9          | 32 T C ---                |                                      | ---                                 |   |
| EST12492<br>1b         | 95 A G ---                |                                      | ---                                 |   |
| EST12492<br>4          | 25 A G ---                |                                      | ---                                 |   |

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| EST12502<br>2  | 52 C G ---       |                           |                        | ATACTAGGGAGAAACCAACTGGAGGCAAGTCCACAGGTCACACTTGTGCA[C/G]CAGCAAGTAT<br>AAACAAAGTGGGTTTCGATGAAGAGAAATGCTCACGGGGAAATGACCAITTTTAAGGGCCATGTG<br>GTCGTCGAGGCAGTTAGAGG    |
| EST12619<br>8  | 105 T C ---      |                           |                        | CCAGAGAAATAGAAATGATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTGCACAAA<br>CAGGTGTTTATTATCCCAAATGACAGTGTGCCTGAGAT[C/G]GATGCATGTGGCAGACGAG                                 |
| EST12620<br>0  | 67 A G ---       |                           |                        | TTTCTCTCTCCTTCATTATTTCATTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGC[A<br>/G]TTGAGAATACAATATTGAAGAAGAGTCACTGCGCTGCGCTCTGGAATAATCAGAGTATTTGA                            |
| EST12817<br>9a | 22 C A ---       |                           |                        | TTGGGTTCTCCAGGATCCAG[C/A]CTCGTAGCTGATGTGCATGAGGTCTCATCCATGCTCCACGG<br>GTCTTGGGAGTGACCGGGATGGGAATCCATGTTGCTTGGGTACTCCATCAGGTCAITGGG                                |
| EST12941<br>8  | 23 T A ---       |                           |                        | TCTCAGCTTCCACCTGACCTGCAIT/AJCAACAGCCCCAGTTATTTACCAGAAATTTTGTTGCGTTTCA<br>ATGTAGTGTAGCTTTAATACACTGCACITGTTTG   |
| EST12949<br>2a | 52 A G ATACTGTT  | GGCTTTAATCA<br>TAACCTAATA | TGTGTCCCTGT<br>GGGTCTC | AGGATTTTCATGAGGCTTTAATCATAACCTAATAACTGTAAAAACAACAC[A/G]TCTGTCACTTG<br>CAGAGACCCACAGGACACACATCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT<br>AAGGAATAA                  |
| EST13067<br>4  | 104 C T ---      |                           |                        | ATTTTTTTTCTTAAATGAAGCATAATAAACAGTTAAAAATTCAGAAAAATCATCTATAGTTGA<br>GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACA[C/T]GGAGCAGAAAGCAGCTTCCCACCCAAAG<br>CACCTCTGAAC            |
| EST13117<br>6  | 66 A G ---       |                           |                        | TGCTGTCTGCATCAGTCCCTTTAAAAATTTAAATCGCTTTATACAATTGACACCAATAAATGCACIA<br>/G]TATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC<br>TTTACTG            |
| EST13121<br>6  | 44 C T ---       |                           |                        | TCTGCTTTTAAAGATCTTCATAGCTGCTTAGGTTTGTCTTCC[C/T]AGCATATTCAGCTATAATCA<br>CCTACATTCCTCCACAAATATTCCTGTGTGTGCGCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC<br>AGTCTTATTCACCTCT    |
| EST13226<br>6  | 74 T G ---       |                           |                        | AACTGTTTACTAACAAGGTGCTTTAATTTGAAAAGCAATTTGAGGAAATAAATTAATGAAATAGTCT<br>GGCCATTT/GIGACTAACCCAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG<br>TCAGAGGAACAAACATG   |
| EST13230<br>6  | 72 G A AGAGACGC  | GCTCAGATGTG               | CCGGCTCCTGT<br>ACAGAGA | GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTTCCCGCTCAATATGCAGCTCAGATGTGAGAG<br>ACGC[G/A]TCTCTGTACAGGAGCGGTACTGTCTTCAATCCTTTGATGCAGGTGTTTACCACAGGCA<br>AACAGTTTACTCCACAT |
| EST13236<br>9a | 70 T C TCTCAGGCT | AACCAGATTT                | TGACAAAAGA<br>G        | AAAGATATAAAACAACCTCCCATCAGTAGCAATACAAGGTTATACATTTTAAACCAGATTTTCTCAGG<br>CCTT/CITTTTGGATACCTTAGTAGTTAACTCTCTTTTGTCAAAACCCTCTTGATATAACCA                            |

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| EST13278<br>2a | 51  | A G G                 | CTTTCACCGAA<br>CAATATTTTAG  | CATATCTGG<br>GTGGTGAGAA                 | TTGCGAGAACGTTTTACAGCTCCAAACCTTTTACCCGAAACAATATTTTAGGAGAGATTTGAAATTTAT<br>TTCTGTAGTTCTCACCACCCCAAGAATATGACAGCTTG  |
| EST13282<br>0  | 99  | A T                   | CCACACATTTTC<br>AGTCCCAAGA  | GATGGAAAATT<br>TGAGGAAGGTT              | GCTCACTAGATGAGATTGACCAAATAATTTAGATAATACCTGTGGGAAAGTGCTGAATTAAGCTAGCC<br>TGCCTGAGAATCCACACACATTTTCAGTCCCAAGAATTAACCTTCTCAAATTTTCCATCTCCCATCAGAG<br>GG               |
| EST13290<br>9  | 39  | A G C T T             | CAATTTT TAGA<br>AGTTGGGTTT  | AAATCAGTTCA<br>TGGAAATTTCA              | AGCTCATCTGCAAGCAATTTTTAGAAAGTTTGGGTTCTTTAGCTGAAATTTCCATGAAGTGATTTTT<br>TTTTCTGTGCTTAACCTTCACTTAAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTTGT<br>ATGTGGGCTTTTTTG        |
| EST13518<br>2  | 45  | C G ---               |                             | ---                                     | GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTGAGCATTTA/C/GIACTTTAAAAATTACCTCA<br>ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCCCTTATAACCTTGATTG                                |
| EST13522<br>8a | 66  | A G ---               |                             | ---                                     | CAGGTTGGTGAATCTCAACTAGGAGCTATTTGCCCCCATCCCCACCGGAGTGCTGGAGAC/A<br>G/GTTTTGATTGTCACAACTGCGAGAGGTGGTGCTACTGGAATCACTGGGTAGAGGCCA                                      |
| EST13568<br>6  | 69  | T C ---               |                             | ---                                     | CTTTAAGGAAGTGAGCCAGATGAATCCCAATGACCACTGGTTGAGAGCCATTGGTCTAGGAGTAGA<br>AA/T/C/GCACACAAGGAATAAGGGAGAAGGAGTTGCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA<br>TTTCAAGCTAAGTAAATGGT   |
| EST13785<br>0  | 101 | C G ---               |                             | ---                                     | AAGATTACGGACCATAGAAGAACTGCCCCCGACCCATACACACACAATTTATAGCAGGTAAACCAA<br>CTGAAAGGAACAAGTAATGACTTTCTTGAACAAA/C/GJTGATTACGAAAGTGAAAGGCTACAGGG<br>TGATTACTA              |
| EST14038<br>1  | 25  | A G ---               |                             | ---                                     | CCTCAACCATCTGTAAACCCGAGCCCCAG/CAGTGACCGGGGACTTGTGCTTCCCCCATCCCGCCCTCT<br>CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG   |
| EST14083<br>7  | 23  | A G ---               |                             | ---                                     | CAATGGTGTCCTATGTGAACATATAGIACCTATTTCATAAAGTTAAAAATAATCCCTTCTTGCAATCA<br>CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCGAACAGGAGGGTAGGAGG                              |
| EST14221<br>5  | 42  | T C                   | GCATGCTAGA<br>CAGAGGCATT    | GGAACAAGTC<br>AAAAATATTTT               | AATATCAATGCATTTCTTGTGGCATGCTAGACAGAGGCATTAT/CJTTTTGAAGATCTTTTAAAAAT<br>ATTTTGACTTGTTCCCTTCACACTCATTTTTAAATTTG  |
| EST14812<br>2  | 50  | A G A T A             | CAAGTCAGCTT<br>CTACATTTCTGA | TAAAGATTTCAC<br>TTAAATCCCAT<br>TATGTACT | TTCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATTTCTGAATA/GIAGTACATAATGGG<br>ATTTAAGTAAATCTTTAGAAGTCCCGGAGTTTGGCTTTTCTAACATTTTCATATCAGGTGAAAAACAAT<br>TTTTTCATATGGGTGATT |
| EST14815<br>3  | 128 | A T A T A C T G G T T | CATCAOCCACC<br>GTACCGGAA    | CGGGAAAAACA<br>GTACCGGAA                | TTTGGTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCCGCTGCCCACTGAACCAAGTAAT<br>TCACCAGACAATGGCGCACCACTTAATAAAGTTCGCCGCTCATCAOCCACCATACTGGTTT/TTTTCC<br>GGTACTGTTTTCCCGTA    |

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| EST15420<br>6  | 109 C A ---          | ---                        | ---                                   | TTTAAACCCCAAGACCTTGATGTCAGGACTCCGATCATTTTCTCGCCTATAGCTTGGATATCTTA<br>ATCTCTCCCTTTTGTCATCATATAATCATATAGCCCAAGGGACTC/A/GGAATTTTGGCTGCTTCAAGTCA<br>TTCCAAAACCTCTCAGG  |
| EST15700<br>6  | 48 G C GGA           | GAAAAGACAA<br>AGACAACAGA   | GGAATAGCTGA<br>AACAGAGATA<br>TTATTCTC | GTCAACGACACTTTTATTAGACGTGAAAGACAAAGACAACAGAGGA(G/C)AGCAGAGAAATAATA<br>TCCTGTTCAGCTATTCCAGGATGTTATGCCAATTATCCAGAGTCCTTGATCTGATGTAGTA                                |
| WI-16739       | 57 G A CACAAGC       | GGTTTGCCAT                 | GATAGTTGATG<br>TTCATTATTCC<br>CTATAA  | AAGGATTGAAAACATACCTAGATCATATAAATTGTGAAGGTTTTGCCATCACAAAGC(G/A)TTATAG<br>GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAATTCCTCCAAAGGT                             |
| WI-16782       | 96 C T CACTGTAAGG TC | GGTGGGAGTCT                | CTTCTATCTTT<br>CTGTTCTCTCA            | CTTCTCTCTCCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC<br>CATAATGGTGGGAGTCTCACTGTAAAGG(A/C)TGATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT<br>GCTGATGAAATTGTGGGG |
| WI-16783       | 64 A G G             | TCCTGAGATGT<br>CTTTTACCTGA | CTGCTTGGTTC<br>AATCCTTATTA<br>G       | AAAAATGTAAACCTTAGAGGTTGCCCTCTTTTGTGTCACCTTTTCTGAGATGCTTTTACCTGAG(A/G)<br>CTAATAAGGATTGAACCAAGCAGTATTTTTTAATGGCAAAAGTCCAGATGTAACTCGAGT                              |
| EST15948<br>2  | 58 T C ---           | ---                        | ---                                   | CAGGACTTAAGTCAATTTTGCCTGGAAAGACTTTAACTAAAGGTGAGGGCAACATAGGAT(C/T)GTGTA<br>CAGCACACTCGGACCAAGGAGTGTGCTGAAATCGTACACTAGCTGCGCCAGCCCTTTTCTCTGGC<br>TGCTCTGCCTCCACAGC   |
| EST16088<br>8  | 89 G C ---           | ---                        | ---                                   | GGTTTGAAGACGACGCTTTATCTCCACCTGCCACTGGGATTCCTATTTGAGAGCTGTTTTGTGACGCC<br>TTTTCCAGAAAGGCCGCTC(G/C)[GGGTTTTCTGAACCCCTCTATGGGCATTTTTAGAAT                              |
| EST16089<br>9  | 96 C T ---           | ---                        | ---                                   | CGTCTGAAGTTTTCTTTTATCACAAGTCACATCAATCCCTCGGGCCCCCTGCTCAATGCCACCTCTTC<br>CTGAAAGCCATCCCTAAGTAGTCTCTC(T/A)AAGAGGCCATCCCTGCCCTTTCTTTGCT                               |
| EST16100<br>1  | 24 C G ---           | ---                        | ---                                   | ATCCAGCTGTGAAGGGACAGGAG(C/G)GTAAACACAGTCCATTTATAAGGGGTGTGCACATTCOCA<br>GGGGCTCCAAATAATGCAACATTGTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC<br>ACTCCAGACAGGTTGGCTC   |
| EST16104<br>9a | 83 A G ---           | ---                        | ---                                   | TTCCTTTAAATAACCCACAGACACCCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTGTCAG<br>CTGGTTCTCCAGGGA(A/G)TTGGCCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC                              |
| EST16118<br>0b | 119 T C ---          | ---                        | ---                                   | ATGGTATAACAAAATCAGTTCAGGTTTTTCTGAACAAATGATCCTTTTGGTCTTTCCCGTGGCATG<br>CTCCTAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCACCTAAGATA(T/C)CGAGTGGCAAGT<br>CTTTCACA             |
| EST16118<br>0a | 32 C G ---           | ---                        | ---                                   | ATGGTATAACAAAATCAGTTCAGGTTTTT(C/G)TGAACAAATGATCCTTTTGGTCTTTCCCGTGGC<br>ATGCTCCTAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT<br>CTTTCACA             |

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| EST16151<br>2  | 53 C T ---      |                          |                         | AGCCAATTCAAACGAACTCTATCAAAACACACAAAGGCCTAGAGGAGAGATTAC/TAATGAACGT<br>AAATAATTCAAGGCAATTTTGTATCTAAAGCAATTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT<br>GGTCACGTTTTGTATAGGA       |
| EST16182<br>6  | 54 G A ---      |                          |                         | CATTGGTTGGGTAGGGAAAGATAGTGTGCAAAATAAAATGGTAAACACAGCAG/G/A/AAATGGAA<br>TTATAGCTTCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGGCAGAAGTAGTA                                |
| EST16183<br>2b | 59 A G ---      |                          |                         | GCAGGTAAACTGTGGTTCACACAGTATTGTTCTTTTCATAAAGAAAGAAATATCTAGTTG/A/GJTAG<br>AGGAAGGCACGTCTCTCTGCGCCCTCTCGTTTCATATTTTATGTCACGTCTCTAAGCGGGCCGTGT<br>GCAAGAGATCTTTGAGA       |
| EST16198<br>4a | 28 G A ---      |                          |                         | AATCTTAGGCTCTTGGCTTCAAAATCA/G/ATACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT<br>CCCCAGAGGAAAAGTCAGCATCATAAACACATGGGTACATGCTCACGCACATGGTGTC                                     |
| EST16229<br>2c | 52 T C ---      |                          |                         | TGTGAACCTGGAATTCGCTTGTCGAAGTCTGAGTCACAGTTTCATTTGGGAGT/CJCCCTGTGCAGCC<br>CTTGCCAGTTTCCACGAGGAGGATACTCCACTAGCTGATTCAGACAGGAGGAGGCTGCA                                   |
| EST16229<br>2b | 45 T C ---      |                          |                         | TGTGAACCTGGAATTCGCTTGTCGAAGTCTGAGTCACAGTTTCATTTCTGGGAGTCCCTGTGCAGCC<br>CTTGCCAGTTTCCACGAGGAGGATACTCCACTAGCTGATTCAGACAGGAGGAGGCTGCA                                    |
|                |                 |                          |                         | CAGACTTTTCTCACACCTCATTTGGCTGGAACCTGGGTGCACATGCACATCCTTGAACATATCATTTGGCAA<br>AGGGAAATGGGTCAATAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA/GJACTGTCC<br>TGAACAAATCTAGGCTC   |
| WI-16816       | 124 A G TGGGTTA | GGAGCATTTGT              | GCCTAGATTTT             | GCACCTCTCTGTGGCTTGTCTGTCTGTCAGCTGCTGCCAGTGCCACA/G/ATGGTCTAGCCTCATGG<br>CAGAAGCATTTAGCCAACTCTGGTGTCTGCTCCACTCTCTCTCTCTCCGCCGCTGGGGCTCACCACC<br>TCCTCTCTCTCAATC         |
| EST16269<br>5b | 49 G A ---      |                          |                         | GTACCCCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCGAGCTGTTGTTCTTATGAAGAAGTCAG<br>AAGCTGATAAAGCTGG/G/AJCTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGGA<br>GCCTTCCATTATGGGAATA |
| WI-16824b      | 83 G A ---      |                          |                         | GTACCCCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCGAGCTGTT/CJGTTCTTATGAAGAAGTC<br>AGAAGCTGATAAAGCTGGGCTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGAGGC<br>CTTCCATTATGGGAATA  |
| WI-16824a      | 47 T C CAGCTGT  | TGATGGTGTG               | TTCTTCATAAG             | TTGCTTTTATTATCCAGAAGGCGATGCTACAGATACTGTACAGCATGAACATTTTATTATTACAAA<br>AATGGCTTCCAAACCAATTAAAATGAAC/T/CJGGAATAAGAGCATAAACGGAAACAGTAACATCA                              |
| EST16445<br>3  | 96 T C ---      |                          |                         | TATAATCCATCTCTCAACACACACACAAATAAGCAGCTAATGGCAAT/G/AJCTAGTGGTCTTCCCAA<br>TTCACAAGACCTGTGCTTCAATTTTCTCTGATAATGTGGAGAAATCTGCTCTTTATGTA                                   |
| WI-16857       | 47 G A A        | CAAATAAGCA<br>GCTAATGGCA | TGTGAATGGG<br>AAGACCACT |   |

|           |         |                                       |                                       |  |
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| WI-16879  | 79 C T  | GATACAGGCC<br>ATATTTCCCA              | CAAGGCTTCT<br>AGAACTAGAGT<br>CC       | AGACAGGTCAACAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG<br>GCCATATTTCCCA/C/TATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCCACCCAG                                 |
| WI-16882  | 99 A G  | GAAAATGCCA<br>CGTCTCTGAC              | GACACATGTCA<br>GGTAAATCGC             | ACATGAATGGCAACCTCTTAGTGGGAGAGACAAATCTCCCCCTTTCACCCAAAGGTTACTCTGAC<br>AAGGCTATGAATGAAATGCCACGCTCTCTGAC/A/G/GCGGATTTACCTGACATGTGTCACTCCCT                            |
| WI-16888  | 70 G A  | GCTAACTTTGG<br>GCAGGTTG               | TTGACCAAAT<br>TAA                     | GTAGTAAATGTTCACTACCCGGGGAGAGCAAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG<br>TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCAAAT   |
| WI-16905  | 75 C T  | ACTGGCCTGT<br>GTTGTTCA                | GCTATACTCT<br>TCTAGGCAGTG<br>GG       | TTTGTGTTGTTATTGCGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG<br>TTGTTCA/C/TCCCACTGCCTAGAGAGTATAGACA  |
| WI-16910  | 74 G A  | AAGAGTAAAG<br>ATGGCGTAG<br>AA         | CAAAATGAAG<br>TATCGTTTCTA<br>TAACAGA  | AGTTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTTCATCTCAGAAAGATAAGATGGCG<br>CTAGAA[G/A]GTATCTGTTATAGAAACGATACCTTCAATTTGGGCTGAACCAAGTGAAGGT                             |
| WI-16918  | 93 C T  | CAGCCATTAA<br>CACCAGCAC               | TCCTGATACAG<br>AAGTGGCATC             | GGAAAGAAAAATAAACTACCACCATCTCTCTGCTACACAGAGCACTAAAATCTAGGAAATTTGAC<br>TTTACTGCAGCCATTAAACACCAGCAC/C/T/GATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC<br>ATGAAAGGTCCTCTGAAAG |
| WI-16947b | 127 A C | GGAAAGCAGA<br>CCTGGGG                 | ATGTGATTGCC<br>CGTGG                  | TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAG[C/G]ACAGG<br>TGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA<br>CGGGCAATCACATGAGATG      |
| WI-16947a | 58 C G  | CATGGAATA<br>GGCCTGGAG                | GCCTCAGCCAA<br>ATCCTGT                | TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAG[C/G]ACAGG<br>ATTTGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA<br>CGGGCAATCACATGAGATG   |
| WI-16966  | 43 T C  | AAATGCACAC<br>TACATAACAA<br>CCTAA     | TGCAAGTTATC<br>AGTATAAAAA<br>CTCATATT | CATTTGTTTTACTTTAAATGCACACTACATAACAACCTAATAT/C/C/CTTAACTTGGTCCAACTATTT<br>AGTATAACTAATATGAGTTTTTATACTGATAACTTGCAATGCCATTAAA   |
| WI-16995  | 55 T C  | GAGCAGTAGA<br>GACTGAGGTA<br>AATAGTATT | CATGTTGATTT<br>CCAGCGGT               | TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATT/T/C/ACGGCTGG<br>AAATCAACATGCCCTCTCTCTGTGTGAAGTTGTGACATGGAGCTGAGAAGGCTGAGTCAATCT                             |
| WI-16992b | 60 T G  | ---                                   | ---                                   | AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAACCTACACTGTGCGCCCTCATCTGAGAT/T/G/GTG<br>TAGGACTGTAAGGGAATGTGTTTGGGGTTTAGGAA   |
| WI-16992a | 46 G A  | AAGCACCCAG<br>AAGTACACTG<br>TC        | CACATTCCTTT<br>ACAGTCTTACA<br>C       | AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAACCTACACTGTG/C/A/CCCTCATCTGAGATGTG<br>TAGGACTGTAAGGGAATGTGTTTGGGGTTTAGGAA   |

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| WI-17010       | 23 T C               | TTCAACAGGA<br>AAAGCCATG                   | AATAATACGGT<br>GTTTGAATGT<br>CA       | ATGTTTCAACAGGAAAGCCATGTCATGACATTCAAACACCGTATTATTAGAAAGCTCATTTAAT<br>TGTTTAATGCAGACAAAATCAAGGCTAACTAAAGCAGATCCAAATGACCCAGTGATCAACCTAGA<br>GGTCCACG                |
| EST17127<br>9b | 74 C T               | CACGCGGCAC<br>TAGACAGAGT                  | GGGAGGGCAGG<br>GGTG                   | ATTCGGTCTCCAAACAGATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA<br>CAGAGTCCTTGGGAGCCATGGGACCCCTGCCCTCCACGGCTTCTTAAGTAACAAC                                     |
| WI-17040       | 94 T C A             | AATTCTTTAT<br>CATCTCAAGCC                 | GGACTATGGCT<br>TATTCAAGTAT<br>G       | CACGCGTTCAATAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC<br>GAGAAATCTCTTATCATCTCAAGCCAGTCATCATCACTGAATAAGCCATAGTCCAGTCTCGTTTTCC<br>AAATCTTTCTCATATTGT |
| WI-17044       | 47 G T G             | GCAAGGGAT<br>TAACGTATAG<br>T G            | GGGATCCCT<br>TGTTAAGA                 | TGTTTGGTTTGTCTCTCTCTGCCAAGGGATTAACGTATAGGTCCTTTAAACAAGGGGATC<br>CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCTGCAGAAATGGCAGGGAATCGAAT<br>CAAAAAGAAAGCAAGTG         |
| WI-17021       | 62 T A A C T C       | TGGACTTGTCA<br>GCCTATAACT                 | TGTAGAGTTAG<br>TGGCAGCTGC             | GCATGTGTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTGAGCCCTATAACTACTCTTAAJG<br>CAGCTGCCACTAACTCTACAGGCACAGTAACACTTATACAGGAGCACATGCCAAAAGTGCCTGG<br>GAGGTGCCAATAAAATCAA  |
| WI-17065       | 90 T C C T T         | CCAGAAAGGA<br>AAAGCATAAA                  | CCCAAGAGAC<br>AATGAAATCCT             | TGTAATAAATGTAGACATGGGGAAAAAACATTCGTAATCAACATGTGCTGTTTTCTACTTCCGGTA<br>CCAGAAAGGAAAGCATAAATCTTTCAGGATTTCAATTGCTCTTGGGT  |
| WI-17066       | 32 A C T             | TGTACAGCCA<br>ACATCACTGTT<br>A            | GAGATGTTGAA<br>AATGTTCTGGA<br>A       | TTCATAAGGTTGTACAGCCCAACATCACTGTTTTCATTCAGAACATTTTCAACATCTCAAAAAGA<br>AACTCTGCACCCATTAGCAGTCACTCCCTGAGCTTCCCTCATAGGCAATGGCAACTGCTGATC                             |
| WI-17074       | 86 T G               | ---                                       | ---                                   | TGCTGACTGTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAAGCAT<br>AACCTCCTACACAGGCCCTTGTACATAGGAGTATATTTGGCCAAGACTACCACTAGAAAGTGATT                     |
| WI-17104b      | 108 T C              | ---                                       | ---                                   | CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTGATGCTTTGCGAGCTTCCCATTCATTCCA<br>AATCAGAAAGCAGTCAGTGGCCCGTGGTTCCAGACGGCTTTCCTCTTTGTTAAGAAATTA                               |
| WI-17114a      | 37 T C               | TTCCATCAAG<br>GACTTTGTTT                  | TTGTATTATAA<br>ATAGCAGAGTG<br>AAGAGAC | AGCGTCCAACAGATGTTTCCATCAAGGACTTTGTTTTCCTCTCTCACTCTGCTATTATAATAC<br>AAGCTACCTCCCAAGGCCAGATGCTAAGTGTCTAAAGAGAGACTGCAGCCACAATCAGAGTTACAT<br>GGGA                    |
| WI-17150       | 76 T G C T C T T     | GATGAAATTC<br>AGATAGTCTTC<br>G C T C T T  | TTCTCAGAATC<br>CTGGAAGATAT<br>G       | CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC<br>TTCTCTTTTGTGATATCTCCAGGATCTGAGAAAGGCCCTCTTGTCTGCTCTAATTT                                 |
| WI-17163       | 43 A G T A A C G T T | CATTCCTTGT<br>AAAATAACAA<br>T A A C G T T | CAGAACTTTGG<br>TTTTGCTT               | GAAATCGAATACGTCCTCTTTGTAAAATAACAATAACGTTTAAAGGCAAAAGCAAGATTCTG<br>TAAACCAACATTGAAAAGGGGACACAGGGGAGGGGAGGAAAGGCCAGATTTTCAACGGTTT<br>CCTCCACATCTGCAGACAAA          |



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| WI-17178                  | 127 T C                            | GGACTCCCTCA                           | CCCTCAATTTT                        | AGCAATGTCCCTCCAAATTTCAATAGCTATGATGGAGTTATCAGTTCAATTCAGAGCGAAATTACTGG<br>GGCGAGGGGTTTAATATCTGATGGTTTAAATCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA<br>GCAGTTGAAAATTGAGGG  |
| WI-17180b                 | 81 C G ---                         | ---                                   | ---                                | TCATGGACATCTGGAAGCAGACACAAAATATAGAGAAATCCTGCACITCCCAGTCTCGTGCACAG<br>GCTTCAACAATTAC/C/GJAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAG<br>GGAGTC   |
| WI-17180a                 | 47 T C TGCA                        | CACAAAATA<br>TAGAGAAATCC              | TGCGAOGAGAC<br>TTGGG               | TCATGGACATCTGGAAGCAGACACAAAATATAGAGAAATCCTGCACITTCJCCCAAGTCTCGTCGCA<br>CAGGCTTCAACAATTACCAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAG<br>GGAGTC  |
| WI-17156                  | 54 G C TCCCA                       | TGTTCTCTAAA<br>CTTTAGATATC            | CAAGAAAATAT<br>ATATTTGATTG         | TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTTTAGATATCTCCCATTC/JTTCCACAGA<br>ATCAAAATATATATTTCTGGTTGGAAATTTTAAATGTTCTTAACTATCTGCCTACCATCCACCTCAAT<br>TAATATTCCTG  |
| WI-17149b                 | 79 T C ---                         | ---                                   | ---                                | CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA<br>ACCCAAATTGTCAT/CJGTGTATGAACACAAAAGGATGGGGAAGAAACACATTTTCCCTACA  |
| WI-17149a                 | 48 C G AGGAGGAACA                  | CAAGGTTTGA<br>AGGAGGAACA              | OCACGCACGTG<br>CATGA               | CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATTC/JTTCATGCACGTGCGTG<br>GAAACCCAAATTGTCATGTGATGAACATACAAAGGATGGGGAAGAAACACATTTCCCTCACA   |
| WI-17197                  | 67 G A CTGGGGCTAC                  | GCAGAAGTAG<br>CTGGGGCTAC              | GGTGAGGTGGT<br>GCATAOC             | ATTTGCTATGTTGCTGGGCTGGACTCCAGGAATCCTCCTGCCTCAGCAGAAAGTAGCTGGGGCTACJG<br>/AIGGTATGCACCACTCACCCTGCTTATCAGTTTCGTTTAAAGAAATTTTGACTTTTAGATGCGCA<br>TGATTTTCAGTACTTTTCTCCCTGCTGCTCCTAGTTTTC/JTAAATTTCTCAGTGGACAAATGGACAA<br>ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC<br>TTC |
| WI-17198<br>EST18753<br>8 | 38 A C CCTAGTTT<br>27 C T GGTCTCAT | TCCCTCTGTC<br>CTACCCAGGCT<br>GGTCTCAT | TCCATTTGTC<br>GGATCGCATGA<br>GCTGA | TCGCTATGCTACCCAGGCTGGTCTCATTC/JTCAGGCTCATGCGATCCTCCTGCCTCTGCAGTGGCTGG<br>GATAAGACACAACCTGCCACCCAGGCTGCCCTAGGAGTAGTCTTAATGCCCTGATGGTGGG   |
| WI-17108b                 | 74 C T CA                          | GCCATTGAGTC<br>TCAAAGTAAA             | AACTACGATTT<br>ATCATATGCTC<br>CC   | TTATTTTAAACATAAACCAGATGCACCTTGGTTTTTACATTCCTGGTTGCCATTGAGTCTCAAAGT<br>AAACAC/CJTTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCATTACAGAGT  |
| EST19067<br>2b            | 41 A G ---                         | ---                                   | ---                                | ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTTC/JAGTGGCATTAAAGTACATTCAACT<br>TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCTCCGTT   |
| EST19067<br>2a            | 40 A C TTC                         | CGTGACCATTT<br>AAGGGTATAG<br>CTTC     | AAAAGTTGAA<br>TGACTTTAATG<br>CCA   | ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTTC/JAGTGGCATTAAAGTACATTCAACT<br>TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCTCCGTT   |
| EST19125<br>8             | 28 A G ---                         | ---                                   | ---                                | CTGTTTCTCAGAGATGACACTGCCAACAC/JGJTCACAGATTTGCATACAATACAGTTATGTATTGGC<br>TATTCACAAATTACAGTAGTGTGTTTTTCCCTCTGAAAAA   |

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| EST20824<br>8  | 115 T G          | AGTCGGGAGT<br>GCTGATTG           | AAGATTTTATC<br>TTGGACCCGA   | GTGTGAAGCCGGAGTTTATTATTCAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA<br>AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTG[T/G]TCGGGTCGAAGATAAA<br>ATCTTAGG                 |
| WI-17347       | 50 A G           | ATCCTCAGAA<br>CTTCTCAGCCT        | TCAAGCATCCA<br>CTTGTCCTA    | TTGGTTAAATGATGCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCTT[A/G]GTAGCACAAAGTGG<br>ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA                            |
| EST21904<br>b  | 128 G A          | TTCATATGGCC<br>ATTTTAATAA<br>GTG | GGCAGGTGTC<br>AGAAAGCAT     | TGATTGGGCTCTGGGAGCAGGTGGGCAGTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT<br>GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTCATATGGCCATTTTAAATAGTG[G/A]TA<br>TGCTTTCTGAACACCTGCC |
| EST22111<br>3  | 82 T C T         | GAAGATCTGT<br>CTGGCATTCTT        | TGGA AAAACA<br>GCCCCAC      | CAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGCTAAGAGAAGAT<br>CTGCTGGCATTCTTTT[C/G]TGGGGCTGTTTTTCCAAGGCACA  |
| EST22197<br>2  | 78 T C T         | AATTATCTGC<br>TATTCCTGCCA        | ACCATGAAGG<br>ATGGGT        | GTTTAATGATCACTCAACAAAATCCACAGGAGAACTTTAAATGTTTACAAGCACCAATATTCTGCT<br>ATTCTGCGCATTT[C/G]ACCGCATCCTTCATGGTAGAGATACAAAGTAAAGTTTCTGGTTGTTTCATC<br>TACTTAAACCA          |
| EST22311<br>9c | 92 T C ---       |                                  | ---                         | TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG<br>TAGCATTCAATGGTTTTTACTCTA[T/C]GTCAAAGCTGGGCAACTATCACTACTATCTAATTTCAGAA<br>CACITTCATCATTCAG  |
| EST22311<br>9b | 54 A G ---       |                                  | ---                         | TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCC[A/G]CCACTGTAAA<br>CAGTAGCATCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTTCAGAA<br>CACITTCATCATTCAG   |
| EST22311<br>9a | 41 T C GAGTTATAA | GGATTAGATC<br>ATCTTTTATT         | TTGAATGCTAC<br>TGTTTACAGTG  | TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAAT[T/C]ACATAAAAAATCCACCACCTGTAAA<br>CAGTAGCATCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTTCAGAA<br>CACITTCATCATTCAG   |
| EST22319       | 19 A C ---       |                                  | ---                         | TCGAGGAGCTCTGAGGAGC[A/G]ACCAAGGGACGTGTGTCCAGGGCCACCGTGCAGGCAAGTGTG<br>GTCCAACTCCTTCCTCCCTTTACAAAACCTCCAGCCTCACCCACACAAACACTGGCTGACAGGCTTCT<br>TAAGCCTTTTTTAACGTG    |
| EST22433<br>c  | 103 A G AA       | AAGACATGTT<br>CACCAAGTGA         | CAGCTTCAGCT<br>TAAC TGACAGA | GATGTTAATGACTTTCCTTTGAGATATGATGGAAAAATATTCAGGTTACACATGGA AAAAGACATGTT<br>CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC[A/G]TCTGTGAGTTAAGCTGAAGCTGAAAT<br>CTGGGAGCTTGACATGCTG |
| EST22657<br>9  | 71 A G           | AAATGGATCC<br>TTATCTGCACA        | GCATGAATTTT<br>T            | TATCCATTTCAAGAAAAAAAATGACTTAAAAAATAGAAATCTATCCAGAAATGGATCCTTATCTG<br>CACA[A/G]CCATTGAAGAAAAAAAATTCATGCAAACTGAAACTATGCTTT  |

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| EST22993<br>5b | 71 T C    | ATCCTTTTGT<br>TCTACCCC               | TTGCCTGTTAA<br>TTTGACTGTAA<br>TG      | GCCTTTTATTGCTCCTTTTAAACATCAATGTTTTATAACACACTTGATCCTTTTGTCTTCTACCCCCA<br>ATTTC/CATTACAGTCAAAATTACAGGCAATATAATAGGTCTAACAGAATGCTTGCAATTT                              |
| EST23021<br>0  | 108 T A   | ---                                  | ---                                   | TTATTCTCAGCTTACCATTGTGTACTTATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG<br>TTAAATCTTTGTGAGGTTAAATTTATTAATCTTTGCCTTTTATGTTTGTGACAGTTTGTGCTTTCT<br>T                         |
| WI-17387       | 55 C G    | CCTTTCAGAT<br>TGAAGAAAA              | GCTTTTGCTTA<br>AGATTAATAGT<br>AACTACT | ACAGAAATTTAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG<br>TAGTTACTATTAAATCTTAGGCAAAAGCCATTTCTTTG   |
| EST23669<br>1  | 101 A C   | AATGTAAGCT<br>CCAGAGGCAG             | CCTTCCCTCC<br>TGTAAGC                 | TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA<br>AGTGCACACTAGGCAATGTAAAGCTCCAGAGGCAG[C/G]CTTACAGGAGGGGAAGGACGCTGAGGC<br>CAAGAGTGTGCTCACTG   |
| EST23733<br>9  | 31 T G TT | GGCTGTTAGTT<br>TTGTTTTGTTT           | TGCACITTTAA<br>TCCCATCAAT             | AAAGGCTGTTAGTTTTGTTTTGTTTTTCTTTT[G/T]ATTGATGGGATTTAAAGTGCATATAACTGAAG<br>GCAAAGTCCAAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGGCGGC<br>TGAAGAATACCCACCTAAA |
| WI-17470       | 83 A G    | GTCCCGTCCCG<br>CCAG                  | CCAGTGACGAG<br>GOOGA                  | CTGACACGTCCCTGTGTGCGGGGTGCTCATGTGCGGTGTGTGAGTGAGACTTTTTTACTGCGTCCG<br>GTCCCGCACGCCCTA[G/T]CGGCCCTCGTCACTGGCCCTTGGTCACTTTGTATTCTGCTTGGTTGGAAA<br>TACCATCAGCCTTCC    |
| WI-17519       | 55 T C A  | GTGTCCTAGC<br>TAATGAATGC             | AATTTATTAT<br>TGCAGGCAATA<br>CTC      | TTTTTAACGAAATCTCACTACTGCAAAATGCAATGTTGTCTAGCTAATGAATGCAIT/CJAGAGTATTG<br>CCTGCAAAATAATAATTGAGATTCTATTTTAAAGACTTAGAACAGTACATGGTGATAG                                |
| EST25356<br>3b | 95 C G    | ---                                  | ---                                   | TCITTTGATACAGGTAACCAAGTTTGTAAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGATAT<br>CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]ATATAATGTCAACATCAGGATTTCTTTTT                            |
| EST25356<br>3a | 26 A C    | ---                                  | ---                                   | TCITTTGATACAGGTAACCAAGTTTGTAAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGA<br>TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT                                 |
| WI-17581c      | 99 C T    | ---                                  | ---                                   | GGGTGACGCTCCAGAAATGGAGACAAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATCAACATT<br>ACTACCAGTTATTGATAAT/CJGATAGAACCCCACTAGGCGCAATTTACATTGACGCGTCATGC                           |
| WI-17581b      | 86 T C    | ATTCAACATT<br>ACTACCAGTT<br>ATTGATAA | CGTCAATGTAA<br>ATTGCGCT               | GGGTGACGCTCCAGAAATGGAGACAAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCAATCAACATT<br>ACTACCAGTTATTGATAAT/CJGATAGAACCCCACTAGGCGCAATTTACATTGACGCGTCATGC                           |
| WI-17596       | 86 A G C  | ACTTCCCTGTG<br>TAAACACTCC            | CATTCTTATAG<br>CTAGAAATCGA<br>CAATAT  | GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAGGCGCTACT<br>TCCITGTGTAAACACTCCCA/GJATATTGTGCTGATTCTAGCTATAAGAATGGGCCACTAAGTGGGTC                        |

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| WI-17623       | 46 T C ---        | ---                             | ---                               | TG TGG TTTTAA TTTTAA TTTCCCATATAATTAATGGTGGGCACATTTC/GCATGTGCTTACTGGGTC<br>ATTTCATATATCTTTTGGAAGCATCTGCTCCAATCTTTTGCTGACTTTGGAGTTTTTTGGT                            |
| EST26419<br>1b | 46 T C ---        | ---                             | ---                               | ATTTTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA/T/C/GGGCAGTCCAAACTTCT<br>TGGGAGGAAGTAAATTCATGTTAAATGTCATGCTGCTGCTCGAGGAGAAGGTTCAAAGGAGGTAG<br>AGAGAGGAGACAGAGAAATG  |
| EST26419<br>1a | 35 C A A G        | CAAGAAAGTTG<br>GACTGCCC         | ATACAAAGGC<br>AACTATGTGC          | ATTTTCATACAGAGATACAAAGGCAACTATGTGCAG/C/A/AACAATCTGATGGGCAGTCCAAACTTCT<br>TGGGAGGAAGTAAATTCATGTTAAATGTCATGCTGCTGCTCGAGGAGAAGGTTCAAAGGAGGTAG<br>AGAGAGGAGACAGAGAAATG  |
| EST26780<br>5  | 69 G C ---        | ---                             | ---                               | TCAGCTTTAA TTTAAGGGACATGTAATAAATAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC<br>AG/GC/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAGTGTCTGCTTCCATCTTTGGCTTTACCA<br>CACTTACAAACTGATACCC |
| EST26900<br>7  | 39 A G ---        | ---                             | ---                               | TACTTCAGTTTAAAGGCAAAATTCACACAGAGACTGTCTC/A/G/GAGACGGGCACAGAACCCAGACACC<br>GTAGAAACACCACCACCACCATGTCATGACGGGAAGCAGAG   |
| EST27152<br>1  | 101 C T ---       | ---                             | ---                               | CAAAGGATTTATTTTGTTCCTAAAAAGTAAAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGTT<br>CTATACTAAACATTTTCAATCATCTCTCTCTC/T/TTCACATGGTGTACTCTTTTCATGTACACAT<br>CATCGGAAAACAGACTGA     |
| EST27504<br>0a | 33 G A ATTT       | GCTGGTGTGAT<br>GCTACTGTAAT<br>G | GCACTTTGCAA<br>CAATTTAATA<br>ATTT | TTTTGCACTTTGCACAATTTAATAATTTATC/G/A/CATTACAGTAGCATCACACCAGCAGTCAAT<br>AATGCCACTTTAGGCAAAAGCTTTTCAAGTATTTCTGTACACATTTCTGTTAACAAAGAACCCATACATT<br>GGTAAATTCATTCT      |
| EST27662<br>4  | 51 C T CTCCAGTCTG | TTATGGAATG<br>GCTTATGTAAC<br>C  | CACATTCTGTT<br>CTCCAGTCTG         | ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTTCTCCAGTCTTG/C/TJAGGTTACATAAG<br>CCATTTCCATAAATTTCTATAGCCTTCTTCTTAGAGTAACACACACTCTTGTTTAGGAATGTTT                             |
| EST27788<br>3  | 100 A G ---       | ---                             | ---                               | ATTTTATTAGGCGGTACAATTCGAAGGTGTAAGGGTGAAGGGAAGGGAAGGCGAGGCAAAATACAT<br>TATTGAGCTGAAAACAACCTTACATTCAGGAC/A/G/GCTTCCAGACAAGCCATGTAGAACCAGCAT<br>GCCTTGGGACTGTGGAT      |
| EST27828<br>4  | 58 G A AGAAGTCTG  | GTGCAGAGAGG<br>TACTCCAAGTA<br>C | GGAAGTCATC<br>AGAAGTCTG           | TCCTTAAACCTTCTCTCTGTTGGATCCAGTGACGTGGAAGTCATCAGAACCCCAAC/G/A/JGTACTT<br>GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAAATTTTACTTGAA                             |
| WI-18369       | 58 G A ACAATC     | TTATCCATT                       | TTATCCATT                         | TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACAATC/G/A/JAATG<br>GATAAGGCTTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC                             |
| EST28036<br>4  | 37 T C ---        | ---                             | ---                               | TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTA/T/C/JAAAAGAAATGATCAATCCTGTTGCCTCT<br>AAGTCAATGGAATGAAGAGCTGTGTCAGGGACACACCACGCCGCTGTGAAGGAGACTGCTGTTGTG<br>TCCACCTCTTATTCATAG  |

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| EST28483<br>7  | 31 T A  | GGAGTAAAG<br>GTGTTCTTCT<br>TTAAA | TTTCTCGCATT<br>TATTTTATAC<br>CA   | CATTTGGAGTAAAGGTGTTCTCTTTAAAT/AJATGGGTATAAAAAATAATGCGAGAAACATTAAAC<br>GGAGAAATGTACAGACACAGACGAGACATGAGTTGTTCTGACTGTGACACATTGGGTGAAA                               |
| WI-17724       | 50 T C  | TGGGCGCTCC<br>TGTC               | TGGGTTGGCAG<br>TGTC               | AGAATTGGTCTAGTAATCGTTCCAGGATTCGGGTGATGGGCCCTCCCTGTC/CJGGACACTGCCAACCC<br>CACAGCTGGAGGGGCACTTAAGGCACGTCATTTTGATTAGA  |
| WI-17730b      | 68 T C  | ---                              | ---                               | TGAGCCTGGGGAGAAAGACACAGAAAGTGAAGTGCATTAGTTACATCATACCAAGTGTACATACTG<br>TT/CJACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA                             |
| WI-17730a      | 39 A C  | GACCACAGAA<br>GTGAAGTGCT<br>ATT  | TCAACAGCCAT<br>AAATCATGTG         | TGAGCCTGGGGAGAAAGACACAGAAAGTGAAGTGCATT/AJGTTACATCATACCAAGTGTACATA<br>CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA                              |
| EST29041<br>5b | 53 G A  | GGAACAAACA<br>CATTAAAGCAT<br>CA  | GGTATTGTTGA<br>TTTGAGGAGTT<br>AGC | TACTCAGAAATGTGAGTTTCATGAGGAACAAACACACATTAAAGCATCATTGTCACT/G/AJGCTAACTCCT<br>CAATCAACAATACCCCTTATTTTAGCCATGAAAAC   |
| EST29128<br>4  | 58 A G  | ---                              | ---                               | CTTTTAGAAGGACACACAGTCTGTTGGACTTAGGGCCTACCCCTATTCAGCAGGTGCC/AJGTTATTT<br>TCACTTGGTTACGTCGTAAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA<br>GTTTGTCTGGGACACT  |
| EST29912<br>3  | 103 C T | TCTGCCAGCTT<br>ACAGGCT           | GCGTAAGTGTC<br>TCATTCCTCTG<br>T   | ATTATTAGGTATCTGCTGTTGGGGTGGGGAGATTGTTGAGATACTGCAACAGACACAAA<br>AGCAAAGAAAGAAACATTCTGCCAGCTTACAGGCT/CJACAGAAAGAAATGAGACACTTACGCATG<br>GCCATGATACACAGCAGTGA         |
| EST29936<br>8  | 121 G C | ---                              | ---                               | TATTGGTATGCTTAGGGAAGATTCTGATTAGAGATATTAATCTTAAAGTTAACTCACCATGAAA<br>TTTAAACCTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA/G/CJAGCTCAGTA<br>TCTGGAATCATGCTTCTCTG |
| EST30223<br>2  | 99 A G  | ---                              | ---                               | AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA<br>TCCAATTACACTCTAAGTTATTTTAAATATCC/AJGGGATTTAATTTCTCCTAGTTCAATCTTGGGA<br>GG                    |
| WI-16260b      | 86 G A  | ---                              | ---                               | CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAAGAACCCAGA<br>GTTTCACAATATAGGTAGC/GAJATAACCAGGCTCACTTCCCTTCCGTGAGAACTTCGTGGGAC                               |
| WI-16260a      | 59 G T  | TGAGGTGGATT<br>CAAGAAGAAA<br>A   | CTACCTATATT<br>GTGAAACTCTG<br>GGT | CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAAGAAA/G/JACCC<br>AGAGTTTCACAATATAGGTAGCGATAACCCAGGCTCACTTCCCTTCCGTGAGAACTTCGTGGGAC                           |
| WI-17835       | 30 G A  | ACAGGAAATA<br>TTGTGCTTTCT<br>TG  | TGGGGTATAGG<br>AAACAGGC           | AAGAGAAACAGGAAATATTGTGCTTTCTG/AJGCTGTTTCTATACCCCAATATCATAAAGAAAT<br>GTTGTGCTTCTAATGTTACAGCTTCAAAATCTTTTGCTTAATCAATCCAAATGAATTACCTGAAT<br>TTCTCCTCTTGTTCAAA        |

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| EST31951<br>4  | 87 C T      | GGGTGTCCAG<br>CCAACA        | CCCACCAAAAT<br>CACTCC                | ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAACAACTTTTCACTCTTTTAGCAATGACA<br>TCGGGTTGCCAGCCCAACA/C/TGGAGGTGATTTTGGTGGGAATTCCTTATCACAATTAATCT   |
| EST31968<br>8b | 95 T G ---  |                             | ---                                  | CGAATTTGTCCTCTTATTTTTGTGATTCTAGTAATCCTAAAGATTGGGGGGCGGGTTACTATAAGT<br>GCATTTTATAATGGGATTTTCTGCTT/GJAAGTCCCACTGATTCCTTACATGGGAAAGGTGCAAAAG<br>ACAGTGGTACTGCTCC  |
| EST31968<br>8a | 75 T C T    | GCGGGTTACTA<br>TAAGTGCAATTT | TGTAAGAATCA<br>GTGGCAGTT             | CGAATTTGTCCTCTTATTTTTGTGATTCTAGTAATCCTAAAGATTGGGGGGCGGGTTACTATAAGT<br>GCATTTT/CJATAATGGGATTTTCTGCTTAAGTCCCACTGATTCCTTACATGGGAAAGGTGCAAAAG<br>ACAGTGGTACTGCTCC  |
| EST32063<br>2  | 103 C T --- |                             | ---                                  | TCCATGGATGAACAGACGCTACCATGCCACATCCCACTCCCTCCGACCAGATGTCGTGGCCAGAGC<br>TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TGTTGAGGCCCATTTGAAATAGCAAAACGCAC<br>AGTCATGTAGCACTCGG   |
| WI-16303       | 65 A G ---  |                             | ---                                  | AAGGCTTTCCAAAGCAATTCAAAGGCACTTGGGTGTTGTGCTCTAAGTTTCTGTCACTGCAGCCCCA/G<br>TCTGTATTAGGGAGACCCCAAGCCAGTAACAATATGGTTCTTGACG  |
| WI-17800       | 29 C G      | GGGAGCACAA<br>GAGAACTCA     | TTTCTACAAAT<br>TAATCCAGTC<br>TT      | TGGACATGGGAGCACAAAGAGAACTCACT/C/GJAAGACTGGGATTAATTGTAGGAAATATTTACACAG<br>TTTCCAAAGTCAGAGAGCTAATCCCAACCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC<br>CCATGAAGGGAAATACCC   |
| WI-17857       | 34 T G C    | CCATAAGTCTG<br>GGATGACTTTC  | TGGCTTAGGT<br>TCTACTTGATG<br>T       | AAACTGTCATTCCTAAAGTCTGGGATGACTTTCCTT/GJATTCATCAAGTAGAACCTAAGCCAAAT<br>TCAGAATCAGAATCCTTTTGTCCATCAAAATTCAGCTAAGTCCCAAGCTGAATTTAAATGTTCAATCT<br>GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAAACAAAATCTTTA<br>TAGTGCCAAAGATAATTAATCTTGGTTAAATCTTTGCCAGCAAGCAAAATAT/T/ACCGACTGAC<br>TGCTCCTTAGTCTGTGATC |
| WI-17860       | 121 T A     | TTTGGCAGCAA<br>AGCAAATA     | ACTAAGGAGC<br>AGTCAGTCGG             |  |
| WI-17866       | 43 A T      | TTTATAGCCT<br>ACTTCTCAA     | CCGTTGTCACT<br>AATCACAAA<br>A        | CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATTTGT/T/TTTGTGTGATTAGTGACAAG<br>GGGGAATCTACAATGCTCACATCACAGTAAACTACCA  |
| EST33301<br>4c | 80 G A ---  |                             | ---                                  | GAAAAAAAAGTCAAAATGTTCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCATGATC<br>AATCGCCACGAGAG/GJA/ACTGGATGCCCCAAAGAGTATGG   |
| EST33301<br>4b | 63 G A ---  |                             | ---                                  | GAAAAAAAAGTCAAAATGTTCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCAT/G/A/<br>ATCAATGCCACGAGAGACTGGATGCCAAAGAGTATGG   |
| EST33460<br>1  | 44 G A CA   | AGCGTGGTTTT<br>CAATACTAAA   | CTGTATTATT<br>GTTAAATATT<br>GCATTGTT | CTATCCAAAGATATTTATTGCAGCGTGGTTTTCATATACTAAACA/G/A/JGTAAACAATGCAAAATATT<br>TAACAATAAATACAGTGATTAAATAAGCCATGCCATATCCAGTTGATGTAATACCTTTTGCAA  |

|                |                        |                                       |                                      |   |
|----------------|------------------------|---------------------------------------|--------------------------------------|---|
| WI-17904       | 50 A G                 | AAAGCATGAC<br>AATAAAATGA<br>ACAC      | CGCTTATGTTA<br>ATAGTAATTCC<br>CG     | CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACAC[A/G]TACGGGAATTAC<br>TATTAACATAAGCGATAAACATCAAAACATCTGGTAAATGCAGTTAAACAAACACAAACAAATGA                                |
| EST34149<br>5  | 69 A G A T             | TGCCAAATAC<br>TCAAGTGTGA<br>GAT       | AACTACTAGCG<br>AGAACAATA<br>ATAAAATC | GTITTTTCTTTGAGTGACACAAGCTTGTTCAITTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA<br>T[A/G]GATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTTCAGC<br>TTACAAATCACACAAGT       |
| EST34343<br>8  | 95 C A                 | ---                                   | ---                                  | TGGGAAACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAAACATTGTAATAGTGT<br>TTTTATCAATGATGCCGAGGTCACTGCT[C/A]TACAAAGATTAAAGAACTTACCATCAAAACACTTC<br>CAGTGCATCAA               |
| WI-17982       | 98 C T                 | GGACCATATG<br>ATATATAACT<br>CCTAAAAGC | CAGAAATTATG<br>TGATAATAACT<br>CCTTCC | GGTACACAAATTTAATGGAAAGGAACACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG<br>GAGGGACCATATGATATATACTCCTAAAAGC[C/T]GGAAAGGAGTTATTATCACATAAATTTCTGGGC<br>GCTACAGAAAGTTTTCATCA   |
| WI-17993       | 118 A C                | ---                                   | ---                                  | CTCAGTAACTCCGGGTATAATCTGCCATTTATTGATTTATTTATGATAAAACACCTCTCATTGTGA<br>AAAACAGCTAAGGGTGACATCTCCAGACCCCAACCACTGTCCCTGTAATGT[A/C]CTGCTGAGAGTCC<br>ACATTTTGGAAATCCAAT       |
| WI-17996       | 84 A G                 | GTAGAGCGA<br>AGGGAACAG                | AGGCACATGGG<br>CAGC                  | CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAAACAACATCTCCCCAGGCCTCGCAGT<br>AGAGGCGAAGGGAACAG[A/G]GCTGCCCATGTGCCTGTCTCTAAAGACGCCACCTCAGGTTGATGT<br>CACCTGTGGAGACCGGGT          |
| WI-17136       | 33 C G                 | ---                                   | ---                                  | ATTCTTTATAAAACACCATGTCCCTAAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGTAT<br>AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT   |
| WI-18041       | 24 A C                 | ---                                   | ---                                  | GCCACTGAAAAAAGGTGCTCTTCC[A/C]GTTTCTAACTCCCTGGACTCCCTCATTTGGAACTGAAGCTC<br>ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT<br>TCAAATACTTAATCA         |
| EST35164<br>8a | 57 A G                 | CACAGCCCTGC<br>CCCC                   | CCCTCTGGATT<br>CTGAATCTCAA           | TGAAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCC[C/A/G]TCTTGA<br>GATTCAGAAATCCAGAGGGTGTCTCAGTCCCTTGGTTTAGGTGCTTCTGTGACATTTCTCTTG                               |
| WI-18052b      | 67 A G                 | ---                                   | ---                                  | AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTATGTCGTAACGAATCTTGGTTACACATCTTAG[<br>A/G]ACAGCAGAGCTGCCTGAGGGAGGGTGTGTTTAAATGTCGTATGTCATGCTCAGCACAGTGTCTGGC<br>ATGGCCCATCCATGCTTT |
| WI-18052a      | 50 T C A T C           | CCTGAGTTCCT<br>TCATGTACGA<br>ATC      | CTCAGGCAGCT<br>CTGCTGT               | AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTATGTCGTAACGAATCTTCTTGGTTACACATCTT<br>AGAACAGCAGAGCTGCCTGAGGGAGGGTGTGTTTAAATGTCGTATGTCATGCTCAGCACAGTGTCTGGC<br>ATGGCCCATCCATGCTTT  |
| WI-18054       | 46 G A G A G A T A A A | GGGAGTGGG<br>GAGTAAATG                | CGTCAACCTGC<br>TTCCA                 | CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAA[A/G]ATGGAAGCAGGGGTGACG<br>CATGSCAGGAGTCCAGACAAAAGACGGGTGATTTTGCTCAGGTTGGTAGCAACAGAGGTAATG                                    |

|               |                 |                            |                                       |   |
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| WI-18064      | 54 G A A G A    | GTAGTGTCTA<br>AGCTGTATTTC  | CCAGTGGTATG<br>ATTGTGACATT<br>C       | CAGTGGCAATCATCTCTCAAAACCCCTGTGGGTAGCTGCTAAGCTGTATTTTCAGAG/GA/GAATGTAC<br>AATCATACCACCTGGGGAGAAAGAGTAAGCACAGTGCTTATTAGGTGCCAAACTGGGGTACCTGGGAG<br>GCAGAAA  |
| EST35347<br>2 | 97 T C A A      | GCATAAAATT<br>TTCCAGTTGGT  | COCTGGCAOC<br>TGCT                    | TTAGCACCATTTCTAGTGGAGCAGGATCTTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCAT<br>GGGATGCATAAAATTTCCAGTTGGTAAGT/CJAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG<br>CAGGCA  |
| WI-18070      | 28 A C GTGTAT   | AACCCACTAC<br>TTACTCAGAGT  | AAAACTAATA<br>AGAACTGGA<br>GGTTTT     | AAACCCACTACTTACTCAGAGTGTGTAT/CJATATTAAACACATGAAAGATATAATCTTAGAAAA<br>ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAAGCATTTTAGGTGCAAAGGATATAA   |
| WI-18080c     | 80 C T ---      |                            | ---                                   | TGGCATAAAGTTTGCATAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATCTACTATGCCGTG<br>TTTGACITTTAT/CJTTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT   |
| WI-18080b     | 65 G A ---      |                            | ---                                   | TGGCATAAAGTTTGCATAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATCTACTATGCC/G/<br>ATGTTTGACITTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT   |
| WI-18080a     | 41 T C AGTCTCTC | GCAATATCA<br>ATATCAAACT    | CAATTTACATA<br>AGAGATAAAA<br>GTCAAACA | TGGCATAAAGTTTGCATAATATCAATATCAAACTAGTCTCTCT/CJTGTAAATTAAATCTACTATGC<br>CGTGTGGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT<br>GTGGCATCCTATATAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATCTTCT/GA/<br>TGGCTTTGTACACGGTTTCTTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC<br>TTAGGAGAGGTGTTTGA |
| WI-18086      | 63 G A ---      |                            | ---                                   | AACTACATAGTATGGTCCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGACCTTTGGTATTCCT<br>TTCTCTTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG<br>TCAGT  |
| WI-18115b     | 71 C T ---      |                            | ---                                   | AACTACATAGTATGGTCCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGACCTTTGGTATTCCT<br>TTCTCTTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG<br>TCAGT  |
| WI-18115a     | 70 C T TT       | TTAGTGTACCT<br>TTGGTATTCCT | AGAGGTCTGTC<br>TTTCATACCAA<br>A       | AACTACATAGTATGGTCCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGACCTTTGGTATTCCT<br>TTCTCTTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG<br>TCAGT  |
| WI-18136      | 78 A G ---      |                            | ---                                   | TTTTGAGAAGCACTCTGTAAAGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTCTTTA<br>GGTAATTTGC/JA/GJTAAGAACATAAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT   |
| WI-18169      | 115 A G GAAGCTC | CCATCTTCCG                 | GAGTTCTGCTT<br>GTGCTCCA               | GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGTCTTTCCACTATGAAGGCAATCGTAGAG<br>TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTCCGGAAGCTC/JA/GJTGAGACACAAGCAGA<br>ACTCGTGGGTAGAGTGA   |
| WI-18190b     | 26 G A ---      |                            | ---                                   | TGAAAGAAGTCGACACAGGGGACACT/GA/JTCATAAGTGAACAAGGATGAAGCTAATCATGGAG<br>GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAATCTCTGGCGA   |



|           |                    |                                     |  |                    |  |
|-----------|--------------------|-------------------------------------|--|--------------------|--|
| WI-18190  | 62 G A ---         | AAATATATAC<br>AACACTCCCTT<br>CAGATC | ---<br>CGTTTTACCAT<br>TTGTTAAGCTT<br>TTG | ---                | TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGAACAAAGGATGAAGCTAATCATGTGA[G/A]<br>GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAATCTCTGGCGA                              |
| WI-18181  | 100 A C            | AGCAGAGTTT<br>CTGCCCTC              | OCTOCTCTCT<br>OCTOCTCTCT<br>OCTOCTCTCT   | TTGTTAAGCTT<br>TTG | GACAGTGAAACACATTGAAACACAAATACAAACAAACATTAGGAACAAGAAATGTGTAAATCCAA<br>TGTGTGAAATAATATACAAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACGTA<br>TGTGTTCTTGAAC           |
| WI-18215  | 78 G A             | AGCAGAGTTT<br>CTGCCCTC              | OCTOCTCTCT<br>OCTOCTCTCT<br>OCTOCTCTCT   | TTGTTAAGCTT<br>TTG | ATTACATACAGCAATTCCTGAGTACAACTAGGGGACAGGATTTTCACAAAACAAATAGAGCAGA<br>GTTCTGCCCTC[G/A]GTGTGCGGGGGAGAGAGGGGATTCAGCATTTGGTGGAGTATGTTAATT<br>CCCTCAAGTTAATCTCTC         |
| WI-18232  | 60 T A A A         | TGGTGTGATT<br>GTGATACACTT           | AAATAAAGGT<br>TTTCAGGGGTT<br>C           | ---                | CATTTCCGAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/GAA<br>CCCTGAAAACCTTTATTTTGAATTTGAAGTTTGTCTCAGAAAACCTGGGCAGAACTTTTCACATTCTG<br>AC                    |
| WI-17892  | 76 T C A C A       | GGAAAACCTG<br>AGTTTGAGATC           | CACAGAAGTG<br>AATAGACTAGT<br>GAGACA      | ---                | TTTAAATAGCTTAGAATTTCTCTCAGTATTTTATCAATAGTGTGTAAGCTGGAACCTTGAGTTTGAG<br>ATCACAAT[A/C]CTGTCTCAGTCTATTCACATCTCTGTGGCAATTCGGCAGAGTGGC                                  |
| WI-18242  | 30 G A AATCGTAACA  | CCCCAAATGTT<br>AATCGTAACA           | GCTAACACTTC<br>TACTGTAACAG<br>CTTTC      | ---                | AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT<br>TGGATGCCACAACTTATCTCACCATTCTTTCAAGCAAGTGAGGTCAGAATGTTCTTGCCTATATC<br>TGCAAAAGATCGAACAAG     |
| WI-18266c | 119 C T ---        | ---                                 | ---                                      | ---                | GCATCAGACATCACCACTCTCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTGCAGGACCTAATA<br>CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC<br>CCGCAACTCCGAGGTACCT  |
| WI-18266b | 124 T C ---        | ---                                 | ---                                      | ---                | GCATCAGACATCACCACTCTCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTGCAGGACCTAATA<br>CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[C/T]TGAGAC<br>CCGCAACTCCGAGGTACCT  |
| WI-18266a | 97 C T T T C A A A | AAATAGGAAA<br>TATGGACTATC           | TTTCATGCATCA<br>TTTGTGCA                 | ---                | GCATCAGACATCACCACTCTCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTGCAGGACCTAATA<br>CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACACAAATGATGCATGAATCCACATTTGAGAC<br>CCGCAACTCCGAGGTACCT |
| WI-18312  | 73 A G A A         | GCTGTGAGCTA<br>TTGTTATTCA           | GGAGAAAAGG<br>GAGCAGAAGA                 | ---                | CTGAGCCTCTTGATATGGTTTAGTGTCTATCATTAATTTTGGAAAGCTGTACGCTATTGTTATTTT<br>AAAT[A/G]TATCTTCTGCTCCCTTTTCTCTCTTTTCTGGGATTTCTATTCTGCATGTGTTATA                             |
| WI-18330b | 66 A G ---         | ---                                 | ---                                      | ---                | AAACATCTACAGCTGTCTTAGGCCATCTGTAAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGGI<br>A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAAATAAAGAACATAATTTTTTGTGAT<br>TCACA                |

|                |     |                |                                  |                                     |   |
|----------------|-----|----------------|----------------------------------|-------------------------------------|---|
| WI-18330a      | 49  | GA             | TCCTGTAAGA<br>AATCAGGGAT<br>AAGA | AGTCTGACTC<br>ACTGCTACA             | AAACATCTACAGCTGCTTAGGCCATCCTGTGAAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA<br>GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAGAAACATAATTTTGTGAT<br>TCACA                    |
| EST37564<br>5  | 85  | T C A G A      | AAATTC AAGC<br>CATCTACAAA<br>AGA | CTATGGAGGOC<br>TCAATGAGA            | AAATTAGTTAGCCATAACAGGCTGGAATTGCTGTTAGTAATACTGCATGTTATTTAAGCTAAATTC<br>AAGCCATCTACAAAAGATT[C/T]CTCATTTAGGCCCTCCATAGGCTGCAAAACACATCAAAGGCATTAC<br>TGTACTGGAGAGGACTGAG |
| WI-18327       | 104 | GA TT          | AAACAGCTTT<br>CGTTAGGCTAG        | CGCATACAATG<br>GCTCAGC              | CAAGGGATTTTATTACCTACACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC<br>CCAAACAATGGTGAAACAGCTTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATCGGAGGCAGA<br>GT                       |
| EST37624<br>6b | 102 | GA ---         |                                  | ---                                 | GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG<br>CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACG[G/A]TTCAATCTACATGGCTGCTTGGCGTCC<br>TCTGACCTCCCATTC        |
| EST37624<br>6a | 58  | CT ---         |                                  | ---                                 | GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGC[A/T]GCTGA<br>TGGCCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGGTTCATCTACATGGCTGCTTGGCGTCC<br>TCTGACCTCCCATTC          |
| WI-18357       | 89  | C G GCATCA     | CCAGCCCTTA<br>GCATCA             | AAGACTCAA<br>AGACTGAAGAT<br>GA      | AATGTTTTAAAGTCTACCGTCTGAGGTGGCCATGAAGCCAGCCCATGGAGACATTTTCAGA<br>TAATCCAGCCCTTAGCATCAA[C/G]TCATCTTCACTTTGAGTCTTCCAGCCAGGTCCTCAAGCTT<br>GTGGACCAGAGACAAGCC           |
| WI-18012g      | 117 | A G ---        |                                  | ---                                 | TTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTCCAGACTTGAAG<br>ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTGGTGA[G/A]GTGTTTCCGTGATACA<br>CGCTGACGTTTCGAGGG      |
| WI-18012f      | 113 | GA ---         |                                  | ---                                 | TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTCCAGACTTGAAG<br>ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTGGTGA[G/A]GTGTTTCCGTGATACA<br>CGCTGACGTTTCGAGGG     |
| WI-18012e      | 112 | CT CCCTT       | GCCACTTTTGC<br>CCCTT             | TCAGCGTGAT<br>CAGGAAACA             | TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTCCAGACTTGAAG<br>ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTGGTGA[G/A]GTGTTTCCGTGATACA<br>CGCTGACGTTTCGAGGG     |
| WI-18012b      | 46  | T C ---        |                                  | ---                                 | TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTCCAGACTTGAAG<br>AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTGGTGA[G/A]GTGTTTCCGTGATACA<br>GCTGACGTTTCGAGGG    |
| EST38390<br>4  | 75  | A G CTCTGCATTG | GCAAAAAGGA<br>CTGATTATAA         | GCTAAAGTCAG<br>CTGATTATAA<br>ACTTAA | CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC<br>TGCATTG[G/A]TTAAGTTTATTAAATCAGCTGACTTTAGCATTGGGAGATTATCTGGAT                                   |

|               |     |                     |                           |                            |  |
|---------------|-----|---------------------|---------------------------|----------------------------|--|
| EST38512<br>7 | 91  | T G                 | TGACGATGCC<br>AATACTTCG   | CAC TGC ACTCT<br>GGGAAGC   | TAATAAAAC TGA CCAAT TGGTAAAC TGTGTG GACTGAGAGAGAAACAATGAAAAATCTGTAAAT<br>ACCTGATGACGATGCCAATACTTCGTT/GJGCTTCCAGAGTGCAGTGATAACTGTTATAGCC                            |
| EST38519<br>0 | 24  | C T T               | CCTGCACTCC<br>TAAAAGATCT  | TCTGT TAGGAC<br>TTGGGGA    | CCTGCACTCTCTAAAAGATCTTTTTC/TTCCCCCAAGTCTTACAGAAATGGTATATTCCTCTGGA<br>AGATGAACGTCATCAATGGATTGTGCTGCTCTCGTTTTCAGCTTTGATTTTTTGTCCCTTGAGAACCTTG<br>TCTCCCTGCTGATTT     |
| EST38575<br>1 | 66  | T C A A             | GAACATCCCA<br>TGTTCTGTTT  | AGGGAAGGA<br>GTATAACACAT   | AGTGGTCAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTTAA<br>T/CJTCTCTTATGTGTTATACTACCTCCCTTCTCTTCTTATACACATAGATTTTCTTAATTGCAGC<br>CCA                      |
| EST38616<br>9 | 101 | C G C T T C         | CCTGCTCGGC<br>CTTC        | GAGGAATGGAT<br>GGTGGC      | CCATCTAGGAGGCTACCTGAGCTCTCTGTGCTCCAGAGTGGTGCTCAGGCCCGGGGCCCTCGTGG<br>AGTCTCCGGGGCCCGCCTGCTCGCCCTTC/GJGCCACCATCCATTCCTCCAGGGG                                       |
| EST38652<br>8 | 59  | T C                 | TCGAACTGGG<br>CATTTCAA    | TTGCAAAAATG<br>AAAGGAAAAA  | TATAGTAGGTACTTTCTTGTGCTGACGAGGAATATTACAGTCTGAAC TGGGCATTTCAA/T/CJGCGTG<br>GTATTTTTTCTTTTCATTTTTGCAAGTAAAAAATCAT  |
| EST38654<br>5 | 42  | T C                 | AATGGTCATTT<br>TAATATATCA | CAGTGATGGTC<br>CTTAATCTTCT | CTCAAGCTGAGAAATGGTCATTTTAAATATATACAGTTTACATAT/CJAGATAGAAAGATTAAAGGACCAT<br>CACTGAGGTACATAGCTCAGAGGCAGAGTTAAGATTTGGACCCAGGAGGTTGGTTCCAGCATATA                       |
| EST38707<br>9 | 75  | A G ---             |                           | ATC                        | GGATCCTCACTCACTGGGACAGCCTGAGAAAGGACATCCACCAGACCTACTGATCTGGAGTCCCA<br>CGTCCCCA/GJAGGCCAGGGGATGTGTGCCCTCTCTCCCTCCCACTCATCTTTTCAGGAACACGAGG<br>ATCTTGTCTTCTGGAAA      |
| EST38759<br>2 | 86  | A G                 | TGTCCTCCTGA<br>GGTGATATGG | TCACCATCGTG<br>GACTTAAGG   | TGACCTTGATTTCTACTAGAGGGGAGAAATCACTACCTCTTTGGATGCCCTCCACTACTTGT<br>CTCCCTGAGGTGATATGG/GJGCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAATCTTGCC<br>TAGCAGCAC                  |
| EST38775<br>1 | 40  | T A C               | AATCAATAGG<br>AGAGGATTGG  | GGCTTTGCTCT<br>GAATTCAA    | GACTCTCAACCAAGAGAAAAATCAATAGGAGAGGATTGGC/T/ATTTGAATTCAGAGCAAAGCCCT<br>CTTACTGAGAGGTGAGCCCCCAGCCCCCTCCAAATGCCCTTTCATGAGTTAGGATCTCCTAAGTGGTAC<br>AAACAAACCAACATGGTGG |
| EST38815<br>4 | 91  | C A C A             | TGTTATGAGA<br>ACCCATTACA  | GCTGACTGGCA<br>CATGCTTT    | CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACATTATGTGTGTTCAATCAACAAG<br>TGTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTAATAA                              |
| EST38858<br>4 | 98  | C T T G A C         | CACGAGTAAA<br>AAGAAACTCA  | GGAGCGAGTCC<br>AAGGAGAA    | TCTTACTGTGCTTACAACCTTCTCCCAAGTTTCGGGTGGTTCCATATGTTATTGTTATTGTTATTA<br>TTCAACACGAGTAAAAAGAAACTCATGAC/C/TTTCTCCTTGGACTCGCTCTCTCCCAATCTCGAT<br>ACCGACTGCACGTGG        |
| EST38865<br>2 | 72  | T C T G T G A T G C | GCTGTAGAATT<br>AGGACACAG  | GGAAGGACGG<br>AGGACACAG    | CCTTAATGGATTTACAGCTCATCTGAGTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTG<br>ATGCT/CJGCTGTGCTCCGTCCTTCCCAATGAGCACATATGCAGGGCAGGCAAGCATGCTGGGA<br>TTTGTCTTAGTTGTTAA          |

|                |         |                                     |                                      |   |
|----------------|---------|-------------------------------------|--------------------------------------|---|
| EST38878<br>9  | 47 T C  | AAACATCATT<br>ACTAGCCTAG<br>ATCCTAA | CCTTCAATAAA<br>TCTCATGTCT<br>CA      | CCAAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAA[T/C]TGAGGACATGAGATTT<br>ATTGAAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAAACATTCCOC<br>TTATTCATGTCTCATCTCACACATCTTTATTTTATTTTATTTTCTCCTTTCTCAAATATCGGATTGTTGC<br>TCATGAGAATAATGGCTGAGGGAGCTGGCAGGCAGTCTCTCA[G/C]GCTCCCTGGATAGCTAAAT<br>TTA |
| EST38882<br>6b | 113 G C | ---                                 | ---                                  | TTATTCATGTCTCATCTCACACATCTTTATTTTATTTTATTTTCTCCTTTCTCAAATATCGGATTGTT<br>TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT<br>TA  |
| EST38882<br>6a | 35 T C  | TGTCATCTCAC<br>ACATTCTTTAT<br>TTTT  | CGATATTTGAG<br>AAAGTGAAAA<br>CAA     | TTATTCATGTCTCATCTCACACATCTTTATTTTATTTTATTTTCTCCTTTCTCAAATATCGGATTGTT<br>TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT<br>TA  |
| EST38909<br>5  | 47 A G  | GCACAGCATG<br>GCTAAACG              | GGTATTTGTTG<br>ATCCCATCTT<br>T       | GCACTAACTAACTTTTCATTTGTGGATTGCACAGCATGGCTAAACG[A/G]TAAAGATGGGAATCAA<br>CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT  |
| EST38911<br>9  | 85 A G  | GTTGAGGAA<br>ACTTATAACCT<br>CAC     | TGTTGTTTGT<br>GAAACAAGCG             | AACCTGAATGGCAGTGAAACACTACACATCAAACTTAGGAAATGTGGTTAGTGGTACGTTGAG<br>GGAACTTATAACCTCAC[A/G]CGCTTGTTCACAAAACAACAGCAGACAACAGAGATTTCCAACTC<br>CAGCAATGACAGGCTAGGG  |
| EST38955<br>5  | 30 G C  | TGAATCCCTT<br>GGTGG                 | CACTGCAATCT<br>CACCCCC               | TAAACATCCCATTTGAATCCCTTGTGGG[G/C]GGGGGGGGTGAGATTGCACTGCTCAAGATAAA<br>TATCACAAATATATCAAAACTTCAAATTTGTCTATGCATTCACACACTGACATGAGCCACAACATTT<br>CCTTCACAGGGACTGTAC  |
| EST39002<br>0  | 42 G A  | GGACCTTTCGG<br>TGACC                | CTGGCAGGGAG<br>CCTG                  | CCTGCTATGATGCCTGGGCAGATCCCGACCTTGGTGACQ[G/A]CAGGCTCCCTGCCAGGCTTGG<br>GCCCTAAGGAAATTTGAGGGGCAGGGGGCGATGCCCGCAGCGAGATGGTCTCTGTAAGCCTGTGGGTC<br>CCCCTGACCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT<br>C  |
| EST39004<br>8  | 79 T G  | GGTGGTAAGG<br>CCTAAGGAAT            | ATCTCGGCTGG<br>CGGC                  | CACGTGGCCCTAAGTTCCGGGCTCTCCTCAGTCTGGATGGCTGTGGAAAAAGCTTGGTGGTAAG<br>GCCCTAAGGAAATTTGAGGGGCAGGGGGCGATGCCCGCAGCGAGATGGTCTCTGTAAGCCTGTGGGTC<br>AAAGACCTAACTTCTGGA  |
| WI-16398       | 90 T C  | TCCCTATTATT<br>CCATGATATTT<br>TCA   | GAATGGTTTGT<br>GAAAAATATA<br>TTGATAT | AAAGATAATGTCTATCACACGCAACATATAGAAACATAAAGAAAAATAAGTATCCACCCATAAAAT<br>CCCTATTATTCATGATATTTTCA[T/C]AGCAACTAGTATATATATCAATATATTTTTCACAAACCAT<br>TCAGTTACAC  |
| WI-16403       | 69 T C  | CCTTTGCTCTC<br>AATTTTAAAC<br>ACT    | TAAGGGCTAAT<br>TCCCTATATAA<br>AAAG   | GGTTGCTTTTCATGATTTTCTCATTTCCCTATCAGGTTTCTGGTCCCTTGTCTCTCAATTTTAAACAT<br>T/C]CTTTTATATAGGAAATAGCCCTTAAACTGTGGTACATGCTGCCAAAAATTTCTCCCAAGTT   |
| WI-16406       | 24 C T  | GCTTTAATGGC<br>TACAGAAAGA<br>AGG    | CCAGAACCCAG<br>ATGTGTTTAAA<br>AA     | GCTTTAATGGCTACAGAAAGAGG[C/T]GGTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC<br>AAGTTATATTATGCAATTAGAGCAATAGGTGCCCTGAA   |

|                |     |     |                                   |  |   |
|----------------|-----|-----|-----------------------------------|--|---|
| EST39236<br>0b | 57  | C G | TCATCTGAGA<br>ATAAACTTCCT<br>GTCT | CATTATAGGTA<br>CTGAGTCATAC<br>ATTAAACA | TCCTTTTATTTCATGATTTGTTTCATCTGAGAATAAACTTCCTGTCTAAATTTTCCAA[C/G]ACTATGTT<br>TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGTCTC<br>TTT               |
| EST39294<br>4  | 63  | G T | CCTGAACAG<br>GGATGCC              | GCACAAATTAA<br>ACATAGTACCG<br>AGAA     | CAAAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAACAGGGATGCC[G/T]<br>TTCTCGGTACTATGTTTAAATTGCTGAGCCAGCAACCCCTCGAGTTACCCGGCCTTTTACCCACGCC<br>AGCTGCTGTTGTCTGCAT    |
| EST39366<br>2  | 72  | T C | ---                               | ---                                    | AGAAAACATTCTGTCTGATCAGAGGAAGATGTATGTAGAAAATCAGAATCTGACTGAATTCCTAAA<br>ATCTATT[C/J]ACACTGAGAGGAAAATGGAAAAGAAAATGTTTGCATAAAAGCTTTTCCCTGACTCTCA<br>GAGGGGTTTCAGA       |
| EST39371<br>9  | 86  | A G | CATTGGATTA<br>GGTGAGAGG           | TGATTTGAGAC<br>ATTTCACATTT<br>TT       | AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTATGTGTGTAAATTTCCAGTTGAGCATTTTTCAT<br>TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAATGTCTCAAATCAAATGCTTCTCTTCTAAAGATT<br>GACATTGCCCAACCCCTGC     |
| WI-17177       | 23  | A G | ---                               | ---                                    | ACAAAGTGACATATCCAAACCAACC[A/G]TCCATCCCCACCTGTGCCCTATTCTTTCTTGTTTCTTT<br>AGAGCCCTTTTCAGCTATTCTCTGTGAAGCAAACTGCAGGAAGGCCCTCCCCGTACTCTCTCCCCCTGGAA<br>G                |
| EST39428<br>8  | 31  | C T | GCTCCCCACA<br>ATTGATT             | GGTCCCTTAG<br>AAGCCACC                 | AGGTTCCCTGGTTGCTCCCCACAATTTTATTGTTGTTGTTTCTAAGGGACCCAGGATTCTGCATT<br>TTCTGGGTGGGCTAGTAATCTGTTGCTTTTGGTCCACAGAGCAACAATTAAGAAGATCAGGTCT<br>GGCTGTTGC                  |
| EST39430<br>2  | 45  | A C | GGCAGAGGAA<br>TAACTGATGTT         | CAGGGGTGGG<br>GTAATG                   | AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAAATGATGTT[C/A/C]CAATAACCCCGACCCCTGA<br>CCAGTACCTTTCCCTCAGGCCAGGCCCTCCGGTGAGGATGTCTGGG  |
| EST39446<br>7b | 117 | C T | CTACTGACAT<br>AGGACTTCA           | TCCTGGAAAAC<br>TGACATAAAC              | AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAAAATAACAGGAACCTATTATAT<br>ACGTAAATCACTTTTCATACCTGCCTACTGACATAGGGACTTCAGAGTAATA[C/T]GGTTTATGTCAAT<br>TTTCCAGGATTGTTCTCCC |
| EST39465<br>2  | 80  | A G | AATGCAGGAG<br>GGTGGC              | CAATCTGGGC<br>CCTCT                    | ATGGTGTCAATTAGAGGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACCTGAACAGAAA<br>TGCAGGAGGGTGGC[A/G]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGGGTGAAGACCCAG                            |
| EST39501<br>0  | 81  | A G | AAAGATTCT<br>GTAGACATCT           | CACCTGCAATT<br>CTGAAGGCT               | TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTCTTGACCAAGCCTAAAGATTCTGTAG<br>ACATCTAACATTAG[A/G]TAGCCTTCAGAAATTCGAAGTGAAGTCAAGTCAACCAATTTC                                |
| WI-18387b      | 84  | A C | ---                               | ---                                    | CACAAAATGGGACTGCTGAAGAGTGACAGTTGGACCTTACTTTGGTGACCCCATACATTGTTGGTCA<br>CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGTGCGGATG<br>GCTATGTAGACATAAAGA |

|               |         |                                 |                                  |  |
|---------------|---------|---------------------------------|----------------------------------|--|
| WI-18387a     | 57 A G  | CTTACTTTGG<br>TGACCCCAT         | GCTAAAGCATG<br>TGACCACAAA        | CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACIAGJTITGTG<br>GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTATGTGCGGATG<br>GCTATGTAGACATAAAGA |
| EST40601<br>9 | 78 A G  | GGGTGAACCT<br>GAAACAC           | TTCTTGAAGA<br>AAGCGTC            | TCCCAGGATGGTTTATCCAAAGCTGTGGACGGTGAACATTAGACGAAAGAGGTGACTCGCGTGGA<br>ACCTGAACACIAGIAGCGCTTCTTCCAAAGGGCTGTGGCGATCAGGCCACTCAAGG                                    |
| EST41935      | 32 A G  | AGTGATCAC<br>ATCTCAGGAT<br>AGGT | GCACACCCTTC<br>ACACTGTIA         | TCCATTGAGTGATCACATCTTCAGGATAGGTIAGJATAACAGTGTGAAGGGTGTGCTCATTTTCTTC<br>AGCTGTAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTGA   |
| EST43091      | 28 C T  | CATTCTGGTCT<br>TTATTTTGGG<br>CA | AAACTGATTT<br>GTTAAACATG<br>CTAC | ATGTCATTCTGGTCTTTATTTTGGACAICJTGTAGCATGTTTAAACAAATCAGTTTTCATAGGCAA<br>CCTTTGAACACATCAAAAGAAATACAATATATTTTCACAAAATTTCTCATCACTGTAAATTCA                            |
| WI-18420c     | 108 T C | TTCCATTAAAC<br>AGGAAGTTTC<br>C  | AAATCTCAGC<br>ATTGCTATAAG<br>C   | AGAGAGACAACAAGAAATAAGGAAATGGGAAGAACAGAGTGAATTAAGCAAATCTTGGA<br>TTCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAIJCJGCTTATAGCAATGCTGAGAA<br>TTTCATAGGTACTTCATGGGA        |
| WI-18420a     | 38 C T  | GAATAAGGGA<br>AAATGGGAAG<br>AA  | CCAAGATTTC<br>TTTAAATTCAC<br>TC  | AGAGAGACAACAAGAAATAAGGAAATGGGAAGAAICJTAGAGTGAATTAAGCAAATCTT<br>GGATTGAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA<br>TTTCATAGGTACTTCATGGGA       |
| WI-18425b     | 101 T C | CACCCTGTCCT<br>AGACAGATTTC<br>A | ---                              | AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCTGTC<br>CTAGACAGATTCAIJCJTGACACAACAACAGGAGGTGGGGTCAACACGGCGGAGAGCCAAAAGAC<br>TAGGGC                  |
| WI-18449      | 81 A C  | CTTTTGGCTCT<br>AAGTGGGACT<br>T  | CTCCCTGACT<br>GTATCCAGA          | AAATTGAGGTCCGGGTGGAACATATAAAAGGAAGAAAGAGAAAGTAATCAAGGGAGGCCAAAGTG<br>GGAAGCTGTATTGCTGATCTAACGTGCTGTCCAGTTCCTCTTTTGGCTCTAAGTGGGACTAICJITTC<br>TGGATACAGTCAGGGGAG  |
| WI-18457      | 120 T C | ---                             | ---                              | ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGCCCCCAAGACATTATTTTATTCTT<br>AAATGTCCAATATCTGCCTGATGTCTGTGTTTGTGCACATTGGGGCCACAGIJCJAAATAGGCTAAA<br>AGGAGTCCCACTGCT   |
| WI-18462      | 39 A G  | CCACAATGGC<br>AGAGGTGA          | TTTAGGCTTTG<br>AGATGGTTTCT       | GGTGCTATAGTCTGTTTACACCACAAATGGCAGAGGTGAJAGJTAGAAACCATCTCAAAGCCTAAAA<br>TATTTACCATACATCCCTCAGCAAGAAAGTTTGCTAATCTCGGGTTTAGGGACTCCATTGAG                            |
| WI-18476      | 60 C T  | GGTGGGGTGC<br>GAGG              | GCACGATGGGA<br>GTGACC            | TGAGGACGTGTGACAAAGCTCCAGCAGGGGTGGGGCCGGCTGAGGGTGGGGTGGGAGGCTJGCT<br>CACTCCCATCGTGGCCCTGGCGGTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT                              |

|               |     |   |             |                          |                                 |     |   |
|---------------|-----|---|-------------|--------------------------|---------------------------------|-----|---|
| WI-18491      | 109 | A | AATACTATT   | AACAAATGGT<br>AGGTTGATT  | CGTGTGCATT<br>TCCTGTAATCC       | CGT | CTAATGAGATGAATACATGGAAGGCGTTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAAT<br>GGTAGGTGGTATTAACTATTATTATTAATCCAGAAATGAC[G/A]GGATTACAAGAAAATGCACA                      |
| EST50757<br>b | 79  | C | TCTGCTCT    | GAGCTGAGG                | ACCTTCAACC<br>GACC              |     | AGCCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGCTCCCGAGAGCTCGAGGGCTGCTCTTTTATAT<br>GTGCAGGGCC[CT]GGCGGGTGAAGGTCAGAGA   |
| WI-17675      | 103 | T | CATGGTGACTT | GGACATTTGG               | GGGGAACCAAC<br>CAGG             |     | GATCTTGAAAGCACTAGAAACTAAACATCTTACCAGGTGCTGAAGAAAAGTGTCTCGTTTTAAAT<br>TGCCAAAGCAGGGATGTGGACATTTGGATGGTACTTT[CT]CCTGGTGGTTCCCCATAGATTCACCAT<br>TGCTCTAATGGTGCTA |
| WI-16543      | 67  | G | T TGG       | CATTGGGTTT               | GATTCATCATT<br>ACAGGGGACTT      |     | GATCCATTACCTAGGGTAAAAATCTCCTGAATGTCAACAAAGAGATAAACTACATTTGGGTTTGG[<br>G/TAAGTCCCTGTAAATGAATCAAGAAATCCTCAAGTCTGTCTTGCCACCCATTTAATACGTATT<br>TTTGTTAAGGCTGAAGTT |
| WI-17687      | 107 | C | TTGGGAA     | GCCAAAAGG                | TTACTTTTGT<br>CCGACCAGCA        | G   | ATCTGAGATGGGAAGAGTTTCATCCAAAACCATCTCCCCCTGACCCCCCAGTCCATGGAATAATGTC<br>TTCCACAAAACCGGTCCCTGGTGCCAAAAGGTTGGGGA[CT]GCTGGTGGTACAAAAGTAATT                        |
| WI-17690b     | 79  | A | G ---       | AGGCATTTTC               | ...                             |     | ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCAATTTTCTAGCTGTGTTGATT<br>GGCTTCCCTA[TA/G]GATTCAGGACCCATACTCTGTTCTCACTCATCTGCTATGCTGCTG                             |
| WI-17690a     | 63  | A | TAGCTGTGTTT | TAGCTGTGTTT              | CAAGAGTTATG<br>GGTCTGAATC       |     | ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCAATTTTCTAGCTGTGTTT[G/A]<br>TTTGGCTTCCCTATAGATTCAGGACCCATACTCTGTTCTCACTCATCTGCTATGCTGCTG                            |
| EST51717<br>b | 128 | C | TGTGAGCTGTT | GCGGAAGACA               | TTGAGGCAATA<br>ATCCAGCTC        |     | GATCCAACTCTCAGTGTCTAACTCATCATCCAGATTATTCTGAAGTGGAAACCCCTCCGACCCAA<br>TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGCGGAAGACAGTGAGCTGT[CT]GAG<br>CTGGATTATTGCCCTCAAA  |
| EST51717<br>a | 39  | C | T ---       | ---                      | ---                             |     | GATCCAACTCTCAGTGTCTAACTCATCATCCAGATTATT[CT]TGAAGTGGAAACCCCTCCGACCC<br>CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG<br>CTGGATTATTGCCCTCAAA  |
| EST53012      | 97  | C | TGGGOC      | TGGTCACTTTG              | GGCTCTGCOCA<br>CGCC             |     | TTTCCAGTTGACAGGTTTATTCCACCCCTTCCATCCCATGCCACCCCGAGGAGGAGGAGACAG<br>GTGTGCTGGAGTGTGTCACCTTTGGGGCC[CT]GGCGTGGCAGAGCCCACTGGGTTTACATTCTCTGT<br>GGGCAAGGTGTGGACAC  |
| EST53349      | 96  | A | G TAC       | TGTTGAAAGC<br>AGTCACAATG | CATCTGGATAT<br>CTTGTACATT<br>TT |     | AAACTGCAAAATAACAAAACAAAACAGAAAGTCCAAGAGGCTAAAGTCTAAGCTATAATTACACATG<br>AAGTATATGTTGAAAGCAGTCACATGTAC[TA/G]AAATGTGACAAGATATCCAGATGTTTAA                        |
| EST53389      | 74  | A | G CA        | GGAGACCTGC<br>AGAACTTAA  | GGCCTTTCTAA<br>CAATAAATGCT<br>C |     | TTTCGAAATGCTCCTCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT<br>TAAACAC[TA/G]GAGCATTTATTGTTAGAAAGGGCAAGCTTACACTCAATAGGTTTAAACATGAAC<br>ACATTAAGGGAGATGGCC  |







|                       |                    |  |  |  |   |
|-----------------------|--------------------|--|--|--|---|
| TIGR-<br>A003P30      | 117 C G ---        |  |  |  | ACAAAGTTCAAAGGAGAACTTCCTTTGTTTAAATGCAGCTGTGCTCAGAAAGCCTGTGATTTCTCCTAGGA<br>AACCATCTGGGTTTAGCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA<br>GGTACCCCTTGGAGATACT   |
| TIGR-<br>A004S34      | 156 C T A          |  |  |  | GCTTGCTTTTATGTTAGGTTCCGGGGAAGGAGGGGCTGACAAACCGCAGACATCTGGACACCAGC<br>AAGGTCACAGGGGAGTTTGCAGAACTCTTTGCTCTGGCTAACAGTCTGTCATGTGACAATAGCCA<br>AACCTCCTCATCTCCTATAAA[C/T]CTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT<br>TACATG                |
| TIGR-<br>A004T44b     | 97 A C ---         |  |  |  | AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGATCAGGAAGATAAAACCAAAATGAT<br>TGAGTATGATAAAGAAATTTGCATGGCGATT[C/A]AAATAGAAAACTATAAATGTAGAAAAAGCA<br>GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG  |
| TIGR-<br>A004T44a     | 69 G A TGA         |  |  |  | AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGATCAGGAAGATAAAACCAAAATGAT<br>TGA[G/A]TATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACTATAAATGTAGAAAAAGCA<br>GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG   |
| TIGR-<br>A004V08      | 60 T C GGCATTCTCTT |  |  |  | CCTACAATCCTATAATATTGCAAGGGTGGGAAGGATGCAGGAAACAGGCAATCTCTTAT[C/G]GCC<br>TTTTGTGGGAAGGATCAATTTGGTGCATGCACITTAGGGGACAATTTGGGCAGTAGCTGCAAAATTC<br>AGTAGCTGTCAAAATTTCAAA   |
| TIGR-<br>A004V26      | 125 A G ---        |  |  |  | TCTAGCTATAAGACCAGATTTTAATATTCTAGATATAGAAATATCCAGAATAATCTATTGAATTGA<br>CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[G/G]AAGGT<br>TTCAGTTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG                                     |
| TIGR-<br>A004V28<br>a | 29 A G CGATCTC     |  |  |  | CCAGGCTATAATGTTGGGTGGGATCTC[G/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA<br>TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCGCCTAACCTAATTTTGG<br>TATTTTATAGTAGAGACATTTGATTTTTTAGTAGAGACAGG   |
| TIGR-<br>A004X20      | 25 T C G A         |  |  |  | TAAGTTTCCCTCTCTCTGTAGGAT[C/G]GCTCCATGTTACAGTCAACTATAAACATGGCTCATGT<br>TCACTCTGGGCTTCGCTTCAGAGGAGTTTGATATTTTGGAAAGTGGTACCCTTTGTTCTGTGCTTTTCA<br>GACCAACCCGCTCTCTTCAATTTCTCAAGGCTTCCCTCCAAAGGAGTTAAATCATCATCATGTCCAATC<br>ATCATCATGTCCCT    |
| TIGR-<br>A004X30      | 26 T C CCAC        |  |  |  | TTTTGAAATCTTAGAGTAGAACCCAC[C/T]CJACTCTAGTAATACTTGTAATAAAATTAATAATAGTTTT<br>AAACACTTCCATAAAGAAATAGGGTGCCAGCTCCTTGATTTCCCCCTAGGGATAAAGATATCCAT<br>GTTAGGGATAAAGATATCCATGTAC   |
| TIGR-<br>A004Z04      | 102 T G ATGCAAAACT |  |  |  | CACGGTATATGCCTTATATATAGGTATATATACAGATCGTACACAATATATTAACAGTTTGACATG<br>GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT[C/G]TTGCTTTCATGAAATTTCTAATTATAAGG<br>ACTGTTGCTTCTTCATATTCATGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC<br>TCITTAGTGATTAAAGACTG |





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|----------------|-----|----|-----|--|--|---|
| D63807         | 101 | CT | --- |  |  | CAGGCAGGACTTCAGTGTCAAGTATCCCTGCCTTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC<br>ATTGTTTAGAGGGAGTGATTTTCCCTGTTCCA/C/TTGAAGAGGACTTTTGTTTACAAATTTGGATCAC<br>AATGCAGAGGAGTCTGTTCTCCCGCTGCTCGGTCGCTGGAGGGTGAOCTGTCCAGATGAC           |
| D90145         | 21  | TC | --- |  |  | TGGGAACATGCGTGTGACCTCT/CJACAGCTACCTCTCTATGGACTGGTTATTGCCAACAGCCACA<br>CTGTGGGACTCTCTTAACCTAAATTTAAATTTATTTATCTATTTAGTTTTTATAATTTATTTTGAT<br>TTCACAGTGTGTTTGATTTGCTGTGAGAGTTCCCGCTGCTCCCTCCACCTTCCCTCACAGTGTG<br>TCTGGTG |
| EST14035<br>1a | 59  | TC | --- |  |  | ATTATCACTCTCAAAAATTTTGGTGTGTGTTTAAAGTACTTTCTTATTATGAGCCCCCT/CJGAGGA<br>CCAGACATGTTATTATCAAGCCCCCTTATATACCATCTAAT  |
| EST16868<br>5  | 71  | CT | --- |  |  | GCATTTTAAATTCACATTTGAATCATTATTACTATTATGATGTTTACATAACAATTCAGTATCATTT<br>ATG/C/TTGTAGATTTTCAAGTGTAGGTCGTCATTAAGTACTGAGCACTTATCT   |
| EST16904<br>7  | 57  | CT | --- |  |  | ACAGACTATCGCCAACTTATAATGCTTAAACTTTTATGATCAATAGTAATAAATTACAC/C/TTGAGATA<br>TTCACACTTTTATTATAAATAGGGTTTGTGTAAGATGATTTTCCCAACTGTAGGTTAACAT   |
| EST21863<br>9  | 49  | AG | --- |  |  | TTTTAAGTACCAGAGGCACCTGCTGGAACAGGATGAAAACGTGATACACC/C/GJGTTACTACTTACTC<br>TTCACCTCTTCAAACTGATCCCTAAAGACTTCTACTTAGCAAA  |
| EST21885<br>6  | 80  | GA | --- |  |  | GGCTGTAAGTAGAATCAAAAGTTTAAAGAACATTTTATGCCTTATTCACAAAACATTTACTGAGCATA<br>CTAGGTGCTGGGA/G/ATGTGACAGTGAGCAAAAAACACAA   |
| EST22623<br>8a | 26  | AG | --- |  |  | ATTTTAGTGCAATGACAAAAGCCCAA/GJAGAACAGAGGATCAAAATAGATTGAAATGTATTACC<br>TTCTCATAAGTATACGAAGTTTAAACACAAAGTATGGGAGT  |
| EST22644<br>2  | 98  | AG | --- |  |  | AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTGTTTAAACAGCACTAAAAATAA<br>AAATTTTAAATGATTATCCATTATTACAGI/GJAAATGTGGAAAAGATGGCTTTTAAACCC  |
| EST23587<br>1  | 31  | TA | --- |  |  | CCTCATTTATTTAAAAAGACGGACATAAAAAAT/ATATACAAACAAAAACCCCAAGTCACATTTTCAG<br>GAGTAAAAACTAAAAAGTCTGATATGAAAAATATGGTGG   |
| EST24246<br>7  | 106 | TC | --- |  |  | AAAGATCTGGCATTATTCACATCATCTTAATATTTTGTAAATTTTCCATGAGTATTTTTTCA<br>TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACC/CJGAATAACCCATAGTTACAGAAATGG<br>GTCTGTGTAACCTCAATT  |
| EST24308<br>3  | 45  | AG | --- |  |  | TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/CJGATTTAAAAATGTATCAAT<br>GCACCTTCTTCAGTAGTACCACATGAAAAATATAAACCTCGTTC  |
| EST24435<br>6  | 73  | GA | --- |  |  | CTTGAACCTTCTGGTCTCAAGTGTAGCTCGCTCAACCTCCCAAAATGATGGGATTACAGGCATAAG<br>CAGCC/C/ATGCTGACCCACATTTCTTTATCCGATCTGTTGATGGACATTCAGGTTGTTTC   |
| EST25089<br>6  | 25  | TC | --- |  |  | TATTGTTGCATTATCAAAATGGTTAT/CJAGTTTTCATTTAAACTGTAATTTCTATGTATAAA<br>ACAGCTTTGAAGTTGTAATGTAGTTTCCAACTCGTTAGTTAATGCTACATT  |

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|----------------|-----|----|-----|-----|---|
| EST25476<br>9  | 33  | GA | --- | --- | AATGATCTTTATTTTCAGACCTGCTCCTAAAA[G/A]CTTTCTCCTCCTAAAAACCAACACA<br>AGAGGTCTCTTGCTGCTTTTCCATGGACTGTGGCGGCTGGACTTGGACCGTCTGCTGA  |
| EST26183<br>2  | 70  | TA | --- | --- | AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACTTTGTAAAGATTGATCTCTAAATAAG<br>ATT/AJACATTCTGGGGTACTGGGAGTTAGAACAAC  |
| EST27231<br>1a | 28  | TC | --- | --- | AGAAATAAGGTGCTACCGAAGTCTATG/CJGATAGCGCTTTCTTTAGGCACATATTATAGCATT<br>CAGATGAAAGTTCTGTAATCACACACACACTGTGCTCTAACACAAACACGGTGACTCTGA                                    |
| EST27816<br>5a | 26  | TC | --- | --- | CAACTCAAGGTACAAGACAAATTGCATT/CJTAACATTGTTATAAATAAAGGAACATCAGATCAAT<br>CATTAAAGGCTCCAGAGTGAACAGCATCTTCATACTTCCATGTT  |
| EST28588<br>0  | 78  | AT | --- | --- | GTTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA<br>ACTTACAATCA/JTGGTAGAAGGCAAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG<br>AACAGACAGAGGGGGGAT          |
| EST30226<br>5  | 25  | AC | --- | --- | TACTCACACCGACATACATATCTCA/JCJGTAGAATTAGCTATAGTGCATACATACTTCACTTGTAGT<br>AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTTCCCTTTGA<br>G                   |
| EST30935<br>9a | 59  | CG | --- | --- | AGCTATGGTAGAGCAAAATCCAGTGGTAAATCAAGAACTCTAAAGTTCAAGTAGAGAG/CJGAGGT<br>GTTTTGAATGTCAAGGAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT<br>CATAAGAGCTTTTGAGG        |
| EST32515<br>7  | 25  | GA | --- | --- | CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCTCTAAACCTGTTGAATAGAATAATGGCCAAAT<br>ATTACAGTTTCTCAGTTTCTCTATGAATACTGGCAGCTTTTATTTTCATGTTTATATGTGAGTTTCTATGC<br>ATAAAAATCCCAGTAAGA |
| EST33274<br>4  | 27  | TC | --- | --- | TGCTTTGTTTCCCTCCAAATCCTAAAAT/CJGTGTGTCTTCAAAGAAATTCGTGGAAAGGACTTTGAA<br>TACGAGTTTGTACCATATTCAGTATTCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCATTT<br>GGACTAGGTA          |
| EST33352<br>7b | 75  | CG | --- | --- | TACACATTATTCAAGAGACCCTGACATGCATCTCCTCCGCAAGATAACATTGCTCCTCTCTTAGAGA<br>AGTTTAA/CJGACACATAGTATTATTTTACTAAGAGAAATATCTTGGTGCATATCTAGGGG                                |
| EST33424<br>1  | 126 | AC | --- | --- | ATTTTCCACAGCAGAGTATATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG<br>GAACAGTACAGAAATGTTCAAAAGATTACAAATCTCAGTCATTACACACTGAGCAAC/JC/JAAA<br>CAAAGGTGTTGAATCCTCTT        |
| EST33488<br>7  | 90  | AG | --- | --- | CCTTTGGGGGAGTTTAAAGCCAGAATGTGACAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG<br>TTGAACTCTAACATCGTCTATAG/JG/JACCATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT<br>GCTC                |
| EST33508<br>1b | 45  | CT | --- | --- | AAAAACATGCTATTTGAACAAACTTTTTATAAAGAAATAAGTTGA/CJTJGAAAAAGCAGTTTTTAAAT<br>AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA  |

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| EST33508<br>1a | 36 A G ---  |  |  | AAAAACATGCTATTGAACAAACCTTTTATAAAGA[A/G]TAAGTTGACTGAAAGCAGTTTTAAAT<br>AACATCAACTCACAATGACTTTTAGAAGCCAAATAA  |
| EST33863<br>4  | 77 C T ---  |  |  | ACAACATAGGACTGGTTATCTTGGTTTGAAGAAATATGTTGCCACTTCCTATTGTTTTAAATGA<br>TCATTTAAC[C/T]CTTTGAACCTACAGCCTGAATCCCCC   |
| EST34739<br>3  | 97 T A ---  |  |  | GAAGTATCCTCCAGTGGCAGGAACCTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA<br>GCTGATAGCTTCTAGGCTGTGGGGAACCTC[T/A]GGTGCCCTTACAACCTCAACTACTGCAGAAATTTCT<br>TGTTGTGCCTCATAAACA  |
| EST34792<br>6b | 104 A G --- |  |  | ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCCACTATCAATA<br>CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCCTAGTCCCTATTACA<br>AAGATTTTGTGCTGTG   |
| EST34835<br>9b | 93 T G ---  |  |  | GGAAATGTCCCTTTGCAAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG<br>TGGGGAGTCTATGTTGCTTTCTGGT[G/G]GCCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT                              |
| EST34835<br>9a | 82 G A ---  |  |  | GGAAATGTCCCTTTGCAAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG<br>TGGGGAGTCTATGTT[G/A]GCTTTCTGGTGGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT                              |
| EST35230<br>0  | 93 G T ---  |  |  | CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG<br>CAAGACATGAGCATAAAGAGGTTCTC[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAGAAACCT                            |
| EST35337<br>9  | 33 C T ---  |  |  | CTTTTCAAATTTTGTATGAGGCATTTAATG[C/T]TATAAATTCCTGCTTAGGAATGTATCTGCT<br>ATATCTCAGAAGTTGGGCATGTTGTTGTTCCATTTTACTAGTTCAGAACTTTTTCATTTTCATCT                               |
| EST35708<br>9  | 32 C T ---  |  |  | CTGCCCCAAATTAACCTTTAGGCAATGGAA[C/T]AGACTTACTGTATGGGACATTTTAAAG<br>ACAGCTTAGTAATATGTTATATGCAGCGTGTGCTCCCTCTGAGGTGGCACCTTTCTGTTGTG<br>ATGTGCAAGTGTGGCT                 |
| EST35747<br>9  | 51 C G ---  |  |  | ATCCAGTGCAGAGTTGAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAACGT<br>TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTCCAGTAGGGTTGAGATT<br>G                      |
| EST35751<br>9  | 89 C A ---  |  |  | TGGTCCATTATATAAACTGAGGGAACAAACGGTGTGCTGACATGGCAGACATTTATTTCAATGGAGA<br>AGTCTCCCTCCATGAACCAAGA[C/A]CTTGCTCCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT<br>ATATAATTAGGCCTGTGA   |
| EST36301<br>4  | 93 C T ---  |  |  | CACCTGTTTCATGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTCTCAGCCTACAGC<br>AGTCAGGAGGCAGCCATGGCCCCG[C/T]GCTGATGGAGCTTGTAAATTTAGCCCCAAACTGATCTTCA<br>GAAAGAGGTACAACAA     |
| EST36519<br>0a | 33 G T ---  |  |  | GCCATCAGCCCCACAAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCCTACTGGCCTCAGCAC<br>CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT<br>CACAGGGGTCTTAGTGT |





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| EST37378<br>9  | 63 T G ---  |  |  | ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCTGTGAAAACT/G<br>JAACATGCCTCAAAAAAGAGGGGAAAAAATTTAACAGAAACACTGTGCTGACATGATTAGCTT                               |
| EST37452<br>4  | 46 G A ---  |  |  | AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAACCTCTG/AJCTTCTCAGGAGTGACAC<br>TAATCATGGTCTGGAAGCTAGCCTATGCAATTTAAACACCCCTAAATCAATGACGTAGAA                                 |
| EST37613<br>6  | 34 A G ---  |  |  | CTAGGCATGGGGCTTTTACAGTCATTTATTACCA/GJGTGATGAATTCATTAATAAACACACGCGAT<br>ATAGCAATGAGCAAAACAGACCCCTCCCAAAATCACCCCTGGTTTCATGGAATCCTCCATTCTAA                           |
| EST38025<br>4  | 56 T G ---  |  |  | TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTATATCATTAT/GJTTATCTCA<br>ACAATCTTGAAAGGGGTATTATTTCCCGCTCTTATAGGTGAAGACTCTGAGGTTTCAGAA                                 |
| EST38068<br>6  | 57 C T ---  |  |  | TCTACAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTA/C/TJCGCATGG<br>AAGAACGCTCTCCTTTAATCCCTAACTCTCTCTCTCTGGGAAGACAGAACGTGCACAA                                  |
| EST38420<br>6a | 100 T C --- |  |  | TAAATCAAGGCCCTCTTTTACATTAACCAAAACAAAAAAGGGAACAAAATACGATGGGAGAGG<br>GAAGAGATGATGCCGAAGTGTCTGCTGACTGACTGAC/CJGTCCCTGCAGTGCCCATGGTCCCGTGCCT<br>TATTCATTCTCCTCTCTCA    |
| EST38950<br>5  | 25 T C ---  |  |  | TTTATTTGCAAAAGTAAGCAGCCGGT/CJGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG<br>CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAGCTT<br>ACAAACAAAGAGCAGCCA     |
| EST39053<br>6  | 90 T C ---  |  |  | TTTTTTGTACTCTGTAGCCAGTCATTAACTCTGAAGTTTAAATATATCATTTTATTTGGGATGAGATCA<br>TAGCTTTACACAATGCTATG/CJAAACAAGTTACTGAATATTTTACCTCGTGGAGTTG                                |
| EST39331<br>1  | 70 G C ---  |  |  | TCCTCTTGCTCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCCATGGAAGGAAAGTA<br>TGC/GCJGTGTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACACAGATGGGT<br>GCCITTTGGATACATCACT |
| EST40544<br>7  | 31 C A ---  |  |  | GTCAACCATGACCTTACATAGTGCCTCTAGT/CJAJACCTATGAGGCACCTAGAACCTCTATTGTACTTCT<br>CACTTTATCACATTAGCTATCGAAGTTTGAATTT  |
| EST40548<br>4  | 37 T C ---  |  |  | TTCTAATAGCATGCCCTGTGACAGGGGAAACTAAGCTC/CJTCAAAAATAACTGAAACTAAATCTGTA<br>AGATAAAATGCTGGAATTTGAGAAGGCACATGCCTTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTT<br>AATAATCTGTGGGACTCA  |
| EST40549<br>1  | 42 A G ---  |  |  | TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCAACA/GJATAAAGTCACATCAAGACTAA<br>TAATCTAATGTTAGTTTGTACCACCATTTCTCATTGAACTAGCTCCCTGCAAGCACCTTTCTA<br>CCCTGCACCTTTGGGGAG      |
| EST40579<br>1  | 81 A C ---  |  |  | TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCATTTCTTACCTAAAGCTGTGCTATCTG<br>AGCTGGTGGAAAA/CJGGACITGGAGACAGCGATTTAAATACGGAACAAGGTCTTCCAGGAAG                             |
| EST40584<br>3  | 68 A G ---  |  |  | TTGTATGGTTGTAGGAATTTGGGAAGAAATTAATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC<br>A/A/GJCTGTACTCCCAATATCCTATGTTTAAAGCT  |

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| EST51340 | 51 GA ---  | --- | GATAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA<br>AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACTAAGAGCCTCTCTAAGCTA<br>GATAGGCCAAGGATTATT  |
| J04162   | 134 TC --- | --- | CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTGCAACCCCATCAT<br>CCTCAGGCCCTCTACAAGCAGCAGGAACATAGAACTCAGAGCCAGATCCTTTATCCAACCTCTCGA<br>T/CJTTCCTTGGTCTCCAGTGGAAAGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCAAGTGTGAGT<br>AGCTG             |
| K01506   | 63 TC ---  | --- | CTGAATCCAGCTGCCCTACAACTCCATCTCAGCTTTTCTCTCCTCATGTGAAAACACTAC/T/CJC<br>CAGTGGCTGACTGAATTGCTGACCCCTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCATTCCCT<br>TAGTAAAGTTTCCAAATAAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC<br>ATTGAGCCTTTTATCCT |
| L18877   | 69 TC ---  | --- | TGAGTCTGAGCAGCAGTTCAGCCAGGCCAGTGGAGGGAGTCTGGCCAGTGCACCTTCCAGGCO<br>C/T/CJATCCATTAGTTTCCACTGCCCTCGTGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG<br>TCAGTATTGTTAGTAGTGAGTTTCTGTCTATTGGATGACTTTGAGATTATCTTTGTTTCTCTGTTGA<br>ATTGTTCAAATGTT   |
| L31848   | 36 TC ---  | --- | GCATTTTACATATCCCAAGCCCTTAGGGCTACAGT/CJC/TCTTGTCTTGACCCCTGTAGGGTGCCA<br>TTTGGAGTTACAGCCTAGAAAGAAAGGCTTTGGCCCTGGTGTGGCATAGGCCCTGTAAATCGT<br>AGCGCTTTGAGAGGCTGAGGAGGAAGATAGCTTGAGCTCAGGAAGTTTCGAGACAAACCTGGGCAAT<br>GT                  |
| L38517   | 137 GC --- | --- | GGTCCAGAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC<br>TCCTGCCATCTCTCTGCCATGAAGATACACCAATTGAGACTTGACTGGGCAACACCCAGCGTCCCCAC<br>CC[G/C]CGTCTGTGTAGTATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGTTGTTGACCCCTCT<br>CTCTAGAGACCTTGAG  |
| L39059   | 123 TG --- | --- | ACTTGAGAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA<br>AGTTGAAGGGACAGGGCAACAAATACAGTAGTATTTCTTTTGTATTTGTATAT/GJCGCCTGA<br>AGATCATCCCGCAAGCAGGCTGGAGGTGCGGTGGGCTGTGTCTGGGATTTAGTCTGTGCTGG<br>GAG                       |
| L41268d  | 173 GA --- | --- | CAAAGTTGCTCTCTGCCATGAGCACCACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC<br>CCTGTCTCAAACTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTGCAT<br>CTTAGGGCATCGCTCTTCTCTACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT<br>AAGGT         |

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| L48728b | 111 T C --- |  |  |  | AAGTGAACAGAAAAGCATGGATTGTGTTCTCTATAAAGCACATAGTTATGTTTACTGGTATCGT<br>AAGAAAGCTGGAAAGAGAGCTCAAGTTTTTGGTTTACTTTTCTTTCAGAAATTCGAAAGAACTTATTCAGAAAG<br>CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCTGTACCTTGGAGATCCA<br>GTC  |
| M18079  | 52 G A ---  |  |  |  | GGCACAGTCCAAAATACAAAATTGGACAGAGATCTATATTGTACCAGAACTGGAAJTTTATTTTACC<br>CCATCAAGTATAAGGTTACTGATTGATGGTCCCTTTATAAACATTGGTATATTTCCATTTCATGCGCAA<br>AGCAAAAGAAAGTAAAAGCTAA  |
| M19169  | 113 T C --- |  |  |  | TAGGATCTGTGCCAGGCCATTGCGACAGCCACCACCCACTCCACCCCTGTAGTGTCTCCACCCCG<br>TGGACTGGTGGCCCCCACCCTGCGGGAGGCCCTCCCATGTGCTGTTCGCGCAAGAGACAGACAGAG<br>AAGGCTGCAGGAGTCTTTGTTGCTCAGCAGGGGGCTCCGCCCTCCCTCTCTCGCTTCTAATA<br>GC             |
| M21539  | 114 T G --- |  |  |  | TCACCTGTTCCACAGCTCCACCTGCATCTTCTCATCAAGCCATCCAGGGATACACAGGGAGCTTCT<br>TTCCCTTAGCCTGTGATCTGCCCATGATGATCCCGACAGCAAAATTCGTTTCTCTGAGGCTG<br>CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCCCTTTCAGAGCT<br>TCTCTTTGGGTG |
| M26041c | 173 A G --- |  |  |  | CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT<br>TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACTTC<br>CTGATTTTCTCTTCTCAAGTGTACCTACTAAGAGTGGAGTAAAGCCACCCAGCTACC<br>TAATTCCTCAGTAA      |
| M26041b | 157 A G --- |  |  |  | CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT<br>TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACTTC<br>CTGATTTTCTCTTCTCAAGTGTACCTACTAAGAGATGCCTGGAGTAAAGCCACCCAGCTACC<br>TAATTCCTCAGTAA |
| M26041a | 45 C G ---  |  |  |  | CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCCTTCGCTCTCTCACCTCT<br>TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCCTGACTTC<br>TTCCTGATTTTCTCTTCTCAAGTGTACCTACTAAGAGATGCCTGGAGTAAAGCCACCCAGCTACC<br>TAATTCCTCAGTAA |
| M53967  | 57 G C ---  |  |  |  | TAAGGCAGCTGTACGGGAGGCCAGTCCAGTCCAGCAATTCACAAACCACCTTGAGCGJAAATGCT<br>TGCCAAGCTGTTTAAAGCCCAAGAACCCCTTTCTTTGTTCCAAATTAACCTTTAGAAGAAACCCCA<br>CAAAATAAGCAATTCATC   |
| M81695  | 34 G A ---  |  |  |  | ACTTACTACCTCACCTGTACGGCTGACGGGGA/GA/GAACCACTGCACCCAGAGAGGCTGGG<br>ATGGCCTGCTCTCTGCTTTGGGAGAAACGCTGTGCTGGGAGGGGCTTGTCTTGTCAAGGTTG<br>CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCCAAAAGGACTTGACTTGCATTTCTACC<br>T                |

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| U06641d | 166 C T --- | --- | CTCCTCCTTTATTTAGCATGGAGGGTTAAATGGAGGATCTCCTTTTCTGTGACAAAACATCTTTC<br>ACAACTTACCTTTGTAAGACAAATTTAAAAAGATCTTTTCACAACTTACCTTGTGTAAGACAAAATTT<br>TATTTCCAGGGCTATTTAAACGTACTTTAG[C/T]TGGAAATTAATCTATGTCAATGATTTTAAAGCTA<br>TGAAATACAAATGGGGGA    |
| U09607  | 39 T C ---  | --- | GAGGCCCTATGAGGGTCTCTACTTCAGGAACACCCCTT/CJGACATTGCAATTTGGGGGGCTCCCG<br>TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTTAAGTTCAAGACAGATGGGCATATGTGTGAG<br>TGGGGCTCTCTGAGTCTCTGGCCCAAGCAAGCAAGCAACCAATTTAAGACTCTCGCATCTTCCCAAC<br>CCCTTA                 |
| U09608  | 82 T C ---  | --- | GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATCCAAAGGCTCATCTGGAGCCTC<br>GGGAAAGTCTGGTCC[C/T]ACATCTGCCCGCCCTTCCAGCCCTTCCCGAGCCCTCCTTGTGTTCTTC<br>ATTCATTCAACAAAATTTGGC   |
| U10694  | 20 C G ---  | --- | GTACATGAGGCCCATTT[C/G]GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG<br>GTGGAAGTGAGCACACTGTATGTCTCTGGTTCCTTGTCTATTGGGTGATTTGGAGATTTATCCTT<br>GCTCCCTTTTGGAAATGTTCAAAATGTTCTTTAATGGTCAGTTTAATGAACCTTACCATCGAAGTTAA<br>TGAATGACAGTA              |
| U13877b | 162 T C --- | --- | AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGTCTATCTTTGTGACCTTGACAAAGTTGTTAAAC<br>CTCTTTGTTTCAAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATAGTGAAGTTACATGT<br>AAAGCACAGAGGAACACAGCCAAAGAGAT[C/T]TACCGTGGTCTTACTAAAGTACATATCCCTAACTTGG<br>GGTTTACCTTCAGCA |
| U15555  | 187 T C --- | --- | TTTCTGCCACTTTTCACTGGTTTAAATAGCCAGCCAGTCATATAATAGTAGAGGAATCAGTCAAGCAA<br>AAATGCTTTGGAAGAAATTAATAAGCAATGCTGAACATCAGGAATGTAGATATCCGTACAGAGAGT<br>TCCAGTAAATTTTATGAGTCCACAGCCCTTTTCTAAGCAGTCTGGTCCATG[C/T]GGTCTCATAC<br>CTCATATGCAGGATTCATTCA   |
| U17077  | 122 T C --- | --- | TCCAAATATTGGTCCCAAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT<br>AAAAAGTCCACGGGATTAAACAGAACGCTTTCAGACTGAGCGATGACACACACAT[C/T]TGTGTTGG<br>ACATTTAAATTTCACTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAAACAACTGTCTCTTGG<br>AATTA                  |
| U18543  | 58 T C ---  | --- | GCACATGCAGAAATAGACTCAGCCTATGTCCTGATTCAGCTGGGTAGTCTAGAACTTT/CJAGAAG<br>CTCCATCTTTTAAATGTTTATTTGTTATGTCCCTCCCGCTCCCACTAAATTTAGAGCTTTAAA<br>AGATGCACTGCCCAATAGGACACAGCATGGTGTAGCTGAAGTTTGTAGCAATTAGGCACCTTCC<br>AAGGCTTTAGTAGAGAGGCC           |

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| U25975b | 164 | C A --- | --- | --- | TCACGTGCTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTATT<br>ACTCTTTTGGGGTTAAAGAAATGGCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG<br>AAGACAAACCAAGAGAAAAATTGCAAAAAGAC/C/AAGTATGACTTTTATATGAACCCCTTCTTTAGG<br>GTCCAGAAGGAATTGTGGACTGA |
| U25975a | 143 | C G --- | --- | --- | TCACGTGCTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTATT<br>ACTCTTTTGGGGTTAAAGAAATGGCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG<br>AAGACAAAC/C/GAAGAGAAAAATTGCAAAAAGACAGTATGACTTTTATATGAACCCCTTCTTTAGG<br>GTCCAGAAGGAATTGTGGACTGA  |
| U25997  | 61  | A G --- | --- | --- | CAGGGAGAGGTTATTCACAACCTCACCAACTAGTATCATTTTAGGGGTGTGACACACCA/C/GJTT<br>TTGAGTGTACTGTGCCTGGTTGATTTTTTAAAGTAGTCTTATTTCTATCCCCCTTAAAGAAAAATT<br>GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATCCCAACCAACAAAA<br>TOC                  |
| U28413  | 29  | C T --- | --- | --- | ATTCTGACAGCTAAATTAGCCCTAAATG/C/JGGGTAATATTTTCCCTCATGTTTTAAATGAGGTT<br>AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTTCCTTGATOC<br>CAGATGTTGTGGCCTGGAAAGCCCTCATTGCTACAGTACAAGTAACACAAAGTCGTTGTACCTCAGTT<br>G                    |
| U30884c | 89  | A G --- | --- | --- | TAGGGGTAGCATTTAAGATTACAGAGTCATTAGCAGTGTGATTTTGGACCTGCCGTATAATCTGTT<br>CTTCTATTTCCACGTTAGCCA/C/GJTTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT<br>TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTGCCCCACAGTTGAACACAAAGT<br>GCTGTCA         |
| U30884a | 34  | A G --- | --- | --- | TAGGGGTAGCATTTAAGATTACAGAGTCATTAGC/C/GJGTGATGATTTTGGGACCTGCCGTATAATCT<br>GTTCTTCTATTTCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT<br>TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTGCCCCACAGTTGAACACAAAGT<br>GCTGTCA       |
| U31216b | 78  | A G --- | --- | --- | GGGACAGCATATGTGGCAACCGCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAACA<br>GCCGTATCA/C/GJCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA<br>CCAGACCAAGAGCCCTTTACAACGTAGAGGAGGAGGATGCCAAGCCGATTGCTTTAGCCCGCC<br>TGGTAGCCCTTCCAT            |
| U31216a | 70  | G A --- | --- | --- | GGGACAGCATATGTGGCAACCGCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAACA<br>GCC/GJATCATCAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA<br>CCAGACCAAGAGCCCTTTACAACGTAGAGGAGGAGGATGCCAAGCCGATTGCTTTAGCCCGCC<br>TGGTAGCCCTTCCAT           |

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| U31416c | 76 GA ---   |  |  | AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC<br>CTCCTCAC[G/A]CCACAAATCTGGTGCCTCTCTCTGCTTACAAATGTCTAGGTCCCACTGCCTGCT<br>GGAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTACCTTGACCCCTGCCACCTCTCC<br>AACCTAACTGGCTTACTTCCT      |
| U31416b | 68 CT ---   |  |  | AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC<br>[C/T]TCTCACGCCACAAATCTGGTGCCTCTCTCTGCTTACAAATGTCTAGGTCCCACTGCCTGCTG<br>GAAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTACCTTGACCCCTGCCAACCTCTCCA<br>ACCTAACTGGCTTACTTCCT     |
| U37519a | 78 CT ---   |  |  | ACGGGTACACAGAGAACTTGAGTCTAGCCATGAGGGCTTATGCTCCCACTCACATTGTTCTCTCC<br>AGACCGCAGG[C/T]TCCCCAGCCTCAGGTTGCTGGAGCTGTCACATGACTGCATCCTGCTGCCAGG<br>GCTGCAAAGCAAGGCTTGTCTTCTATCTGGGGACGCTGCTCGAGAGAGGCGGAGAGGCCGCGAGAAC<br>ATGCCAGGTGTCC           |
| U37690  | 54 AG ---   |  |  | GACCACGCTGAACCCACCCACCCGCTGTGCTGACCATGGGGCCTGAGCGTCTT[A/G]CCCCGAATTC<br>ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCTGGCCGAGTGTGTGTATCCCATACCCCACT<br>CTGGAAGGAACCATCCAGTAAAGGCTTT  |
| V00540  | 39 TC ---   |  |  | TGAACCGTTTCAACATGGAATGATCTGTATTGACTAAT[C/A]CACCAGTCCACACTTCTATGACT<br>TCTGCCATTTCAAGACTCATTTCTCTATACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT<br>TCAGGAGTGTAAAGGAAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT<br>A                       |
| X15943  | 106 AT ---  |  |  | TCAAGAAGTGACTGCCCTTGTATGATGGGATGGAAGATGAATGACTGGTTTTACTGGGTGTAA<br>AACCACCTGAGCCTCTCTGAGACCATGTGGTTTTAAA[A/T]ATCCATAAGGGAAGGTACCCACAC<br>CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAAATTTGGATTCTCTGTTTTTTCATGTCTCTCCTT<br>GTAAACCCTGAGATCATCAG       |
| X52011b | 148 CT ---  |  |  | AGGAAGATCCCACCGACCCCTTCTGGCCTAATCCTTAGATTAGTGCACATTACATTAAACATTTAGGA<br>ACCCAGACCGAAAAAGTTGCTGAAAGGGAAGGAGACACATTCAAAAGAAAAAGTTGCGAAAAATGCG<br>AAATCTGTTGTGCA[C/T]GCTCAAATGAAAACGCCCTTCGGCTTTGGGCTTTATTTTTTGGAACTG<br>CGAGTGGCTTAGGCTAGCCT |
| X52011a | 118 A/C --- |  |  | AGGAAGATCCCACCGACCCCTTCTGGCCTAATCCTTTAGATTAGTGCACATTACATTAAACATTTAGGA<br>ACCCAGACCGAAAAAGTTGCTGAAAGGGAAGGAGACACATTCAAAAGAAA[A/C]GTTGCGAAAAAT<br>GCGAAATCTGTTGTGCACGCTCAATGAAAACGCCCTTCGGCTTTGGGCTTTATTTTTTGGAACTG<br>CGAGTGGCTTAGGCTAGCCT  |

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| X54741  | 24 A G ---  | --- | CAGGCCACCTGTCTTCTCTCCAC/GJTGACAGCTTCTGAGTCACCCCCTGTGTCCAGCCAGCTCCT<br>GCACAAATGGAATCCCCAGGGCTCCAGGACTGGGCTTGCCAGGCTTGCAATAGCAAGGCCAG<br>GGCACAGCTGGAGACGATCTTGCTGGCAGGGCTGGCCTTGTCOCACAGCCCCCACTGGCCCCCTTCTCC<br>AGCAAGCAGTGC  |
| X54869  | 99 A G ---  | --- | AAGCATTGGCGTTACAGTGCATCAGATACATTTATATTTCTTAAATAGAAATATTATGATTGCAT<br>AAATCTGAAATGAATATGTTATTTGCTCTA/GJATACAAAAATCTAAATCAATTAATTGAAATAG<br>GATGCACACAATTACTAAAGTACAGACATCCTAGCATTTGTGCGGGCTCATTTTGCTCAACATGGTA<br>GCGTGTCTGACACCTCCAGAACGCGAGTGTGCGCCCGTCTGCTGGACCCCGGGAACTCTC<br>CTGCCGGAAGCCGACGGCAGGATGGCCCAACTTCCCTGCCCCACTTGACTTCACCAATCCCT<br>TCCTGGAGACTTG/AJAACTGGTCTCAGGAGCGAAGGACTGTGAACCTTGTGGCTGAAGAGCCAGA<br>GAAATGTGAAGAAATGTGACAAAGCCTTTAAGCGTTGTACACACTTGATTGTATATAAGATAA/TGJT<br>CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAATTTAATTAATTCATACCTTA<br>TTGCACAGGAAAGCATTTATACTTTGAGAAAAATTTGTATAAAGAAATGGAAGAGTCATTAATATCTGCT<br>CATATCTTAACATCAGCGAGTT |
| X66924  | 147 G A --- | --- | CTCAACCCATAACCTCAACACATCT/JTATCTCTCCACCCACATCCCACACATCCACCTCCATCC<br>CCAAACCATCTCATCCCACTACAGCCCAACCCAGCCAGACTAATCCACAGCCATCCCCAA<br>CTCATCTCATCCCACTGCAGCCCAACCCAAACCCAGGGCCATCCCCAACCCATCCCCAAGCC<br>AAACTCAACACCATCC  |
| X78932  | 62 T G ---  | --- | ACCCCAACTCAAGTCCAGGCCCATCTTCTGCCCCCTGCCTTGTGGCCCATCCAGTCCAGG<br>CGCTGGAGCAAGTCTCAGCTACTTCTCTG/CJCACTTTGAAAGACCCCTCCCACCTCTGGCCTCA<br>CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG<br>ACCCCAACTCAAGTCCAGGCCCATCTTCTGCCCCCTGCCTTGTGGCCCATCCAGTCC<br>AGGGCTGGAGCAAGTCTCAGCTACTTCTCTGCACTTTGAAAGACCCCTCCCACCTCTGGCCTCA<br>CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG<br>GGCAOCCAGAGTGACACAAAGTCCAGAGGGAGGCGCGCCCTCGCGGTGTCGGTGTCTTTT<br>CAGCCCCGAGAGGTCTGACCTGGGGCTTCTCAAGCCTCACTGGCCACGCTCCCGCCGCTCT<br>CTTTTCTCCCAAGC/G/AJAAACCAATGCGCCCTTCACTCGCGTGGCGGAGGCCGGGGCTT<br>CTTTCAGAGC                                       |
| X80197b | 99 G C ---  | --- | ACCACAGCCATGGTCTAAGGACATGGATCGGGTGGCCCCCAGACGTGTGACAGGGGACCCCTCTGCC<br>CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTT/GJGGC<br>ATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACGTGTCCAGGCTGAGATAAATCCC<br>GGGA   |
| X80197a | 28 A G ---  | --- |  |
| X85106  | 150 G A --- | --- |  |
| X87160  | 128 T G --- | --- |  |

[illegible]



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| 1282  | 130 C T | --- | --- | GTGCGATCACCCTACAGTCTAATTTTCAGATGTTTTTCATTACCCCTAAAAGAAATCTTTGTACCCCAATTA<br>GCAATTTATTCCTCAITTCCTGCCCTCACCCCGAGGCCCTACTCTTTATCGCTATAGATTTGCCQ[C/T]ACT<br>TGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACTGAGAATA<br>ATGTTTCAAGGT                            |
| 6810  | 68 C T  | --- | --- | AGTATCAGACATACCTTAATATATTAGATATACACAATAATAAATCACTCCCTACCTTGAAAACTTT<br>A[C/T]JAGAAGCATTTTTAATTTTACAACACAAAGCTCAACGAACCTACAATAAGTCTAGTAGCTG<br>TTACGTGCCAAGGATAAGGCTGAACAATAAATTAACCCCTTTAAAATGCTATGAAACAAGTACAA<br>TTTTCTTTTGTGTTCTGCAGAGCAATGACCACCTAAGAAATATTTTTAAAGGC |
| 6817  | 118 A C | --- | --- | CCAGTACATTGGGTGAACGATGAGTAGCTGTTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCA<br>TCAGCATATACAACATCATCACTAAGCTCAACAATGTAGCTGCAGGGTAAC[A/C]JGTGGATACCCCTG<br>TGTGCTCTACTGGCTCCAAAGGCATTGAGGGGATCAAAAGATGTTGGACACCTTGTGTTCAAATC<br>TTGGTTCAGGTGGCGCTGTGCAGATCGGCTTTTGGTTGGTTGCTTAG     |
| 6819b | 212 C   | --- | --- | CCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAACACATTTAGTACCATCATGTCA<br>CCCTGAATGCCAGCAATACCTCGACTTTTACACGCGAGGAGCCTAGTAAAGCCCGTCAGTAGT<br>ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTCTGCTATTTGCTTTAGCAAA<br>CAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA                  |
| 6819a | 166 G T | --- | --- | CCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAACACATTTAGTACCATCATGTCA<br>CCCTGAATGCCAGCAATACCTCGACTTTTACACGCGAGGAGCCTAGTAAAGCCCGTCAGTAGT<br>ACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATTTTGTCTTAGC<br>AAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA             |
| 681xx | 39 A G  | --- | --- | CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[G/T]TATACTATGGCACCATTGGGACA<br>CAGATTATATATGTCAGACACCCAGCAATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGGT<br>TTAACAAGAAATGAACGTCTAGG  |
| 6972b | 149 G T | --- | --- | AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCT<br>CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCCTGGACTCTTTTGGTTGGTAAACTATTGATTATG<br>CACAAATTCAGAG[G/T]CCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA<br>GAGTGTATGTGTCAGGAAT                                 |
| 6972a | 122 A G | --- | --- | AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCT<br>CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCCTGGACTCTTTTGGTTGGTAAAGTAA[G/C]TATTGATTA<br>TTGCCACAAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA<br>GAGTGTATGTGTCAGGAAT                            |

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| 7598k | 210 A C --- | --- | AAAGGTAATCAAAGTCCCTCTATAAATATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA<br>ATGAAATAAGCCGCTAACGAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTTTTA<br>ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCCT<br>CAATGCAG[AC] |
| 7598j | 208 A T --- | --- | AAAGGTAATCAAAGTCCCTCTATAAATATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA<br>ATGAAATAAGCCGCTAACGAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTTTTA<br>ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCCT<br>CAATGC[AT]GA |
| 7598i | 192 G T --- | --- | AAAGGTAATCAAAGTCCCTCTATAAATATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA<br>ATGAAATAAGCCGCTAACGAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTTTTA<br>ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT<br>CCTCAATGCAGA     |
| 7598h | 144 C T --- | --- | AAAGGTAATCAAAGTCCCTCTATAAATATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA<br>ATGAAATAAGCCGCTAACGAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTTTTA<br>ATATTTGATCC[CT]ATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT<br>CCTCAATGCAGA |
| 7598g | 142 C T --- | --- | AAAGGTAATCAAAGTCCCTCTATAAATATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA<br>ATGAAATAAGCCGCTAACGAGATTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTTTTA<br>ATATTTGAT[CT]CCATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT<br>CCTCAATGCAGA |
| 7598f | 120 A G --- | --- | AAAGGTAATCAAAGTCCCTCTATAAATATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA<br>ATGAAATAAGCCGCTAACGAGATTTACCTTGGAGAAATGAAAATATTTCTTG[AG]GGATGCCTT<br>TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT<br>CCTCAATGCAGA  |
| 7598e | 83 C T ---  | --- | AAAGGTAATCAAAGTCCCTCTATAAATATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA<br>ATGAAATAAGCCGCTAA[CT]CAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT<br>TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT<br>CCTCAATGCAGA |
| 7598d | 77 C T ---  | --- | AAAGGTAATCAAAGTCCCTCTATAAATATGATTTACAAAAGACACCCAAAGGCCAAAGGAACTCA<br>ATGAAATAAGC[CT]GCTAACGAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT<br>TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT<br>CCTCAATGCAGA |

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| 7598c | 56 A G ---  | --- | AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCA[A/G]AGGAAC<br>TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTT<br>TTAATATTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT<br>CCTCAATGCAGA                                  |
| 7598b | 47 C G ---  | --- | AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACAC[C/G]CCAAAGCCAAAGGAAC<br>TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTT<br>TTAATATTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT<br>CCTCAATGCAGA                                 |
| 7598a | 30 A G ---  | --- | AAAGGTAAATCAAAGTCCCTCTATAAATT[A/G]TGAATTTACAAAAGACACCCAAAGCCAAAGGAAC<br>TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTT<br>TTAATATTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT<br>CCTCAATGCAGA                                 |
| 7998c | 116 A T --- | --- | GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA<br>ATACTTTAAATGAATGGGTGATGCTCTATCTCTCAAGGTCCCAATA[A/T]CCTTGAGGTTTCT   |
| 7998b | 94 A C ---  | --- | GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA<br>ATACTTTAAATGAATGGGTGATGCTCT[A/C]TCTCAAGGTCCCAATAAACCCTTGAGGTTTCT   |
| 7998a | 75 A T ---  | --- | GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA<br>ATACTTT[A/T]ATGAATGGGTGATGCTCTATCTCTCAAGGTCCCAATAACCCTTGAGGTTTCT   |
| 8071  | 119 A G --- | --- | AAATACAGAAATTTATTTAGAACTGTTTAAAGTAGAAAAAACCCTGTCAAGAAAGACCAGGTGG<br>AAAATGGGTTCCCAATAAAATGGAATTTTAGGCAACAAAGCTAAAAGGCC[A/G]CAAAAAGAGA<br>AATAGCACTGCTCAATTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTGTTAATCACTGAATC<br>TGGGTTTCTCTGAAATTCACACAGAGCATGCACACACATTTTATCAT      |
| 8467b | 93 C T ---  | --- | AAGGCTTCTCTAAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCACTT<br>TGACGCAAAATCCACTTTGCTGTA[A/C]TGGTCATCCGAACCTCCCTCAGAGAGCAAGCAAGCAAAA<br>TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTAATG   |
| 8467a | 70 A G ---  | --- | AAGGCTTCTCTAAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCACTT<br>TG[A/G]CGCAAAATCCACTTTGCTGTAACGGTCATCCGAACCTCCCTCAGAGAGCAAGCAAGCAAAA<br>TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTAATG   |
| 8498  | 84 C T ---  | --- | AGGTTTCAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTATGTCA<br>AACTGGCTTCAGCTAG[C/T]AATACTTCATTAAATCGAAAAAGAAAAATTTGCTTTAAGGAAAAAA<br>AATCCAGTTTAAAGAACAAATTAACATTAGCTTTAAATAAAGGAGGCTAATGTTTTCATGTTGCT<br>TTATACATCTCTCTCAATACAGAACCAAGGAATGTAATTTCTCTAATCTCAG |

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| WI-18562  | 29 G A ---  | --- | CTAAGGAAAAATTTAATGATGGAAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG<br>CTTCTCTTATTTACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATCTTACATT<br>TAGCATTAAATCAGAAACGA   |
| WI-18618  | 51 A C ---  | --- | ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG<br>TTACAATGAAGAAATGGTTTCTTTTCGATGCAAGTATAATTGTAAACCCACAGTGCTCGCACAGTTC<br>AC   |
| WI-18683  | 22 C T ---  | --- | TAAGCTGTTCAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA<br>CAAAAATAAATTTCTCTCCCAAAGCCTGCGCTGCAGT   |
| WI-18520  | 75 G A ---  | --- | GACTTTGGTGATTTAATTGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT<br>ACTACA[G/A]CCGGAGTGGTAAATACTACTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA<br>TGCTCTTCCGTGAGAC  |
| WI-18563  | 94 A G ---  | --- | AAATAAGTTTTATTGGCACACAGCCAAAGCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA<br>TACAATAGCAGGGTCACTAATGTGAC[A/G]GACATGGTGGCTCACAAAGCCAAAGATATT  |
| WI-18582b | 69 T A ---  | --- | GTCTATTTCAAATTTAGCTAGACCCATTTCATCTGTTTAAATGGCTACATTGTTTTCATTGTGAGAC<br>[T/A]GTGCCATAATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG   |
| WI-18723f | 94 G A ---  | --- | AACTTTATTTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGTCTGTAGATTTTGTAAAG<br>TGTTAACAGGTACATAGGTAAACCAA[G/A]TATATAGCTTATTTGGTGAATCTTCATCCT   |
| WI-18723e | 71 T C ---  | --- | AACTTTATTTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGTCTGTAGATTTTGTAAAG<br>TGCT[C/A]ACAGGTACATAGGTAAACCAAAGTATAGCTTATTTGGTGAATCTTCATCCT  |
| WI-18723c | 96 A G ---  | --- | AACTTTATTTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGTCTGTAGATTTTGTAAAG<br>TGTTAACAGGTACATAGGTAAACCAAAGTATAGCTTATTTGGTGAATCTTCATCCT  |
| WI-18619  | 44 G A ---  | --- | TTTATTACAATAATTTAGGTGGCACAATAACTAACAGCTTCTGA[G/A]ACAGGAGGTAAACATTCTCA<br>TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA  |
| WI-18715  | 76 G A ---  | --- | TTATTCACAAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG<br>TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTTTAATAAAAAATAA<br>TGGAGCTACAACCCACCCCG  |
| WI-18535  | 107 G A --- | --- | GTAAATAAGTTTTATTGGCACAGCCAGCTCGTTCATTCATATGCCATTGACATCTGCTGTTGCCCT<br>ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC<br>CTTCTGGTCCCGGTG   |
| D17525    | 107 C T --- | --- | AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGCAGGTGAC<br>TTTCATCTCTTCGAACCTTCAGTTCTTCATAGATGGAAC[C/T]GCTATACCTTACCTACCTCGTAAAA<br>GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT<br>TCAATAAATGCACCTTAGCAGAGGTGATGTGTCTACCCAGGCAGACGAAG |

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| DWU-133c | 313 | A G --- | --- | TAATTGGCCACTGCCCTATTATTACAAAACAGAAAATGCTCATGACTTTTTTATGTGTTACCATCCT<br>TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAATATTTTGTGGGCAGTCCT<br>GATTTAAAACCTAAGACTGGCTTGTTGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACTCC<br>AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT      |
| DWU-133b | 236 | T C --- | --- | TAATTGGCCACTGCCCTATTATTACAAAACAGAAAATGCTCATGACTTTTTTATGTGTTACCATCCT<br>TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAATATTTTGTGGGCAGTCCT<br>GATTTAAAACCTAAGACTGGCTTGTTGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACTCC<br>AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT      |
| DWU-133a | 199 | C T --- | --- | TAATTGGCCACTGCCCTATTATTACAAAACAGAAAATGCTCATGACTTTTTTATGTGTTACCATCCT<br>TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAATATTTTGTGGGCAGTCCT<br>GATTTAAAACCTAAGACTGGCTTGTTGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAA[C/T<br>TTCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT |
| DWU-36   | 102 | C T --- | --- | ATGAGATCCTTTAAATCCTTCCATGAACGTTTTGTGGTGGCCCTCCTACGTCAAAACATGAAGTG<br>TGTTTCCTTCAGTGCATCTGGGAAGATTCTAC[C/T]GACCAACAGTTCCCTCAGCTCCATTCGCC<br>CCTCATTTATCCCTCAACCCCGCCAGCGTGTATTACAGCTCAGCTTTTGTCTTCTGAGGAG<br>AAACAAATAAGACCATAAAGGGAAAGGATTTCATGTGGAATATAAGAT                    |
| DWU-387  | 169 | G T --- | --- | GTGTATAAATGCAACTGTTGATTTCCTCAACATGGCTCACAATTTCTATCCCAAATCTTTTCTGAA<br>GATGAAGAGTTTAGTTTTTAAACTGCCTGCCAACAAAGTTCACTCATATATAAGCATATTTTTTA<br>CTCTTTGAGGTGAATATAATTATATTACAATG[G/T]AAAAGCTTCTTTAATACTAAGTATTTTTCA<br>GGTCTCACCAAGTATCAAAAGTAAACACAAATGAAGTGTCATTATTCAA             |
| DWU-447b | 172 | --- --  | --- | ATTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT<br>GGGCTGTTGCCATTTAAATCACTGTAATTAATAGTTTGATTAGAGCACAAAGCTTAGCTAATCAA<br>CCATTATTTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAGTTAAATGCTTTCTGTTAG<br>GCCTTCTTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA                   |
| DWU-447  | 85  | A G --- | --- | ATTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT<br>GGGCTGTTGCCATTTAA[G]ATCACTGTAATTAATAGTTTGATTAGAGCACAAAGCTTAGCTAAT<br>CAACCATATTTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAGTTAAATGCTTTCTG<br>TTAGGCCCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA                 |
| DWU-476  | 63  | C G --- | --- | GTAAAAATCAGTTTTTTCCAGTTCTCTTTTGTGCTGCTTCTCAATTAGCGTTTAAAGTGAG[C/G]AT<br>AAATCAACTGTCCATCAGGTGAGGTGCTGCTCCATACCAGCGTTCTTCATGAGTAGTGGGCTATGCA<br>GGAGCTTCTGGGAGATTTTTT  |

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| DWU-505   | 67  | A T | --- |  |  | TCATACTAGGCGAGTATCTCCTCTAGCTAGTGGCCATACAGAAAAATTCACCATACAAAAATTA[<br>ATJTGCAATATTTATGTTTAAAGCACAGGTGTACCGAAAACTGTGAAAGTCTGAATTTATGGTT<br>CTATGCATGCAATTTTGCCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT<br>TAACITTTGACITTTGAGCTTTAAACTTTTAA                        |
| DWU-512   | 131 | A G | --- |  |  | AAATCCAGGCAITTCGAATCTGTTTTCATGATTATAGAGGGTTTACAAAAAGTGCCACTTATTA<br>AGAGCTTCCACAGTGAAGATGGAGAGGTGAACCTTGTTGAATATCCAGATGTGTTTGGTC[A/G]<br>TGCGTATGGGAGTGAGCAGGTATGTGTTGCTTTTGCTTGCACTGAAAAATTAATTTGCTATCAAGAGC<br>AACTATGAACGGTTTTTATTCAGATGTCTCCAGAGTGAAGATGCCGAG        |
| DWU-525   | 97  | A C | --- |  |  | AACTGCATATAGATAATTATCCAGGATGTGGCTCATCTTTTCAGCTTGTTCATCTACTGTTTGT<br>ATATACAGTTTTTGTAAACCATATGATTGA/CJAAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA<br>CCCAATTTAAAAAATAACATATCTTGCTTTTCAAAATATAGTTGAACAAGATTTCCCTAAAAAT<br>CCACCAGGATTAATCTCTAAATCTAGTCTCTGATTGG                     |
| DWU-59    | 94  | C T | --- |  |  | CATTCTTTGTAAAGGTAATGGACTCACAAAGGGGAAGAACATGCTGAGATGGAAGTCTACCGG<br>CCCTTCTTTGTGAACGTACATTGGC/CJTGAGCCGTGTTGAGTCCAGGTGGCAGACTCGTTTGTG<br>GTAGTTGTTTAACTTCAAGTGGTTTACTTCTGATAGCCGGTGATTTTCCCTCTAGCAGACATG<br>CCACACCGGTAAGAGCTCTGAGTCTTAGTGTTAAGC                          |
| EST11     | 68  | C   | --- |  |  | CTTGATCATGGGTGGAATTTTGTTATCTGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAAG<br>CAGCAGGTGCCGAGGCTGGATCAGAAAAAAGGCA   |
| WI-19856b | 63  | C T | --- |  |  | CACACTGGCATCTAGGCCTTGGCTGCATTGCAGAGGAGAGCCAGGTCCCTCTCTGGAGAA[C/T]G<br>CTGGTTCCCGAGCCACACCCGCTTTGCACCACACAGGCTGTTGAGGCAGGAGGTGGTAAAGACGT<br>AGCTGTAGACCCAAAGCAACCAACCCAGCCCTGGACCCCTGGGAGAGGAGCAGCTTTAGAACATGGAA<br>AAGTGTGGTCAATCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT |
| WI-18014  | 40  | A G | --- |  |  | TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA/JGGAATGAAAGTGCAACCATCAGAGT<br>GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT<br>A  |
| WI-18036b | 97  | T A | --- |  |  | TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAAATACAAAGAGAACATGATAAAATCTG<br>ATCACAGTGGAAAAATTTAATTTCTTTCATAA/[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT<br>TAGGGATCTGAAGG   |
| WI-18036a | 27  | T C | --- |  |  | TTCCAATGTAAGAGTCAAGTACCAAGT/[C/JAAACTTCTAGAAAATACAAAGAGAACATGATAAAAT<br>CTGATCACAGTGGAAAAATTTAATTTCTTTCATAATCTGACAGGTCAAGTAAAGCTAAAGGAAACATAT<br>TAGGGATCTGAAGG  |
| WI-18046  | 72  | C T | --- |  |  | TGTAAGGTGACTTCTATAAGCTTCTCTAACTGTCAAACTTTCAATTTACTGAGATTTATTCAGGCCAAT<br>GTGTC/TGTTGGGTCTGAGATTGATTATCAGCTGGGTAAAGTTAACTGTCTCTGTTTCA   |







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| EST5          | 93 A ---    | --- | --- | CTGGTGGGAGGAAACAAATTGTGGTATATTCATACAATGGAAACTCTTCAGAAATAGAAAGGAA<br>CAAACACTGAATCACACAACATGGACAAATCTCAAATCATTATGCTGATGGAAAGAAACCAATTC<br>TAAGAATACACAGTACAT  |
| EST6          | 48 C ---    | --- | --- | TTAGCTACTTTTCAGAATTGAAGGAGAAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT<br>GAACA/AAAGCTTTCTTTCTTTTGCAACAAGACAAGCAAGCAACATTTTGCAATTAGACAGAT  |
| EST8          | 158 A ---   | --- | --- | GGACAGGACCTCTATTCCCGCTGGTGCAGCAGCGGCTGATGGACTGAGGCCCGCCAGGGATCTGGGOC<br>CTCTTCTAGGGGGCTCTCAGGACCCAGAGCTGTTCTGCTTTGAGTTTCCCTAGAGCTGTGGGGCA<br>GATAGCTGTTCTGAGTTGCAAGCACGATGGAGATTTGGACACTGTGTGCTTTGGTGGGT   |
| WI-<br>18740c | 104 G T --- | --- | --- | TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAATTAAAGTAACAACGACCTAGAAAAGT<br>GAGAACAACTCTCATTTACCATCATGTATCCAGTAGTG/G/ATAATTTCATTTTGATGGCTTCTATTTT<br>TGGCCA  |
| WI-<br>18740b | 96 C G ---  | --- | --- | TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAATTAAAGTAACAACGACCTAGAAAAGT<br>GAGAACAACTCTCATTTACCATCATGTATC/G/AGTAGTGGATAATTTCATTTTGATGGCTTCTATTTT<br>TGGCCA  |
| WI-<br>18985a | 105 C T --- | --- | --- | CCAAAGTCTCCTGTTGCTCATAAAGAAGTTTGGGATGGGAGAGAATCCAGACCCTTTGGGGCA<br>GCCAGGCCCTTGCCCTTCATTTTACAGAGGTAGCACAA/C/TTGATTCCAACACAAAACCCCTTCCOC<br>TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCTCAGAAACCAATTGTGTTTCTCTTT<br>TGAAGCAATGACAAGCACITTTACTTTCACGGTGGTTTGTGTTTCTTAT        |
| WI-18746      | 114 G A --- | --- | --- | GCCAGCAGCTGAAGTCTTTTCTCTCTCGGCTGGAAGAATCAAGATACCTTTGCGTGGATCA<br>AGCTTGCTACTTGACCGTTTTTATATTCTTTTGTAATATTCTTG/A/TCCACATTTCTACTTCAGCT<br>TTGGATGGTTACCG   |
| WI-19112      | 212 G A --- | --- | --- | CCGTGTTACACACACACAATGGCAAGCATAAGTCGCTGGTTACGGCCAGGGGAATATGCCAAGG<br>GACCCCTTAATGGAACACAGATCAGTAGTGCTATCTCATGACACCACAAAGAACCCGACGACAAA<br>TCTTTTGCAGATTTTCTTCTAGTGGCTTAGAACATGGCTTTAAGAAACACGGTGATATCTTTGAG<br>GGTGACAAGGC/G/A/TCTCTTCAAACAGTTCCATACCAACTGCTTTGCTCTAG   |
| WI-19092      | 232 A C --- | --- | --- | TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTGCTCTCTATAGAAGGCTATTCTTAGATCATGT<br>CTCAATGGAACACACTCTTCTTCTTAGCCTTACTTGAATCTTGCTATAATAAGTAGAGCAACACAG<br>ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTGTTATTAAGTGAATTTTC<br>TTTTAAGCTAACAAAGATCATAATTTTC/A/C/ATGATTAGCCGTTGAAC |
| WI-19057i     | 175 G A --- | --- | --- | CCCAATTTATTAGGCCAGTGATGTCTCAAAGAGTAGAGGCGTCTACTGGTCTTTCAACTCCTTCA<br>GTCTTCTGACGGCGGACTTTACCGTGACAGGGAGTGGTATTGTACGTCCAGGCAACCGACGCACTG<br>TCTTCATGCAGGAACCCACAGTGCCAGATCCCCACAGCTC/G/A/TCTCTTCTATCTTGGTTTGCCACA   |

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| WI-20103  | 168 | C T --- |  |  |  | TGGGACTTCCAACCTCAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT<br>AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG<br>TGGGCTTCTGGGCTGGAGCTGGGTCTCCCA/C/T/TTCATTCTGCTCAAAGCTTCTTGAAGGAGC<br>TGGTTGACTTCAACTTGTAGAGCTAGCCTCATCTTTCAGTCAACTGGGA    |
| WI-20441  | 111 | G A --- |  |  |  | GCCTTACCCATTTTGCACATATACATATGCACCACCTTTCAGTGGCAACATATATATCCACACTA<br>TAAACATACCACATTTATAATCTTGTAAAGGACAAGAAATGGA/G/JTTGAATAAGTACCCCCCAA<br>CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCTACTACATCAGAGGCAAAATAAGAAATCTTT<br>TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG |
| WI-19911b | 116 | A G --- |  |  |  | TGGTTACAAACCTAAGCCATATACAAATTAGGAACACATTTAGATGCTCTTTTGAAAGAACGT<br>TTTAGTCTTTTAAACTGAGTTTAAAAAAATAACAATGCAATTTTAA/G/ACACTGTTTTGAAA<br>ACTTAAAGTGCAGCAATA   |
| WI-20613c | 165 | A G --- |  |  |  | GTCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA<br>GATACGTAGTACATCTGTAGTATTAATAATGGCATGGGAGGAGGAGTTAGAAAAAACATCTAAAC<br>AGCTCCTTAGAAGGCCAATAATAAGTTGGAA/G/JAAAGGGAGTTTCCACGCAGCCAGTGGTGAGC<br>TGC   |
| WI-20613b | 156 | A C --- |  |  |  | GTCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA<br>GATACGTAGTACATCTGTAGTATTAATAATGGCATGGGAGGAGGAGTTAGAAAAAACATCTAAAC<br>AGCTCCTTAGAAGGCCAATAATA/C/JAGTTGGAAAAAAGGGAGTTTCCACGCAGCCAGTGGTGAGC<br>TGC  |
| WI-19984  | 47  | A G --- |  |  |  | CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA/J/GJTATAACATTAGAAAA<br>GCAAAATTCITTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAAATACAGG<br>TAGGCAAGAGTTTTTCCACACTGGAAATGAAGGCAGTTTTCCAAATACTGTGAATTTACAAACAT<br>TGGGGGAAGG   |
| WI-20122  | 135 | T C --- |  |  |  | GCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA<br>ATTGTTTCTTGGAACTCTGCACCGACTGCCATGCTCTGTGGGACTTACACATTCAAGTTTGACAGI<br>T/C/JTGA AAAACCAACTGGAGCTGCTTTTCCAAAGATGTTCTGTCTTCAATAGGAATCCATG<br>TTATTTCTTCTTGGCCTTAACTCTTATATCTTTCAATGACCTAAGCTGA       |
| WI-18846a | 49  | G A --- |  |  |  | GAGTGCCATACCTTCTCCAGGCTCTGCCCCAAGAGCAGGAGTGCTG/JAAAGCTGGGAGCGT<br>GGGCTCAGCAGGCTGTACCTCCATCCCGTAAGACCTCCTTCCCTCCTCAGCAGGCCAAACATG<br>GCCAGACTCCTT  |
| WI-18959  | 123 | G A --- |  |  |  | AGCAGTGGCCTTATGCATCCCAACCAACCGCCTCTTGACCAGGCTGCTCCCTTGTGGCAGCAACGGC<br>ACAGCTAATTTCTACTACAGTGTCTTTAAGTGAATAATGGTCGAGAAAGAGGCACCG/J/GGAAGCCG<br>TCCTGGCGCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCAT<br>GTCGTGGACACACACAGACTATTTTAGATTCTTTTGGCCTTTTGCACCC |

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| WI-20146  | 31 T C ---  |  |  |     | TGAGTCTTCTGTAATTCATTGAGCAGTTAGCTG/CATTTGAGATAAAGTCAAAATGCCAAACACTAG<br>CTCTGTATTATCCCATCATTAATGTAAGGCTCATTTGAATGTGTGAATTCATTAACAGGC   |
| WI-18922  | 74 G A ---  |  |  | --- | TAGGAATTGGTTTACGCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTACCTGGAC<br>TTAAGC[G/A]TCTGGCTCTAAATTCACAGTCTCTTTCTCCTCACTGTATCCAGGTTCCCTCCAGAG<br>GAGCACCCAGTTCTC   |
| WI-18763b | 53 A G ---  |  |  | --- | TTCTGTGTGTGGGGTCAACCGTACAATGGTGGGAATGACGATGATGTGA/GJTAATTTAGAATG<br>TACCATAATTTTGTAAATTAATTAATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCA<br>TGTTTTTGCCAA  |
| WI-18763a | 38 A G ---  |  |  | --- | TTCTGTGTGTGGGGTCAACCGTACAATGGTGGGA/GJTGACGATGATGTGAATATTTAGAATG<br>TACCATAATTTTGTAAATTAATTAATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCA<br>TGTTTTTGCCAA   |
| WI-18771b | 75 G A ---  |  |  | --- | CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAATGTTGGG<br>AACAGAA[G/A]AAATAAACTGAGTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGA  |
| WI-18771a | 57 A G ---  |  |  | --- | CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG/GJAGATGTT<br>GGGAACAGAGAAATAAACTGAGTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA   |
| WI-18820  | 70 T C ---  |  |  | --- | GGGAAAAATTTGAGACGCAATACCAATACTTAGGATTTGGTCTGGTGTGTATGAAATCTGAG<br>GCC[C/T]GATTAAATCTTTCAATTGTATTGATTCTCTTTAGGTATATTGCGCTAAGTGAAACTT<br>GTCA   |
| WI-18742b | 51 C T ---  |  |  | --- | ACAAAGTCTGTAGCCCCCTCACCTTTCTCTGTTTCACTTTTGCCAAATGTA[C/TA]TCGGGTTTGTTT<br>TCTTGATTATTTAAACGGTTGTGGTTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA<br>GTTTTACC  |
| WI-18882  | 94 C T ---  |  |  | --- | GTGTGTCAAAAATGGGGTCTGCTCTGCTACCTTGACCCCTTCCCTTTCTCTGCTTCTCTCATCA<br>TCATTTCCCAACAAACATCCTCTGCCA[C/T]ACACAAACAAACGTAAGTTTTCATTTGGGCAAAAAATTGA<br>GC  |
| WI-19970b | 167 G A --- |  |  | --- | TATAAGCCCGAGTCACCAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCTGTGGAGCCTGCCCAOC<br>GGCCCCCGGAGTCAGTCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCACTGCGGGGACC<br>AGCAAAAGGCCCTTCTCACTGGTTGGTCAAG[G/A]TAGTCACTTGGCCTGGTGCATCCACAGAGGA<br>TGTTGTTCAAACCCAGAAATCTTTAAACGACTGACCTTCTTTAAAAACAGA |
| WI-19970a | 126 T C --- |  |  | --- | TATAAGCCCGAGTCACCAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCTGTGGAGCCTGCCCAOC<br>GGCCCCCGGAGTCAGTCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCACTTCTGCGGGG<br>ACCAGAAAGGCCCTTCTCACTGGTTGGTCAAGGTAGTACCTTGGCTGGTGCATCCACAGAGGAT<br>GTTGTTCAAACCCAGAAATCTTTAAACGACTGACCTTCTTTAAAAACAGA     |

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| WI-19067d | 202 T G --- | --- | TATTGCTGCTTGTCACCTGACATTACGGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTC<br>ACATTCCCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTTCTC<br>TTGGGCTCTAGGTCCTGGAGATGTTGTAGGGGTTATTTTTTAATAGTTCATAAGAAAT/<br>GIACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC                         |
| WI-19067c | 153 G C --- | --- | TATTGCTGCTTGTCACCTGACATTACGGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTC<br>ACATTCCCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTTCTC<br>TTGGGCTCTAGGTCCTG/CJAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAGAA<br>ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC                        |
| WI-19067b | 151 T C --- | --- | TATTGCTGCTTGTCACCTGACATTACGGGCAGAGGCTGCTGCAGCCTCCCTGGCTGTC<br>ACATTCCCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTTCTC<br>TTGGGCTCTAGGTCCTG/CJGAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAGAA<br>ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC                       |
| WI-19067a | 57 C G ---  | --- | TATTGCTGCTTGTCACCTGACATTACGGGCAGAGGCTGCTGCAGCCTCC/CJCTGGCTG<br>TGCACATCCCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTT<br>CTCTGGGCTCTAGGTCCTGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTTCATAAGAA<br>ATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC                        |
| WI-19106  | 247 T C --- | --- | TAAATCCAGCCTACCTGTTAGTATTTAGGAGACAGTCTCAAGCACTAAAAGTGGCTAATTC<br>AATTAATGGGTATAGTGCCAAATAGCACATCTCCACGTTAAAGACAGTGGATCATGAAAGT<br>GCTGTTTGTCTTTGAGAAAGAAATGTTGTTGAGCGCAGAGTAAATAGGCTCCTTCATGTGGC<br>GTATTGGCCATAGCCTATAATTGGTTAGAACCTCCTATTATTTAA/T/CJGG             |
| WI-18944  | 147 A G --- | --- | CAAGCAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGCTGAAACAAA<br>AATGCCAGAGGATAATATTGATTCTCACATCTTTAACTTAGTATTTACCTAGCATTTCAAACCC<br>AAATGGCTAGAAC/A/GJTGTTAATTAATTAATTTCAAAATATAAGTTCTACAGTTAATTATGTCATA<br>TTAAACAATGGCCTGGTTCAATTTCTTCTTCTTAAATTAAGTTTT              |
| WI-18952  | 232 G A --- | --- | CCCATCCCTGTGAAGGAGTAGGCCACTTTAAGTGAAGGATTGGATGTTTCATAATACATAAA<br>GTTCTCTGTAATTACAACATAATTAATAGCCCTCTCTCACAGTCAAAGGAAGTGGTGGTTGGT<br>TTTTGTTGCTTTTATAGATTATTGTCCCATGTGGGATGAGTTTTTAATGCCACAAGACATAATTA<br>AAATAAATAAACCTTGGGAAAAGGTGA/G/AJACAGTAGCCCCATCACAT         |
| WI-18932d | 177 C T --- | --- | CACACCTCATGCTAGCCTCACGAACTGGAATAAGCCTTCGAAAAGAAATGCTTGAAGCTTGTA<br>TCTGATATCAGCACTGGATTGTAGAACTTGTGCTGATTGTGACCTGTATTCAAGTTAACTGTTCCC<br>CTTGGTATTTGTTTAATACCCTGTACATATCTTTGAGTTCAA/CJCTTTAGTACGTGTGGCTTGGTCA<br>CTTCGTGGCTGAGGTAAGAACGTGCTTGTGGAAGACAAAGTCTGTGGCTTG |

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| WI-19042  | 193 A C --- | --- | --- | TTTGTGAGTGTGCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGAGTTTGGAGATAGATG<br>GATAAGGGAATAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTTGGTGAGAGTCCACAG<br>ACACAAATTTATAGTGGACAGAACTTCAGCATTTGTAATATGTAATAACTCTAACCA[A/C]GGCTG<br>TGTTAGATTGATTAACTATCTCTTTGGACTTCTGAAGAGACCACCTCAAT |
| WI-18984  | 208 A C --- | --- | --- | ATTGGCCCTGTACAGTTGCTTATTTATAAATTCATTTAAACACTACAGGTGTGAATGGTTAAAA<br>TGAGGCCCTCAGTTTCAATTTTCAAGTATTTCTGAGTGCAGACAGTATTTCCGACTGTATTAAT<br>GTAACCTATTAAATGAATCAGAAGCAGTAGACAGATTTGGTGCAATACAAATATTGTGATGCATT<br>TATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGGCATGTTTGACT   |
| WI-18851  | 90 T A ---  | --- | --- | GCTTCAATTGGCGATTGATTCAAGTGGCCACAATGTAAACAGGGTGGTAGTTGTACTCATTTTGAAT<br>ATACCTTTTCCATTATTGATTCTT[A/G]ATAATATAGGATCCTGGAATGAGACCTGGTGGAA  |
| WI-18821b | 76 T C ---  | --- | --- | TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC<br>ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCATGGCCCGGGGAACTTGCCAACTTCGTGTCAG<br>GTGCTGTGT  |
| WI-18821a | 69 C T ---  | --- | --- | TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC<br>A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAACTTGCCAACTTCGTGTCAG<br>GTGCTGTGT   |
| WI-19021a | 20 C G ---  | --- | --- | ACTCCTCTGCTGCTGCCAT[C/G]ACTGTCTTTTGAACAGGAAAGTCAAGAGTTTAAAGAGAA<br>GCAAATTAACATCCTGAATCGGGAACAAAGGTTTATCTAATAAAGTCTCTTCCATCACGTTG<br>CTAGCTACCCACACTCCCTCTGATTTCGTGAGGACGTGGCATCTACTACGTACGTGGCATAAC<br>ACATCGTGTAGGCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTCT         |
| WI-18908  | 70 G C ---  | --- | --- | TGGAATTCCTTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA<br>TGG[G/C]TTAGGGAACATTCATCCTTGAGTCAAAAAATCTCAATCTTCCCTATCTTTGCCACCC<br>TCATGCTGTGTGACT   |
| WI-19037b | 155 A G --- | --- | --- | CACGGTTCTCTGCATCGTTACCAGAGCGCTTCTGGTCTAGCCAGCCCTGTATGACCGCGCAATA<br>TCCCCAAAGCTTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC<br>CCCTCCCTTACGAACAC[A/G]AAACCCAGCCCATGACTAGCAGCTGAGCTCTGCAGGGACCA<br>GTGCAAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG       |
| WI-19037a | 47 C A ---  | --- | --- | CACGGTTCTCTGCATCGTTACCAGAGCGCTTCTGGTCTAGCCAG[C/A]CCTGTATGACCGCGCAA<br>ATATCCCCAAAGCTTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG<br>GTCCCTCCCTTACGAACACAAAAACAGCCCATGACTAGCAGCTGAGCTCTGCAGGGACCA<br>GTGCAAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG       |
| WI-19064  | 66 T C ---  | --- | --- | TTGAGGAGGTGGGTGAAGTCTCTTGGCAGGGATTTGTGACACTGCATGCTGGGCTGTGTTCTCT/<br>CJCGGGCTCTCTGGACCTTGCAACCTGGATACAGGCCATGTGCCATGGTATTTGGGTCTGGAGGG<br>TGGGTGAATAAAGGC   |

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| WI-18972a | 112 A G --- | --- | --- | AGGCTGTGGCTTATGTACCCACAGAGGGTCTCTGAGAAGTCTGGCTGCCTGGGATGCCCTGCC<br>CCCTCTGGAAGCTCTGCAGAGATGCTGGCTGGGAGAGAG/GJTGCTTCTGGCCATGGAGCC<br>TCATTGCAAGTTGTTCTTGAACACCTGAGGCTTCTGTGGCCACAGGCACCTACGGCTTCTCTCTCC<br>AGATGTGCTTTGCCCTGAGCACAGACAGTCAAGATGGAATGCTCTTGGCCA        |
| WI-19016b | 184 C A --- | --- | --- | GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATGACATGGTAGAGAAGATAAG<br>GTTTATGGCAGGTAATTTTTGTAATGTGATTAACGAAGTTCAAGATTAGAAATACATCTGTGTC<br>CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTTCATCAAC/AJCTCAACACTATTGAC<br>TTTTGGGGCTGGATAGTCTCTGTGTGGGGTTTGTCTGTGCACTGTAG      |
| WI-19016a | 161 C T --- | --- | --- | GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATGACATGGTAGAGAAGATAAG<br>GTTTATGGCAGGTAATTTTTGTAATGTGATTAACGAAGTTCAAGATTAGAAATACATCTGTGTC<br>CTGAAAACCTTAGATACATAGCCGAG/C/JTGATACAGAGGTTTCATCTCAACCTCAACACTATTGAC<br>TTTTGGGGCTGGATAGTCTCTGTGTGGGGTTTGTCTGTGCACTGTAG    |
| WI-20096  | 21 T C ---  | --- | --- | GGTTTGGGGCATTTATTTCT/CJGATAGAGACTGGCACAAAGCTTTGGGCTAAGGACACCCGCCOCC<br>ACCCTCATCTAGAACAAATCTCTCGCCAGACTTG  |
| WI-19591b | 156 C A --- | --- | --- | TGGGGCAATTTTAAACAAACAGGCAAAATATACATATACCTGAATAAGGTAACCTCAAGCCATG<br>AGTATAAGATTAAAGCAGTTACTTTATTTTGAACAAGGAGTGCCATAAGCAACTCAGTGTGCCCC<br>CTTAGGGTGGGAGCTCTCC/CJACTACCCTCCCAAGGATCATTTTGGGAGAAAAA<br>GTGCTCTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG             |
| WI-19591a | 45 T A ---  | --- | --- | TGGGGCAATTTTAAACAAACAGGCAAAATATACATATACCTGAAT/AJATAAGGTAACCTCAAGC<br>CATGATATAAGATTAAAGCAGTTACTTTATTTTGAACAAGGAGTGCCATAAGCAACTCAGTGTGT<br>GCCCCTAGGGTGGGAGCTCTCCCCCTACCCTCCCAAGGATCATTTTGGGAGAAAAA<br>GTGCTCTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG           |
| WI-20310  | 125 G A --- | --- | --- | TCTCCAGCTCTGTCTCTTGTCTTGAAGGTTCTGTGTTACGGCCCCCTCCAGGCTGTTTCTTCAT<br>TTAGGTAGGAACAAAAGGCCAAAAGAACATACAGCCAGCTCTCTAGAGGCTCCA/GAJTCAGAA<br>CTGGACCTTTAACTACAAAGGAATCTTGGATGAATATTTTAGCGGGCTTCAGGAGCAGGTAGC<br>AGAGCCAAAGTGCACTCAGGCCATCTTCTCCCAATGTCTCCCGGGGG           |
| WI-20860  | 224 G A --- | --- | --- | CTCTCCCTAAGGAGCCTTGGCCTTGACGCCCTTACAGAGGGATGGAAGTCACAGACAATGAGT<br>GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTTATCTGTCTCTCT<br>CCCCAGTGTGTACACCTTGGGCAAGCAGAGTGTGGGAGACCCAGCCTTGAGAGCTCTTGTAGACC<br>GGAAGGAAGGGCGGTCTT/GAJGGTATGGCTTCTGGCTCTCTGGCTT       |
| WI-19359a | 39 T C ---  | --- | --- | GACGTGGACAAAGGAGGTTTAAATGAATACCTTGTGTTTGT/CJCATGTTCAAAAAAGAGATTAAAT<br>ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACTTAGGTTAATAATAA<br>GGCTATTTGTCCACCCACTCTCTGGGCATTGTGCAATATCTGGCCCTCAAGTGGGAGGCCACGTG<br>GGAACAAGGCCCTCAGAAAACAAGGACATGACGCTCCCTGAGCCAGTTCT |

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| WI-19766b | 93 A G ---  | --- | TGGCCTCAATGACTGGTACATTGGAGAAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGGAGGGCAGGAGATGAACCATAGGAGCCAAAGTC/GJGACAAACAGAAAGGCACACCAAGCCTGAACCCCTC   |
| WI-19766a | 31 G A ---  | --- | CGGACAACAGCAGAGTTACCAGTACAGGTGCTCCCTGGAGTTTCTGACCCATGAGAGGCCCCCTCACCTCTTACCCCTCCTCTACCAAGCTCTCCGGCAGTCATGGACTTAT                    |
| WI-20512d | 126 C G --- | --- | TGGCCTCAATGACTGGTACATTGGAGAAAGCTG/AJTGACAGCATCCTTTCTGTGGTGGGAGGGCAGGAGATGAACCATAGGAGCCAAAGTCAGACAAAGAAAGGCACACCAAGCCTGAACCCCTC      |
| WI-20512c | 59 T G ---  | --- | CGGACAACAGCAGAGTTACCAGTACAGGTGAGGGATGCTCCCTGGAGTTTCTGACCCATGAGAGGCCCCCTCACCTCTTACCCCTCCTCTACCAAGCTCTCCGGCAGTCATGGACTTAT             |
| WI-19599  | 230 C G --- | --- | CTTCCCTGTTTGGCTTGCATTTGTGCGATTGGAAAAACCACTTGAAGAAGGGACTTTCTCTGCAAACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/GJAAAGC |
| WI-19599a | 29 T C ---  | --- | TTAGAAAGGAACTGAAATTGCTTCTTTGAATATGGAATTTAGGGCGGGCGTGGTGGGCTCACGCCCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA                |
| WI-20341  | 221 G C --- | --- | CTTCCCTGTTTGGCTTGCATTTGTGCGATTGGAAAAACCACTTGAAGAAGGGACTTT/GJTCCTGCAAAACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC |
| WI-19599  | 230 C G --- | --- | TTAGAAAGGAACTGAAATTGCTTCTTTGAATATGGAATTTAGGGCGGGCGTGGTGGGCTCACGCCCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA                |
| WI-20679  | 82 T C ---  | --- | GGGCTTAAATCCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAAGGATCGCACCCCTTTTCCATAACCCCTTCTACATTGGAAGAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTTAAACG |
| WI-19909a | 29 T C ---  | --- | GACAAAGGTAAATCACAGCTAACAAACGTGATGTTGGCTCACAGTAAACCAACACCTCTTTTTCAGAACAGAGAGCGTTAAAGTAAAGGGCA/C/GJTTCCAAGAGTAACACTGCTA               |
| WI-20341  | 221 G C --- | --- | TGTTTGAATAAAAAATTTCCATGGTCTTAATTGAACGTATGTTACTTTCTTTTGAATATCCTTTT   |
| WI-19599  | 230 C G --- | --- | TTCAATTAATAATTC/CJCTAAACCACTCTATGTGTTCAACCTCTGTTTAAACATAAGATATGGGT  |
| WI-19909a | 29 T C ---  | --- | TTTTGAAAGGCCACAAAGTCACCAAGTCCATGAAGTGGGCGAATGGTCTTGTGTTTGGAAAGCTCTC   |
| WI-20679  | 82 T C ---  | --- | CAGGGTGTCTTCTCCAGAAA  |
| WI-19599  | 230 C G --- | --- | CCAGAAATAAAGCCTGAATATCTCTTCT/CJTTAAAAATAAATTTTCTCTTTGCTCTTCCAA  |
| WI-19909a | 29 T C ---  | --- | GTAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTAACACTACCTAGGCGGG   |
| WI-20341  | 221 G C --- | --- | TTTTTCCCTTATACCTTGTCTGTACTGTTGAATCAACTAA  |
| WI-19599  | 230 C G --- | --- | TTGAGAGGCTGAGAGAGGCTGTTGAGACATTGTAATAAGTCTTAGGGGCATGAGACATTAGGAAG   |
| WI-19909a | 29 T C ---  | --- | GCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTAGCAGGA   |
| WI-20341  | 221 G C --- | --- | GGCAGGAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGGTAAATATTGGGTGACGTCATGC   |
| WI-19599  | 230 C G --- | --- | ATCCCCCATGCATTGGTTT/GCJATGCTCCAGTGAGCTGTTGGGCAAGTCT   |

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| WI-20113  | 60  | T C --- |  |  | TTCTGGTACATGGTAAAGTCTCAGTATTACTAGTGAATGAGCAAGACCTGAAATACGTGTCJGGA<br>AACAGTAAAAGCAAAATACCACACAATTAGGAGGAATATTTTCAGACATAGGATATTTAAACAT<br>CACTCAAACTACTGGAGCATGATTCAGCAATAAATCTATCCATAAACCCAGGTAGATAAATGTCACA<br>GCITTAATAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATCCGTAAT |
| WI-20895  | 107 | G C --- |  |  | TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCGCGCAGTGCGGTGTGGC<br>CACTTCCACCAGGAGAACACTTGACTTCATTAAGGCAAJGJCJTCTACTCTGTACTTTTCCTC<br>CCACATAGTTTAAACCAATAGAAAGGCATTCCTTCTCACACTACTGCTCTCTAAGGTCCTAGGAA<br>TATAACTGGTACTATAGGCAACAGATGCA                                |
| WI-20721  | 72  | T C --- |  |  | CCTGCAATCACAAAAGTGAAGTGTGATATTTTGAATCATACITTGATTTAACCCACTTCAGAAA<br>TTCTATTCJAAACACTAGCAACTTCCTTTATCAGA  |
| WI-19415c | 161 | A G --- |  |  | CTGGATTTAATATTTCTGCTTAATAACCAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC<br>ATTTCTGCTAACATGTTTTGCAAGATCCCTAAGTAAGGTATTGACACTGAGACTAGTCCGGCAA<br>GTCATGAGACCCCTTAGCTGATCTCATJGJAAGTCCACCTCATGAAGGAGATGATTCACATCTCAA<br>GCTAAGGTATAAAGTGTGGACATACAAAGCTTACAAGTTTACACTTCCTG      |
| WI-19348c | 103 | C T --- |  |  | GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG<br>GCGGTGATGAAGAGACTGTTGGTATGCGGTGACJTGTCCTTCTCCAGGCTCATATGGATGTCT<br>CGAGTTGCACAGGGAAGTCTCTGCTTGTAGAAGCTTCTCC  |
| WI-19348b | 98  | A ---   |  |  | GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG<br>GCGGTGATGAAGAGACTGTTGGTATGCGJGJGTGACGTCTCTCCAGGCTCATATGGATGTCT<br>CGAGTTGCACAGGGAAGTCTCTGCTTGTAGAAGCTTCTCC   |
| WI-19635  | 98  | A T --- |  |  | ATTAGTTGTTGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAACACAATG<br>TTAAAGGTACAGTAAAATACAGTATTATJATCTTATTGTGTAGCACGGCTGTGAGGCTCAT<br>GTTGAATGAAGCATCCTTAGGCAGCAOCTGACTGCATGCAGATATGTGTCTGAAAGAACTTTGCCTT<br>T   |
| WI-19641a | 46  | A G --- |  |  | TCAAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGJGJTATTATAGTCTCATGTT<br>TTAAATTTATGAATAACGCTGATTCATTTGATTTTGTATTTACAGAAGATGTCAGGGCTATCTCATTC<br>AGTTATTAATAAATGGATCAGAGTAGTAAGTCAAGAATAAGTGATATGTGTTTAAATTTTAAAA<br>AATACTCAGAAATGAGTATTTTAAATTTTAAATTCATCCACCCACCTTG    |
| WI-19642b | 52  | C A --- |  |  | ATATAGAGTACCATCCATGGTTTCAAGCATGGCTGGACACATTATCCCCCTJCJAGGGTAAACCAG<br>GACTATTGCATGAGCATTCITTAATACGTATTTTGTATGGACACAAGTTTTCATGCTATTA  |
| WI-19673b | 180 | C T --- |  |  | TCTGCCATGATCACATTGTATGAAGAACATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCCT<br>TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGATCACCAGTGAATCTAAATAGT<br>GAAAAGGCAATGATGTCTCAGTATCACTGTGAAAACATTTTTCJCTCTTGACCCAGCTGAAAGAA<br>TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAAACACAGCCC    |



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| WI-19673a | 35  | G A --- | --- | TCTGCCATGATCACATTGTGATGAAGAACATGATG[A]TTCACCTAGTAGGTAACCTTCTGTGTCAATTG<br>CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGATCACCACCTGTAATCTAAT<br>AGTGAAGAGGCAATGATGCTCAGTATCACTGTGAAACATTTTCCCTTGACCAGCTGAAAGAA<br>TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAAACACAGCCC    |
| WI-19724  | 35  | A G --- | --- | TTTATTGGGAACAAAGGATTGTAATTTGGGTA[A]G]CTGAGTCACGGTGGCCCTGAGTAGTGTC<br>CTAGAAAGCAAAACAGAGTTTGGTTTTCTCTT   |
| WI-19307  | 196 | T C --- | --- | TCCTCCTCCCCAACTAGATGGTATTGATCACTCTGCCACAAATGGTACCCCCCTCAGCAAGAACTG<br>CAAGCCCTTCTTGGATTTGCCCTCATGAGAAATGGTGGCTTGGATGGAGGTGACATTCTTGTCTGT<br>GGTGAACCTGCAAGAGGAACACAGGCAATGATTTCCATAGAGGCTTTAAAGAGACCCG[T/C]TGG<br>AAATGGGCCATGGTCTAATTTGGTGTGAAATAAACTAACCTCTTTGGCTG    |
| WI-19269  | 85  | A T --- | --- | CTTCCCTCATCCCTCTCCACACACCATCCCGGAACAAGTGCTCCAGGATTCCCTGCCACTGGC<br>CATTTTGGAGTGTGTCQ[A]T]TGGGTAGCAATGTGGAACACACAGGGCTTTGTGGAGAAATGG<br>AGGGGTTGAGGAGTCCAGGAGGGCTTATTTGAGGGCTTTGCCACTTGTCTCATAGGCGAGCTCG<br>ATCTCTCATCATCTGGACAGGTGGAAGCGAATTTCTCCCGGGCGTAGGCA           |
| WI-19946  | 122 | C T --- | --- | CAATGGACTGAATGAGTGGTGGTGGGTGGGGGCGACACACACCTTCAATACACGTCAAGGTG<br>CTTCCAGTTT TAGAAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGAGT[C/T]CTTCCCTG<br>ACCCAGACGCACTCAGGAGCCAGTCTGGTTTTCAAAACCTGCATTTAACCTGCGCCAGAGATTCAAC<br>CGTAGGCATCTTTAATAAACTAACCTCCAGCAAAATGTGGGTACGGTTACTAA   |
| WI-19956  | 141 | G A --- | --- | CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCAATAAATAATATA<br>ATAAATATACATCAAGTAACCTTACAGCACACATTTTGGGCCAAGTTTGGATCTGTCTGGACCT<br>CAATGT[G/A]CTCTCGGAGAAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTCTACTCA<br>GTGATGGCCCAACAGAAGCTTCTGAACCTCCTCTGGGAGGTAGCTGACAAG          |
| WI-19076  | 40  | G A --- | --- | TTGGTTGGATACTTGTGGAAAAAAGCAGTTTAAAT[G/A]GTATTCAAAATACCTTTTAAAA<br>GTATTCTAGCACAAAGATTTTCTGTAACTAGATTATGTTGTAACATTTTCTTAAATCTTGTAGGAG<br>TGTCGGTTGTTAAGAACTAGAGCTTATTCCTATTCCTATCTGCTCCTGAAACCACTGCAG<br>AAGGCATTTGAAAGCTGTTCTTTAAGATATGGGATTCTTTTATTCTT                 |
| WI-20218  | 26  | T C --- | --- | CCACACACTCTGGTTTTATAAAGCTA[T/C]JAGGACAGAGCAGAGATGGAACCTGAAACACAGGTAG<br>AAAATAACATAAATTTGAGGGGAACAGTGGGATGCAGAAAGAATGACAACAGCCACATGTGCCCCA<br>GTCAAATACTTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATCTGCTGGGATCCTGCC<br>ATGGATGCAGGAGAAAAA                                  |
| WI-20295g | 154 | T G --- | --- | CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG<br>GGAATTCTCTTTTAAATATCTCAGGCTTGAATTTGGGAGGGCTGGGCTCTACCCCTTCTCTTCCCA<br>TCCAGTCTATTGCCAGAT/G]CCAGAGAAAGCGCGGGAAGCCAGCTCTCCAGCATAGCCACTGTGG<br>GTCCGCTTCACCTTCTGTGCTGACTCTCTCATGCTGGGACTTGTCTTTCGGG |

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| WI-20361a | 192 | G A --- | --- | CTGGAGTGTGACCTAAGTGACATTTTTTAAATGCCAAATACAGTAATCTCCAAAGCTTTTAAATGG<br>CTTATGCAAGATGACAGAAATATGTGAATCTGATTGTGCCAGATACACTCTGCAGCTCCAAAGCTA<br>CAACAGTCCACAGCTGAGAGTTTCCCTATCTCTACTACTGTGACAAATTTAGC(G/A)ATCCTTC<br>AAATGGGAAATTCCTAAGTACAGAGACAATGGGTCTCTACAGTAGGCCCG     |
| WI-20572  | 75  | A G --- | --- | GAGCCAAACCCAAACAAATAAAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCT<br>TCAGAAAT(G/G)TCATAAAACATCATCTTTTACAACATGGAGAAGCGAGGTAGGCCATAATTTGTTCA<br>AATTCATCTTCTCAAAATTTTAAATTTGTTTAAATCCAAAGGTGCCTATTGAATCTTCCAAAAATA<br>AACTGCCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT |
| WI-20588  | 133 | G A --- | --- | CATGACAAAGACAAAGATCAAGGAGTAACATAAATTAAGTTGAATAAATAGTATACAGCAATC<br>TTCACITTTTAAAGAAATGTGAGATCCTTTGTTGGTTTTTATTCCTTAAGTACAAAATGCTAAAC[<br>G/A]GGAGCCGAGCTCTCCGCATTCAGG   |
| WI-20593  | 79  | A G --- | --- | TGACCTCATACTGGGTTCTGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTG<br>CTGTACTTCAG(G/G)TTAAATCTGGGAATGAGCATGCAGCAATGCTCCACAGATGAGGAAGAAA<br>AGCTGTTAAAGGAACTCAGGATGTTGTTAGGAAGGGGAGTGATGCCAGGCCCTCACCAGACTAT<br>CCAGAAAGCCATTCCATGGGTAATTTGGTCTGCATCTGTGAGACACTGAGCT     |
| WI-19765  | 57  | T C --- | --- | TTCTTTGCCAAGCCTGTTCTTCAAGTTATCAGAACTGGGGTGATACCTTGTCCTCAAT(C/A)TGATCT<br>TGCCCTGCTGTTTTAGTTAGCAAGGTGATGAATACTTTTAAAGTTTGTGTTCTTTCTCTCGT<br>GGTATCAGTGAATACTGATCTATTCTCTGGCTAGGGTCAATTTACAAAATGGCCATGGAACCTGAGC<br>AAAAGGCCACGTTGGGATAAAATCACTACCATCGAGCCCAACAGTATT      |
| WI-19066i | 239 | A G --- | --- | TGACAAAGGAGAGAGGGAAATTTCTACTATTGCAAGGAAATCCTCAGTTCAGTGAGCCAC<br>AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGAACTGG<br>CATATGTTCTTGGTTGGTCAACCTGTAGCTGAATTAATCTCCATATCCGGATGCTCAATTACAGT<br>ACCATTCAGGCAAACTTTTCTTAAACGCCCTTCACT(G/G)TTCTTTTA              |
| WI-19066g | 184 | C T --- | --- | TGACAAAGGAGAGAGGGAAATTTCTACTATTGCAAGGAAATCCTCAGTTCAGTGAGCCAC<br>AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGAACTGG<br>CATATGTTCTTGGTTGGTCAACCTGTAGCTGAATTAATCTCCATATTC(C/T)GGATGCTCAATTAC<br>AGTACCATTGCAAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA         |
| WI-19066f | 148 | T C --- | --- | TGACAAAGGAGAGAGGGAAATTTCTACTATTGCAAGGAAATCCTCAGTTCAGTGAGCCAC<br>AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGAACTGG<br>CATATGTTCTTGGT(C/T)GGTCAACCTGTAGCTGAATTAATCTCCATATTC(C/C)ATTCGGATGCTCAATTAC<br>AGTACCATTGCAAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA |

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| WI-19066e | 147 GC --- | --- | TGACAAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC<br>AAGCATTAAACCCCATGAACCTTCAGCTGATC[G/A]TCTTAGCCAGTCCAATCTCTACGAGGAAC<br>CATATGTTCTTG[C/G]CTTGCTACCCCTGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC<br>AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA |
| WI-19066c | 100 GA --- | --- | TGACAAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC<br>AAGCATTAAACCCCATGAACCTTCAGCTGATC[G/A]TCTTAGCCAGTCCAATCTCTACGAGGAAC<br>TGGCATAATGTTCTTGCTTGCTACCCCTGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC<br>AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA  |
| WI-19066b | 87 CT ---  | --- | TGACAAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC<br>AAGCATTAAACCCCATGA[C/T]CTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC<br>TGGCATAATGTTCTTGCTTGCTACCCCTGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC<br>AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA   |
| WI-19066a | 72 CT ---  | --- | TGACAAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC<br>AAGCA[C/T]TTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC<br>TGGCATAATGTTCTTGCTTGCTACCCCTGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC<br>AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA |
| WI-20660  | 105 GC --- | --- | TTTACAGCGAGTTTTTCCCGTCAATAAGTATGAATTAATAGATTAGGTTGAAAGAAATGTTG<br>TGCTAAATAAATCTCCCTTTTGAATGATATTTG[G/C]TTAAAGGGAAGCATTAAATATTA<br>CAGACATAATTTACAAGGTTCTGAACATGAGTGATCCATTAATCTGTTCTGACAGATAGAACA<br>AAGCTATCCACCCCGCCCCCAAAATACTGTTTAAACAACACTATGTTTAAAGA              |
| WI-18768  | 120 CT --- | --- | CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGGGTCTCCTGGCAGCCTCCCTCAGTCTTCC<br>TCCACCCGCTCTTCTTCCCTTCCAGCCTGCCTGCATGTCACCCCTTGG[C/T]TTGCTCCATCGCC<br>TTGAAAGCTCTGAA   |
| WI-19087  | 37 AG ---  | --- | TTCCCAAGGGTTCTGTATTGCAGCTAAGCTCAAATG[T/G]TATTTAACTTCTAGTTGCTCTTGTG<br>GTCTTCTTCCAATGATGCTTACTACAGAAAGCAAAATCAGACACAATTAGAGAAGCCTTTTCCATAAA<br>GTGTAATTTTAAATGGCTGCAAAACCCGCAACCTGTAACCTGCCCTTTTAAATGGCATGACAAGGTGTC<br>AGTGGCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC   |
| WI-18790  | 49 AT ---  | --- | GAAAGCCAGAGATTAGCCCCGCAATCCGCATCTGTCAACAGGACAGAA[T/G]CATGGACAAGGGA<br>TGAGCTTTACAAAGATGATGCACITTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACA<br>CAGTGATTTGGGAATGCCT  |
| WI-18987  | 35 GA ---  | --- | AGGAGGCTGTTCCAGGAGTCTGCCACAGCCTC[G/A]GTGGCCCAAGCCAGACACTCACCCACCTT<br>CCCCAGTGGCCCGTGGATCCTGGTCTAGGCTGGACAGGATTCAGAAAGACACCCAGGCTGCACA<br>GAAAGAGCCAGATGGACCTGAGTGTGGTTCACAGCCCTTACACTCAAGGCTGAGAGGCTCAGGAA<br>AGTCA   |



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| WI-19236  | 54  | G A --- | --- | TACACAGAGGGTGCACCTTGGACTCTGAGGGTTGGGTGGGAGGGGAAAGG[G/A]GATGGAGAC<br>CTGCTCCCCAGCTCTTCTGTACCGGTTTACATGGGAACAGGGTTAAACATCTGTGTAGGGAGGT<br>CACCCTACCCCTTTTCATAGGGGAAGAGTGCACACTCTCTGGCTATCTCAGGGGAATGGGAAAG<br>AATCTTTCAAGGGCAAGAACTCGTGGGAGGATGCTGTGTATGTAATACT             |
| WI-19144  | 222 | G C --- | --- | GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTACGCTTCTGACCTCCAGCCCTTCTAAGG<br>CTCAGCCCCACGGGACTCTGTGGCTGCCAGCTTGTAGCTATCTATCTATATTCATTTCATAGCCAA<br>ACAGGAGACCCCTTTGCAGGACTTGCACACAGGGAGGCTGTAGCCAGGAAACCCTCTCTCCCTGGT<br>CTGGCTCTGCTGGAGCG[G/C]TGGGAACCAACACCTTCAGTCTGGTG         |
| WI-19139b | 110 | C A --- | --- | CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACAGAGGGTAGAC<br>GGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACACTAG[C/A]ATTTACGGGTGTGGGCAC<br>ATGGTGTGGCACTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG<br>GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG        |
| WI-19139a | 66  | C T --- | --- | CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACAGAGGGTAGA[C<br>C/T]GGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACACTAGCATTTTCACGGGTGTGGGCAC<br>ATGGTGTGGCACTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG<br>GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG     |
| WI-18910  | 112 | T C --- | --- | GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAAGGGTGCCT<br>CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTG[C/G]GGCTCATGGCAGAGCAT<br>CAGTGCACGGTTTAGG  |
| WI-19235  | 173 | A G --- | --- | TTACAGGAGGTGGAGTTCGTGCTCAGCTCTCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA<br>CGAATGTCTCTGTAGCTTCTCTTCACTGCCCCAGTATTGCTGTATTTATCAGCGATGCCCTCTGT<br>CACTCATGCCCTGGCTAATTTGTTCAACAATGGTGGAA[G/G]GCTTCATGTAATATGATCAGGACCCACC<br>TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCAGCACTA |
| WI-19222  | 179 | C T --- | --- | CGTTTTCCCTAACTACCCAGTTTAGTTGGGATGATTGATTTCTGTTGTGTGATCCCATTTCTAA<br>CTTGGAAATTGAGCCCTCTATGTTTTCTGTAGGTGAGTGTGGGTTTTTCCOCCACCAGGAAGT<br>GGCAGCATCCCTCCTCTCCOCTAAAGGAGTCTGCGGAAC[C/T]TTTCACACCTCTTTCTCAGGGAC<br>GGGGCAGGTGTGTGTGGTACACTGACGTGTCCAGAAGCAGCACTT               |
| WI-19117  | 134 | A G --- | --- | AAATAATGCAACGCGAGGAGGAGAAAGAAATGCACCTAAGACAAGAACATTCCTCATAGAACATTG<br>ATCTGTTTTACAGGAACAACCTTGCCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA<br>A[A/G]TAGCTATTTTTCTCTAAGACATTTTTCATTTCATGAATATTTCAAGTTTTTCATACTGTACA<br>CATTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAAATTG      |

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| WI-19134c | 263 C T --- | --- | CTCCTGTTGCTGACCTGACAGGGTGACACAGCCCTTTACACTCTGTCTCCTCTATCTTCTCGGTAGA<br>TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCCAGCAAGGGGTGAGCCAGGCCAGGTCAG<br>GCCCTTCAGAGCCAGGGCTAGAGGATGACAGGTGGCTAGAGCCAGCTGCACTATCCTTTTCAGAGCAC<br>TTATCCACTTGTCTCCTCCTACCTCGGCACCCCTGGGTGGAAAGGG    |
| WI-19134a | 162 T C --- | --- | CTCCTGTTGCTGACCTGACAGGGTGACACAGCCCTTTACACTCTGTCTCCTCTATCTTCTCGGTAGA<br>TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCCAGCAAGGGGTGAGCCAGGCCAGGTCAG<br>GCCCTTCAGAGCCAGGGCTAGAGGATGACAGGTGGCTAGAGCCAGCTGCACTATCCTTTTCAGAG<br>CACTTCATCCACTTGTCTCCTCCTACCTCGGCACCCCTGGGTGGAA       |
| WI-19224  | 112 C T --- | --- | GGTTTACCAGTCTTCCAGGGAACTCCGATGAAGTGTCCAACAAAATGAGCGAGTGAACCAAGA<br>AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATAATCTTCAGGATGCCTGTGAAGA<br>AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTTCATATCCAGCAGGCCAGAGACTTCC<br>AGGGAACCTCATTCAAGGAGGTGAAAATGATGGATGACTCCTCCAGATGAAAA          |
| WI-19201  | 179 T C --- | --- | GCAGCTCCTAAGGAOCCACTGGCCATTAGCTCTTGTCTTGTGATGGCATCTCTTCCACCTTGTCTCTC<br>CTTTGCTCCTCTGTGTAGTGGCAGGTATGACAACCTCAGTCCAGTGGAAACAGACAGCCCTCACACTGCC<br>CTTCGCCCCCCACACTTTGCCCTGCAGGTGCACCGAAGGACCTTCCTGGGGGATAAAATCAAAAAA<br>GTGTGATGTGCTGCTCAGAGGTGAGTCCATGCTGCTGCTTGGCCTCAA |
| WI-19034  | 45 T C ---  | --- | GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAATCJACTTCTTATACATTAAAG<br>GCAACAGAGTGTAGTAAAGGTTTACAGTGTCTGCTGTTGAAAGTGAATATAAAATTTTGTG<br>CTAGCCCATGATCAATCGACTCTATTGTTTGATATACACTCAGCATTTAAGTCTGTGCGAATTGAC<br>ATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTTATGCTGTGCTATATA         |
| WI-19102  | 25 C G ---  | --- | TGTTCTGAGTCACGCTGAGGAGAGC/GCTTCACTCAGGAGTTCATGCTGAGATGATGAGTTCATCA<br>TGCGACGTATATTTCTTTGGAAACAGAATGAGCAGAGGAAACTCTTAATACTTAAATCGTTCT<br>TGATTAGTATCGTGAGTTTGAAAGTCTAGAACTCCTGTAAAGTTTGAACCTAAGGGAGAGGTAT<br>AGTGGATGAGTGTGAGCATCGGGCTTGCAGTCCCATAGAACAGAAATGGG          |
| WI-18548b | 65 A G ---  | --- | AAAGGAGGGAGAACTCTTTTACATAAATGCCCTGCATCCTCCAGTCCCTCACTGGGGGA/J<br>GJAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC   |
| WI-18548a | 62 G A ---  | --- | AAAGGAGGGAGAACTCTTTTACATAAATGCCCTGCATCCTCCAGTCCCTCACTGGGGG/JA<br>AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC   |
| WI-18700  | 97 T C ---  | --- | GGCAGCAGCTTTTAAATTTGAACACTTTCTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT<br>TACACCTGAAATCTGCTGAGAGCAGAGCTT/CJAGATCCACAATTGCAAGGCCACTGCTGGCTCA<br>CTTCTCTACA  |
| WI-18501  | 121 C T --- | --- | CAGAGGGGAAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAAGGAGGTTCTGTGT<br>GCATGGAGGAAATCAGGGCGCGNACAGCTGAACCTGCGCAGGACAGAGGGCGGCTGGACAGCA<br>GGCATGCCACAAACATTCA   |

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| WI-18017    | 87  | C A --- | --- | ACAAAGAAATGAAATAGGTTGCGAAACCTTATCTGCATGTACAAAGTAATCCCGTAGATAA<br>GGAGAGGCAACCCNGGAACA/C/A/ACTGCTGGATAAAATCGTTCAATTAATAATCTCTTTGCAT<br>CAGAGCTGGTGGAAATCAT   |
| WI-18148b   | 101 | A G --- | --- | TTATTGCGTTCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA<br>GTGATTTCAGAAACCNCTCGATTCTGAATATCCC/A/GTTGGGCGCATATGCAAAGGAAGATGA  |
| WI-18254    | 64  | T C --- | --- | TATACGGATCATGTATTTGTGTGACCACTACACAGTCAATTTGTAGAGCAGTTAAATCACT/C<br>JGCCAAATCCCTCTTGCTTCTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT<br>TCCGTTCTAGACATTT   |
| WI-18265b   | 117 | C A --- | --- | CAATGGTGGAGTGAATAAACGCATATTGAGAACAAAGACGGCCTTCTGGCCNCTCTGCGTCC<br>AAGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG/C/A/GTTTTCAACCTTTC<br>CTTGGGTGGTTCTTCAG   |
| WI-18295    | 40  | C T --- | --- | ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG/C/TJTTGGGAAGTAAAGGTTGATTACT<br>TCCTCTCCAAGGATGATATGTTTAATGAATTCCTTTNCCCTAGCTTCATCTTCATAATGCCAAA  |
| WI-18459b   | 64  | T C --- | --- | GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGTGGGAGACACAAAT/<br>C/GAGTAATTAAACAACATAATATTTANATGACAGTGCAATTAATTAACTCCTGGTAAGCCAGAG<br>GGGAGGAGGGCGTCTTCA   |
| WI-22585    | 56  | A G --- | --- | TTTATTTAAATTTGCATCTGAGATAATAAAATTTATCTGACAAGTGAACAATG/A/G/CAGAAAGC<br>AGCAGTGAAGTTTCGGAGGGCAGGTATCCTTCATTTTGGCAGAGCTGTATATAGATTGA   |
| WI-21155    | 36  | A G --- | --- | GGGCTGTGGAGTAACAGAACTTGATGGAAATTTGGC/A/GJCTGTGTAGAATGATTTCTAAAGCTTTC<br>AGACAAATGGCAGA  |
| STS-F02766b | 88  | G A --- | --- | GCCTTTGCTCTTTGCTGTCTCAGAGGCCTCAGATGGATACGCAACCTTCTTTTGAACCTTTTAT<br>TTTCCTGGCAGGAAGAAGA/G/A/JGGATCCAGCAGTGAGATCAGGCAGGTTCTGTGTTGCACAGACAG<br>GGAACAGGC  |
| WI-19888a   | 98  | C T --- | --- | GGCAGGATCAACCCATAACAGAGAAATAACTCCTTATTGGAACAAGGTTTTATTTTATGATATGATG<br>AAATATTTTGGAACTAGAAAGTAGCAGTGA/C/TJGGACAACGTTGTAAAGATATTAATGCCACT<br>GAACTGTTCAITTTAAATGGTAATTTCAITGTTATGTTATTTTCACTCAATTAAGAATGGAACATGT<br>CTTATAATTGTAATACATGAGANCATATTTATGTTGGAAGTGAACACAAG |
| WI-21485    | 82  | C T --- | --- | TGAGACCATCCTCCTCAACAAAGATCAGTCAGTTTCAGCACTAATTTTCCACACTGAAGTCTACG<br>CAATTTTCATGCAGA/C/TJGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTTGTAATT<br>CATATCATCCGTTTCCAAA  |
| WI-20601a   | 125 | T C --- | --- | TCAGAAATGCTTTCCACTGCCCAACCAAGAAATTTAATGAATGCNCTTACAATTGAGATGACTT<br>GAAGTTAAAGAAAGGTACCTTCTTGGAGGTTGCATGACAGGATTAGTCTCTCTGTTT/CJCTGGT<br>GCAAGTTTGAACACAGTATTATGACCATTCATGATCAGAGCACTGTTTCCCTGTCAGATCCCCACTAG   |

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| WI-<br>20561b | 94 T C ---  | --- | --- | CGTTGCTTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTG<br>TACTTCAGATGAAAAATCCTTACATGTCGAGAAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT<br>NCATTTGAGGAGACATACAATTGTAA   |
| WI-<br>20561a | 25 A G ---  | --- | --- | CGTTGCTTATTAAAGATGGCTGTTTAAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTAT<br>TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT<br>NCATTTGAGGAGACATACAATTGTAA  |
| WI-<br>20116e | 69 T A ---  | --- | --- | GCCTTCATTTTGTCAACCCACCCCTGTCCACAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT<br>AAT/ATAAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA<br>CTAGGCTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA<br>GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA |
| WI-<br>20116c | 59 T A ---  | --- | --- | GCCTTCATTTTGTCAACCCACCCCTGTCCACAGTTATGTTGGCCTTCAATATATGGCGTT/ATAGAA<br>CATATAAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA<br>CTAGGCTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA<br>GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA  |
| WI-<br>20116a | 22 C G ---  | --- | --- | GCCTTCATTTTGTCAACCCACCCCTGTCCACAGTTATGTTGGCCTTCAATATATGGCGTTAGAA<br>CATATAAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA<br>CTAGGCTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA<br>GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA     |
| WI-<br>20466b | 133 G A --- | --- | --- | AAAGATTGCGAGTCTCTGGGACACAGTTTGGAAACACTATTTATAAGTTGACATATTACAAACAG<br>NTCCCAATGGTGAACTGGTATTTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGCJ<br>G/ATGTGAACATAATGTTTAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT<br>ACAGTAACACTACTTTTTATTTCTTGGCTTTTATCCCTTCAGGTTGATT  |
| WI-21444      | 39 A G ---  | --- | --- | CTGGGCGAGCAAGTAACCATTTTAAAGAAATCTCTCAACG/AGTTCTTTTATGGGGTATTTCA<br>GTTGTTAACAAGTTAAATACTTATTGGAACATAATCTTTGTTATTTCGAGGAAGAAGAAATCT<br>ATAAGATTGACTTACTACTTGTGACTGGTTTGTGAAGCCTTACTGGGG   |
| WI-<br>21034b | 148 T C --- | --- | --- | AGAAATGGACAATGATGCAGATGATTGTGAGCATTTTGATGAGAAAGTGGTATTAGAAGGATACAG<br>CATAAATTTAATTGTAACATGCTTATCTAGCTAACCTAATCTGTTCTGTAGAATTACTGGTCATGG<br>GAGATTGGATAGAT/CJGGCTAACCTATCTCAATTTTAAGTAATGTGAGCAA   |
| WI-<br>22091c | 205 G A --- | --- | --- | GGCGTATTGATGCAATGTCCAAACCAGTCAAGCTATCATTTGAATCCAAATATTTCCAGTAGAG<br>ACATGCAGAGCAATGTCAATGTAAACATACAGCATATTACCTCCCCCTTAAGTGACTCATAATTC<br>ATTACTTGCTGTAGCTTTTAAAGGTTTAAATGTTAGCATTAAAGTGGTATTACTTGAGGGCA<br>ACA/G/AAATTACGGCTTAACAACACACTAAATCATGAGGCTCAGGGATTG     |



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| WI-<br>21805a | 45 A T ---  |  |  | CAACTGCTCTGAGGCTTTCACTAGCTGATTTATAATCCTATATTATJAAAAAAAAATCTATAGTCTG<br>CAGTCTTTTGACATACTTCTCAAGGGTGGATATGTGGTGAATGCAGACTCCATCAATATGTGGT<br>TTGTTGCTTTTGTAGCTTAAGTCTGTTTAGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA<br>CATGGTTCATATAAATTCGAACAGTTGAAGGCTGTTTGTGTAATTGCTG             |
| WI-<br>21778b | 155 T C --- |  |  | AAAAATCCATAATTATTGAACCCCAAGTTACAGAGAAAGTTCGTAACCTTTTATTGAATTATTGAC<br>TCTGCCCGGTGTCGTTCTGCTCTTCAACTCCAGTCTGTCAATGCCCTGTGTAGGTGGGGTCCCCAG<br>GTCTGGGCTTCTGAGGTCCTCJGGTAGAAGGAGGECAGGTGGT  |
| WI-20907      | 241 A C --- |  |  | TGAGTCAGTGTGTCAGATGGGGCAGTTGCGTCAAGCTGCAGTCCCTGACTCCGGAAACACTGTGCTCT<br>CAATGATCTAGAGCTCATCTTGGGCGTACATGAGGGCAGTTGTTCTAGTACCCATTTAGCC<br>ATGGCTCTCAAGCCAAATTCACACTGGGAAACACACCCCTACAAGATGCCTATCCATTTGAGTTC<br>ATACAGGTTTGTAGTACTAGAACTAAAAACAATTTTAA/CJAATTATCTA             |
| WI-<br>21449b | 222 C T --- |  |  | AACAGCAGCAGTCACCTTCCAAAATGCAAAAAAATTACAATTTTGAATAAAAAATTAATGTTTA<br>TAATGCGGGTCAGAAAGANTGAAGGTACACAGATCAATCAACGACACTGGAGCGGCTGGAG<br>AAGCCAAAGCCCACTGTGTCAGGGGTCCAAAGCTGACAAGAGTCCCAACCTGAGAGGTCTCCACACCC<br>AATCATACCCCTCAGCTTCCCA[CJ]TGACAGAGCCAGTCTCTGGGTTAG              |
| WI-<br>21558a | 157 G A --- |  |  | GCTTACAAGGAAGCCTGTGGACAGGCGAGNTGGTGGAAACCGACTCCAGCCTGGAACCTGCCCTC<br>CCATCCCCCTTAGCGCTTCTGGCCTTCCGGCTGATTTCTTCGACAGCAGTCTGGCCAGGGCAAGG<br>AGCTGTGGTGGGGGCGAGT[G/A]AGCCAGGACTCCCTTCCACAGATGAGGCCCTAGGGCTGCAA<br>AAGGGCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGCTCTCCACC             |
| WI-<br>22187b | 178 G A --- |  |  | TTTGCTGTGAATCCATGAGAGCCGGAAGCATGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA<br>GTCCTGGGCCCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAAAACAAAAATACCAAGA<br>ACAGATCAGTTGCCATGGACATCAGTAATCTATTGGTAATGGTG[G/A]AAATTTTCATGAAAAATTTCC<br>CCTAAACCATAACAAAAACTGTCTCTCTTACCCCAAAAGTCTGGAGGAAAG |
| WI-<br>22187a | 110 C A --- |  |  | TTTGCTGTGAATCCATGAGAGCCGGAAGCATGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA<br>GTCCTGGGCCCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAAAACAAAAATACCA<br>AGAACAGATCAGTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTTTCATGAAAAATTTCC<br>CCTAAACCATAACAAAAACTGTCTCTCTTACCCCAAAAGTCTGGAGGAAAG      |
| WI-<br>21609b | 146 G A --- |  |  | TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAACGTGCAGTCCGTTACAGCTGTAAA<br>AACAGCCCCAACCCAAAGACATCAAGAGGCAAGAGCTGGCAGTGAGAAGGGAGCCTGTAAAG<br>GATGTTCAAAG[G/A]AGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGTCCAGGC<br>TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG               |

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| WI-<br>21609a | 42 C T ---  | --- | TCATGAATATGAGCGCTCCATAATCTTCTCCCTTGTAACAAAC/CTGTGCAGTCGCTTACAAAGCTGT<br>AAAAACAAGCCCAACCAAGACATCAGAAGAGGCAAGCAGTGGCAGTGAGAGGGAGCCTGTGA<br>AAGGATGTTTCAAGAGGGTCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC<br>TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG        |
| WI-<br>22512a | 104 T G --- | --- | ACATTCCGAGCGAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCTCCCTAGGGCTTCA<br>GGGTAAGCCCTGACATCATGGTCTTTTGTGATCTGT/G/ACCTCACCCATGTCTCCACACCTNAGTTCC<br>CACATTTCCCCACGCTAAGGGCAGGCAGCTACACTTGACTGCA  |
| WI-<br>21028b | 139 A G --- | --- | ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAGGGCTCA<br>CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTACAGGGG<br>TTTC/G/CTGACTGTTACAGAACACACAGGGGAGTTTCACAAATTTTTTATACAAATGCTTGGGAAT<br>CTACGG   |
| WI-<br>21028a | 121 A C --- | --- | ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAGGGCTCA<br>CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGG/A/C/CTATGTGACAG<br>GGGTTTCATGCACTGGTACAGAACACACAGGGGAGTTTCACAAATTTTTTATACAAATGCTTGGGAATC<br>TACGG   |
| WI-<br>18829d | 58 A G ---  | --- | ACAACATGCTGTTTACAGGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG/A/G/TTTCA<br>TCATACAAGACAAGCACAAAAGCACCACCCCATGCCTCTGAGGAAACATTGGACCATGCACCCCTTGAAA<br>AA   |
| WI-<br>18829b | 35 T A ---  | --- | ACAACATGCTGTTTACAGGGGGGAAAAATCCTAGG/A/ATAACTTATGTGTACTTCTTGATTTC<br>TCATACAAGACAAGCACAAAAGCACCACCCCATGCCTCTGAGGAAACATTGGACCATGCACCCCTTGAAA<br>AA   |
| WI-20964      | 87 G A ---  | --- | AGCCAACTAAGGCCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAGGA<br>GCACAGGTAGTCCACAGAATA/G/A/GACACAAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA<br>AAGAACTACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAAGGAAC<br>AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG |
| WI-<br>20059a | 59 T A ---  | --- | CTCTGAACATAAGGGCCGTGAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCAAT/AJACAT<br>TGGCTGGAATGAGGTGGTCAGGAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA<br>GTTCTGGAGAAAGTTAAGTGTAATAATTACAAAGACTGACATGCAACTCTTACCTTACATTATT<br>CATCTACAGACTATTTCTCCCTTAGGAGATGAGGAGTATGGCCTTAGGT         |
| WI-<br>22130b | 165 C T --- | --- | TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCCTCCCTCTCTCTGACAC<br>CAGCAAGGGGGAGGCCACCATCACCGGCCCTGCCCATCATGCAATCAATGATTACTAGCAGTAGGAA<br>GCCAACGGAANAGGACCCCGCGCTTGCT/G/CTGTTTAATCCAGGTTAAGCTATACACCGTTTAA<br>ATACATGTCGGAGGTTACATGGTCTCATGCAAGTCCCTGTGATGGGAATGAC     |

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| WI-21661  | 117 | G C --- |  |  |  | GCCTAGTCTCCACCCCTTTAAATGTACTGTAGGTACAAAATAAACATTATACACATATAAGATCAGT<br>CTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAAATA[G/C]TTTAGTCACAGTC<br>ACACAAAACACTACCTTCTAAGGAAAACGTCCAGTGAAGCCGTTAAATTTGTGCTTTTCAGCTATGAAG<br>GA   |
| WI-21980a | 25  | T C --- |  |  |  | TCAGTTAAACACATTTCATCAAGGA[G/C]AGATTAAATTAATGTGAGGTGAGCATAAAAGGGAGATTA<br>TAAACCAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTTATTAATTTTCAT<br>GGGTGAAGCCCTCGGATAAAG  |
| WI-21636  | 71  | A G --- |  |  |  | TGCTTGATTAAATGTGGTGTTCACATTATCCTATTTCACAGATGGAACAGAAAATACCAGCTTTTTT<br>AAI[G]TAGCAATATCTATTATAATAAATTTGAAATAACACCATATAATATCACTAAGGA<br>AGTAATCTAATTGTGTTGATTTGCAGAGGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGC<br>TCATGCAAACTCCAATCTGAAGGTGTGAGAACTAGGAAGGGACAGGGATTTC        |
| WI-22457a | 112 | G A --- |  |  |  | TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGA<br>CAACAGTAACATCTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACTAAAG<br>GAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAACTACCTGGGGCC<br>AAAACCACTGAACCTCACCCAGCTGAAACACACTGAAGGATACTGGGTAAAGGA |
| WI-21524b | 97  | C T --- |  |  |  | GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATCTTAT<br>AATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTCGCAATGGACTATTTGCC<br>CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC<br>CTGTCAGAAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG    |
| WI-21524a | 35  | A C --- |  |  |  | GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[AC]GCCTGATGTACGACCTTCGCGTCATACT<br>TATAATGGTTAATAACAGCATTCCTGTCTACCCCGATGATGCTTCTCTCGCAATGGACTATTTGCC<br>CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC<br>CTGTCAGAAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG    |
| WI-22652a | 32  | G T --- |  |  |  | TTACCTTCCAAACCAGGCCACTTTGGAGAAAAG[G/T]AAGAGAATGCTATTATCAATAAGCCAAAGAC<br>AATAGGGACTACCTGGGTAGACCAAGATGGGCAGTCACCATACACCATCATTCCTGCCACAGAACCC<br>TTTGACATGCTGCCCTCCCTACTCCGCACCTCACCTGTCTAATTTGGACCTGAAGCTTCAGCATCCCTT<br>CTTTAGGG  |
| WI-21703d | 197 | A G --- |  |  |  | CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTC<br>TGCAATCCCTTTCTCAGCACAGCACCATCTTCACCCCTCTGGGAAAGCAGCATTGGAGCCTACACCA<br>CTTGCTTTTCTCACCAGGGTAAGAAATGCAGTATTTCAGAGGGGAGTGAGTCTGGGAA[A/G]G<br>TGGGCAGAGCAGACTAGGGGCAAGGACTTAAGGGAACCTTTGTTGGGGAAGAG      |

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| WI-<br>21703c | 134 A G --- | --- | CAACAGGCTCATGTGAACAGAGCGTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTC<br>TGCATCCCTTCTCAGACAGACACCATCTTCACCTCTCTGGGAAAGCAGCATTTGAGCCTACACQ<br>A/GCTTGTGCTTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAAAG<br>TGGCAGAGCAGCAGTAGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG    |
| WI-<br>22663c | 139 G A --- | --- | CCCTTGTGAGTCTGTGCTCGCTTCTCACTGCAGTGGCAGGTGACCGGCGCTCGCTAATCTTATTC<br>CCAGTCTCGGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCAGCTGGTGCACTTACAG<br>GC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCCGTGAATCCGTGTTGAATGTGGGT   |
| WI-<br>22663b | 55 C T ---  | --- | CCCTTGTGAGTCTGTGCTCGCTTCTCACTGCAGTGGCAGGTGACCGGCGCTC/GCTAATCTTA<br>TTCCAGTCTCGGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCAGCTGGTGCACTTAC<br>AGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCCGTGAATCCGTGTTGAATGTGGGT  |
| WI-<br>22663a | 38 C T ---  | --- | CCCTTGTGAGTCTGTGCTCGCTTCTCACTGCAGTGGCAGGTGACCGGCGCTC/GCTAATCTTA<br>TTCCAGTCTCGGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCAGCTGGTGCACTTAC<br>AGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCCGTGAATCCGTGTTGAATGTGGGT  |
| WI-22668      | 99 A G ---  | --- | TCTTTTATCTGCTGCTGCTGAGTATTTCTGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATT<br>CCAACTAACAAATTAGTTTCTGTAATATTG/GTCTAGTCCATTTAGATTGTGTAATGATCTAA<br>ATGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTGAAGAAACTTTTATT   |
| WI-<br>22631a | 52 T C ---  | --- | AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTTCAGTTCGAT/CJAGCACCATTTT<br>CAAGTTTATAGGCAAGGTATTTAACCTCTCAGGCTCATTTTCTCTTTTGTAAAATTGTGATAATGGACC<br>TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTT   |
| WI-20258      | 157 G T --- | --- | AATCCACACTTTCACGGAGGGGAOCAGCCTGCCATGTCTGCCAGGCTCACAGCAGCGCGGCTAC<br>TCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGAOCGGCAATTGGAACCGTAAGGCATGACAACG<br>GGAGCCCGCGGGGTGTTTCA/GTJCGCGTTGACGAGGTGCATGGCTGGCAGCGGCGCTCTACAGA<br>AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAGTACC    |
| WI-22714      | 212 C A --- | --- | ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAAAATCTAGGGTCT<br>ACTAAATAATCTAGTACTTGTTCACCTCTCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAAGT<br>CTGAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT<br>ACCAACCCCA/C/ATGAGTAGGGGGCAAAACATCCTTAACAAGTAGTTGCT |
| WI-<br>22734a | 44 G A ---  | --- | TGGGGCTACTTTAGATGGGATGGCGTCAGGGTCTGGGAAGCCCTG/ATCTTTAGAAGACATTACCCA<br>AATGATGAGAGGCAGCCAGTCTCGAAGCCATAGTTTGGATGGCGAGACTTTCCGGCAGAGGAAAT<br>AGCAAGTGCAAGGGCCTGAGGGAGAAATGAACCTTGGGCTTGTCTACAGGGTGAAGGGCGGCGGT<br>NTGGCTGAGGTTTAGTGGATG                               |

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| WI-22724  | 117 A G --- | --- | --- | TGATATGATGCTGAGATTGCTCCAAATATGCCTAGGAAGGGAAGTGTATTAGAGATATAGGA<br>CAAAATCAAGATTGTCAAAATGTATAGTAAGTGTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT<br>TGGGATATGTTGGGAATT   |
| WI-22750  | 48 G A ---  | --- | --- | TGTAACCTGTGTTTTCCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAA[T/G/A]GGCTCATACAAAGGT<br>TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTCTGACCATTCTGACTGTGCT   |
| WI-22775a | 60 A G ---  | --- | --- | TGCTGTTTCTTTAGTTTCATGACGTTTATCACAATGTGCTACTGTTTCCATTGTTACATCA[G/T]TAGTA<br>GGAAAGGGGAAATAAACTCCCTAAGGGCAGCAATAATTTCTGCTTTGAATCCCTTCATTACAGGCAAA<br>TATTTGTTGAGCACCAAGGGCCAGATGGGAAGTGGGATGATGAGGTGTTGGGAGCCAGGAAAGGAAG<br>GGT  |
| WI-22808  | 143 C T --- | --- | --- | CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCAAGTCCTGAGGGAG<br>CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGCTTTAGCAACCAGGA<br>GGATGAAGA[C/T]AGCAAACTGATTAAAGAGAGTAGGTATAAGAACCAGGGAGAGTGGGGTCCAAAT<br>ATC  |
| WI-21016  | 207 G A --- | --- | --- | TCTCTGCTGCTTGAGCCCTCATCCCCACCCCTCCAAGCCCTCATGCCACACACCGTGTCCCACATT<br>CCCCATCCTCCCTGTCTGCTCCCCATCTCAAGTCCAAATCCAAGGCCAGAGCCCTGGCAGCTTTTCTG<br>GGAGACAGCATGAAAGGAGGGAGTGAGATGGCAGAGATGGGTGGAGCCAGTGGCTGTGGGTC<br>CT[G/A]TTGGCTGGTGATGGGGGCCAATCCTGAGGCCAGAGTTCA           |
| WI-21031  | 31 C T ---  | --- | --- | TTGAAACACTGACCTGACCTGACATGGG[C/T]CTCTGGTCCCCATTTGTCTCCAACGGTGGCACA<br>TCTTCATCTTTGTTATATATCTGCAGGAACACCTCAGTCTCTTCAGCAGCCGAGAAAACACACACA   |
| WI-21314  | 122 A T --- | --- | --- | CCATATCCAGTCTCTTTGAAGCTTTCTATTGACTTTTAGGGTTCAGTTATTATATCTTATCACTAT<br>GACTTTCAATTTGATTTTATTTATTTGTTCTCCATTTCTGTCAAACCTTT[C/A/T]TTTGTATTATAA<br>ACTGTTTCTAAACTTCACCTTAATCTCTATCTGTATTNCTTGTAGTCCCTGAACCTCTTTTAGAGG  |
| WI-21186  | 95 G A ---  | --- | --- | AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAACAGACTCTGGACCCAAACCCAGAGCTTCT<br>GATTGAGTAGGCTGAGGTGGGCTTAC[G/A]AATTAGTATTGGAAGACCTTCCCTAAGTGTGCAG<br>ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTTTAAA<br>GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATATGTTGAAT             |
| WI-21187a | 94 A G ---  | --- | --- | CCACGATAACTATAAAGCAGAAAATTAGCTTTGAAATCAAAATAACATATTATTAGTAACACACATT<br>CATTTTTATAACACACATAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCCAGGGTTCTCAA<br>AGTATGGCTTCAGACAAGCCCCATTTCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC<br>CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT |

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| WI-21190  | 39 T C ---  | --- | TTTTCCCCACATACCAATGCACCTGTTGTATAACTATT/CJGTGGGGTAAGCCCTCTTTGGAGAC<br>CAGTGACATAGACATGATCCCATTTATTTAACAATAATATTATTAATCTGTACTATTACTGC<br>TTTAGTTATCTAGTGTATTGAGAAAGGAGAAGTCAGCATAGTTTATTTCCATGTATAAAGCTT<br>AACACA  |
| WI-19937d | 186 G A --- | --- | ACCATGTGCATTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA<br>GAACTATTGCACAACCAACATTTGACATATCTGATTTAGACAAGCAAAAGCACTTTCATGTTGTCT<br>GTAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCCTCAGCAAGTC[G/A]TCCAAACCTTC<br>CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCGCTCAGGAAGAA |
| WI-19937c | 185 C T --- | --- | ACCATGTGCATTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA<br>GAACTATTGCACAACCAACATTTGACATATCTGATTTAGACAAGCAAAAGCACTTTCATGTTGTCT<br>GTAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCCTCAGCAAGTC[G]GTCCAAACCTTC<br>CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCGCTCAGGAAGAA  |
| WI-2117b  | 227 C T --- | --- | GAAAACGGGGTGCTAAACAAGAAAGTCTCAGATCCCACTGAAATCTGTTTCAGTTTCACAGGCTC<br>TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAATACATTCGGGG<br>TCCAATCAGATACCTCAGGTTTCAGACTCTAGTCCCAATATTCACAGTCTGAAGANTTAGCAGT<br>CCTCTCATTTCTACAGTCTGTTTCTTCTACTGAATCTGGGTGGGAG           |
| WI-21122a | 42 C T ---  | --- | TCACITTTGATCATAATCCCTGTAAAAGCTAAAGTTATTCA[C/T]TAACAGGAACCTCTGTTTTCC<br>TTATTCAAATGTCACAAGCTGACGCTTACTGTACATATTGCTAGCAGGAGACAACCTGGAATACT<br>AAACAAATCTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT<br>TTGTAGGTTTCACAGAGAGCCTATTTGTGGGTGCT                    |
| WI-21254  | 53 A G ---  | --- | CAGTTTGGTACAGGAAGGGCCCATGAATGTGGCGGAACATTTCACAGGAG[A/G]CAAGGAGAAG<br>CTGTTCTCTGG  |
| WI-21054  | 23 G T ---  | --- | AAGGAAACTGCGATGGGTACAAAT[G/T]TCCAATTTCATCTTAACAAGGTGGGGAACGGGTCATTCT<br>TGGCCTGCTCCAGAACAAAGGGCGAGTCTATGCACTCTG   |
| WI-21059b | 181 T C --- | --- | GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTCCCACTGAGCCTGGTGAA<br>CTACAGCTGCCAGCATTTCTGGGCTGCAATTTCCAGCTTCGTCACATCTTAATTTCAAGCTGAAA<br>AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTCTCTATTCT/CJATTGTAGCCAGGGCAAAA<br>TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT    |
| WI-21059a | 63 C T ---  | --- | GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTCCCACTGAGCCTGG[C/T]<br>GAACTACAGCTGCCAGCATTTCTGGGCTGCAATTTCCAGCTTCGTCACATCTTAATTTCAAGCTG<br>AAAAATCCTGGGAAGAGACATACTTCACTGAAGTCATTCTCTATTCTATTGTAGCCAGGGCAAAA<br>TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT    |



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| WI-<br>21627b | 153 A G --- | --- | GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG<br>TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCAATTATGGATATTTATGCTAGGAATGACAA<br>CAGTAAGGGCATTGCAAA[A/G]TCCAAAGTCATCTAATAATTAACCATATTTACATAAATTTGTAGG<br>GACAGTATACTAATACTACATAAATAAGGGTTTAAAAATGTGTGCTTA  |
| WI-<br>21627a | 106 A G --- | --- | GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG<br>TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCAAGTATGGATATTTATGCTAGGAATGA<br>CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATAATTAACCATATTTACATAAATTTGTAGG<br>GACAGTATACTAATACTACATAAATAAGGGTTTAAAAATGTGTGCTTA      |
| WI-<br>21399a | 75 C T ---  | --- | GGATTGAGTCCCAACTTGATCTCAAAATTCACCTCTTGATGTAACCAAGCTCAATTCCTCTAAAGTT<br>TCAGTTT[C/T]TTCACCAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTCCTTGGTAA<br>CTGCCCTCTGCAATTTGCTCTGAGGTTGTGTGCTGCTAGGACTAGGAGGATCTCTCTGCTTTCTGCC<br>TTACCTAGGCATAGTGCCCTGATAGCAGGCTGAAGGCCCAATTCATCTTGT |
| WI-<br>20323a | 68 G A ---  | --- | CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGGTGGGTCACAGACAGACATCAAT<br>C[G/A]TCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCCAAGAGTACAAATCCCATCTATGAGAC<br>AGCAGTGTGGCTTCTTAAACAGATAAACCAATCAAAAGAAAGATTTAGAGGTTTCAGACATT<br>AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGGAAGGCCCTCACT            |
| WI-21249      | 155 T C --- | --- | TTCTGGCATTCAAATGTACATGTAAATCCAATTAACAGATCAAAATGTTACACTAAGTTTCACT<br>TAGTATCTAAGTATCCAATCACAATGTATCTAAGTTTCACTTTAAGAAACATTATAAAGGTAAT<br>AAACTCTAGGTGTACTT[A/T]CJATGGAACAGTATTTTCCNATTTAACTACTGTTCAATTGCCGTA<br>AAGTATGTTGCCCAATTTTCAGCTGTTTAAAGGAATTATAAACATTGAGA       |
| WI-21504      | 147 C T --- | --- | TGACACAGCATCAATTTTCATGAATACTTTGAAAGGGCCATTAGAAAAATAAGAGCCAAATTTGGGTC<br>ATTTGAGAAACATTTTCAGCACAAATACAGTGGGGGCACGGCCGTTCCGCTCCAGCTGGGTTTCCOC<br>AGATGCAACAAT[C/T]GCGGTTCTGCTTCTCCACTGTGGGGATGGGATCGCGCTTCGGAGCTCT<br>CAGGG   |
| WI-21242      | 115 G A --- | --- | CTGCACAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGT<br>CTCTATGGACCGAGGCCCTGAACCGCGGCAGGGAGGGGCAGAGAAC[G/A]CACTAGCTTGGGGGTG<br>GGCACCAGCTTCAGACCCCTT  |
| WI-<br>21475c | 181 A G --- | --- | TAGCCCTTCTGCCAACATCTGGCAATNTGAGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG<br>GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTCACTTGTCTACTAAGCACAG<br>CAGTCTGAAGCTTGGGACTGGGCAAGTGCCTTTTGGAGAAAGGCA[A/G]AAAAAGCCACAGCAAC<br>ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCCTATTTCCTCCCTGAAG  |



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| WI-<br>21475b | 117 | A T --- | --- | TAGCCCTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGCCCTGATGTTGCCAGGAGTAG<br>GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTC/A/TCTTGCTTACTAAGCA<br>CAGCAGTCTGAAGCTTGGACCTGGCAGTGCCTTTGGAGAAAGGCAAAAGCCACAGCAGCAAC<br>ACTTAGGAGCAAGACCTTCCCGTTCTCCACCCTATTCTCTCCCTGAAAG           |
| WI-<br>20893d | 207 | A G --- | --- | TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAGGG<br>CTGTCTTCGGCGTTAAAGTCTACTGAGGAATACAATCATTTGTCAGTAAAGTTATCATCCCGCACTCC<br>AGGTCAGGCCAAACCTTTCGGTGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT<br>TTC/A/GIACATAACATTGGTAGAGTAAACAACAACCAACCAAGCCTAAATG          |
| WI-<br>20893c | 179 | T C --- | --- | TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAGGG<br>CTGTCTTCGGCGTTAAAGTCTACTGAGGAATACAATCATTTGTCAGTAAAGTTATCATCCCGCACTCC<br>AGGTCAGGCCAAACCTTTCGGTGACCTGGGNAACCTGCCAT/CJTTCCTCTCTTTTACAATGC<br>AGTTCAACATAACATTGGTAGAGTAAACAACAACCAACCAAGCCTAAATG           |
| WI-<br>19941c | 71  | C G --- | --- | GAGCTCAAGGGAAGACCCCTTACCAGATAGGGACTAACTGGAGGGTGGAGGAAACAAGGTGAAA<br>GGTATC/GGGTCTGTTGAGACAAAGCAGGGGGGCTGAGAACACAGAGCAAGGTGGTGGAG<br>GGAGCAGCAGGGTGCAGGAAGGGAGATGGGGGACATTCCTATTCAGTGATGCCCTTAAAT<br>AAACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAAGACAAAGCG                   |
| WI-<br>21552b | 166 | C A --- | --- | TGGGTACATGGACAGATGTATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG<br>TAATAATTACTTCAGAGTAAATGCGATCTCCTCACCTCAAGCATTTATCCATAGTTTACAAGAA<br>TCCAAGTACTCTTGATTATTTAAAAATGTAC/A/AAATTAATTTATTGAATTTAGTTACCCC<br>ATTGCTATCAAAATTCATCTTATTCATCTTTGTAACATTTATTGTGA                  |
| WI-<br>21552a | 66  | G A --- | --- | TGGGTACATGGACAGATGTATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG<br>/A/TAATAATTACTTCAGAGTAAATGCGATCTCCTCACCTCAAGCATTTATCCATAGTTTACAAG<br>AATCCAAGTACTCTTGATTATTTAAAAATGTACAATTAATTTATTTGAATTTAGTTACCCCA<br>TTGTGCTATCAAAATTCATCTTATTCATCTTTGTAACATTTATTGTGA                |
| WI-21512      | 54  | C G --- | --- | TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGTC/GITAGAGAGGA<br>AAGAGCTGGTGCCTGCTGAGGCAACGTCAGGTCGGGAAAGGCACTGGTGGTCTGTGATCTGTC<br>TCAGTGATGGGAGGTCTCACTCGCCCCACAGGAGCCCTCGGGGCCAGAGATGAGAAATGCTGTAA<br>TCCAGTACAGGGGCTGGTGGTGGGGTCCCCAACAGCTCTCTTTGGGGG             |
| WI-<br>21513b | 192 | G A --- | --- | CACATAGTTTCTCAAGAAGAGGATGAACCTGAAACTCCTCTAAGCAGGAGCAAAAGCACTTCCATT<br>ATTCTTAGTTTAGACCAGAAATCTTTAATTTTATATTTCTCTTTAATAACTGTCAAAATACACCAATA<br>CTTAGAGGAAATATTCACAGTATACCAAAACATTTTAAAGATAAAGAGGCAAGTGTAA/G/AJAGTAG<br>TATTCTCTACATACCACAGTACATAATGATGCCTTCTGTCAGGTTTAGGAAC |

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| WI-<br>21514b | 133 C T --- | --- | --- | TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTGTGATGAGCTGACAAGCATAG<br>AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGCJC<br>/TACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG<br>ANTTTAAGGCTCAGATGGGTTAAGGGTGAATTTGTCAAGGGTCATAAGGAACT     |
| WI-<br>21514a | 100 A G --- | --- | --- | TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTGTGATGAGCTGACAAGCATAG<br>AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGGA<br>GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG<br>ANTTTAAGGCTCAGATGGGTTAAGGGTGAATTTGTCAAGGGTCATAAGGAACT       |
| WI-22020      | 27 C G ---  | --- | --- | ATGAACATGTTGCAGTGGGATGAATTC/GJTATCATGATGCTAAGTGAATAAGCCAGACACAAAA<br>AATCCAAATGTATCATCTACCTGTATGAGGGTACTT   |
| WI-<br>19576a | 113 A G --- | --- | --- | TTATCGGTTCTTAATACAGTACAATCCTTTTGTGAAACAAAGTCACACTGGCAATGATTATTTACA<br>GATCCAAATAGACTCAGGCTTCAGACATAAAATTTAACATTCTA/GJTCTAGTTCAGTGATTAGT<br>CACAGAAATTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGA<br>G  |
| WI-<br>21695a | 141 A C --- | --- | --- | ATACACAGGCCACAATTGCAGGATGGAAGGACGTGGGCACTTGGAAAGTGAAGTACTACACATGGCAATA<br>AGCAGCCTATCTCTTACCAACCCAGAGTTCTTGGGGCATGTGATGTAGGCCAGACCCCTTTCCAA<br>GGGAATA/CJTACTACACTAAGCCTACACTGTACTGTGAGAGTCAATGTGTGAAACAAGGCCACAGGC<br>AGTGGGAGGAAATGTGATGACTTCACTGTGTTCAGANTTCTAAGGCCCCAGCAT |
| WI-<br>21574a | 235 C T --- | --- | --- | AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAACTCACTATACTAGGAAGCAACTTATGAGTG<br>TGTAATATTTGATCTAGCAGCAACTTTCACCTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC<br>TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT<br>GGGCAGGCCAGGGAACCTTACTGCCCTACTTCCJCTJTGCTGTGAGGTGGGA   |
| WI-<br>21644c | 151 T A --- | --- | --- | TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACCTTAACCTTTCAGGAAGTCTTGGGT<br>GTGACCCACTGCATAAATGGATTTTACCATANATTTAACAGACTCAAGTGTACATACAAGCTTG<br>TTTCATAAATAAGGGAIT/AJTTCAATCAAGATCCATGGAAATGATGCAGTTAACATGTGTTCTCAGC<br>TTGCCTACTGACCACCTTTCCTTTCTAAATATGGCAACAGCACAGCAAGTC          |
| WI-<br>21614b | 55 G A ---  | --- | --- | TGCTTTAACCTCAAAAGTCCAAATAACATATAGACATTTTGANTATAGCTATC[G/A]TTTTAAACA<br>AACCTCATTATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTAATAAACA<br>TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGATTTCTAAGGTACTAGGGAGTT<br>GGAAACAGCTACTACGGGTCAATGGTATTTGGGCAGTTGGCTGTGTGGG            |
| WI-<br>21615b | 151 C T --- | --- | --- | GACCGAGAAAACCTGCAAGGCATATGATGTTTGTGGAAGTATACATGACTATTTCAAGCTTATAGA<br>GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTCATACATATTAAGATAAGGATGGACT<br>CTTTCAGTGAATATTATTC/TAGGACACAATCGACGGATGTAATCTATTTTGANTTATACCATAGGCC<br>TATTCTATATTGGCCAAAGGGAAGGTAGGATGGGTACTGTGTGGAACGGA         |

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| WI-21981  | 61 T A ---   | --- |  |  | TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTTCTTGAAGAAAAAAATTTAAGTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAACATGCATGGGATAGA<br>CACTCTGTTCTCTACAGATCCGTCTTTGGGAATTACAGGAACATAAAAGGATATAATGGATGGGTT<br>ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTGG    |
| WI-21660  | 120 C T ---  | --- |  |  | TOCCAACCTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCCTCTCCACTGCTT<br>TACTGTGTGTACCAAGAGGAGGAGAAAGCAGCTCACCCAGCCTAACCTGGCC/C/TJTGCTCTTTTTCAG<br>GCTTCTCAGGATGCCACAGACACATAGTGGGGAACCTGGGATGCAGGAGAGAGCCAGGGTCTGTCTTC<br>AGGAGGGTCCACAGC                           |
| WI-19105c | 211 C T ---  | --- |  |  | TGGAAGTAGCCCTTCTGGACAGAAAGAATATTTGTGGTCCATGTGGTTGAGTCTGTTAAGAAGGA<br>CACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTT<br>GTCTGATAGTTTCCAGGGCTGGCCACAGAGGTGAGGCGAGAATNTGGGGTCCCAGTGGATCTCCCC<br>ACAACTTC/C/TJTCAGGGGCGAGGATTTCCACCCAGGGGCCAGGGTGCCCCG |
| WI-19105a | 33 T C ---   | --- |  |  | TGGAAGTAGCCCTTCTGGACAGAAAGAATATTT/CJGTGGTCCATGTGGTTGAGTCTGTTAAGAA<br>GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTC<br>CTTGCTGTAGGTTTCCAGGGCTGGCCACAGAGGTGAGGCGAGAATNTGGGGTCCCAGTGGATCTC<br>CCACAACTTCTCTCCAGGGCGAGGATTTCCACCCAGGGGCCAGGGTGCCCCG  |
| WI-21760c | 81 C A ---   | --- |  |  | CAACCTTAGTCACTCTACTGATGCAATGATTTGGAGGTGTCTTCTAGCTTTACAATAAGNGGAGG<br>GACCTCTGACTGCA/C/A/CCTCTGTCTCAGTTTCAGGGCA  |
| WI-21760a | 35 A G ---   | --- |  |  | CAAACTTAGTCACTCTACTGATGCAATGATTTGG/A/GJGGTGTCTTCTAGCTTTACAATAAGNGG<br>AGGGACCTCTGACTGCACCTCTGTCTCAGTTTCAGGGCA   |
| WI-21569b | 198 T C ---  | --- |  |  | TCTGCCATATTGTTCCAGCACCACTATTACTGTTATTTCTCTTTGAGGAAAACCAGGNATTAAG<br>AAATCTGGTTTGAATTTCCATGATGCCTAACTCTATGGTTAAAAATCCTTTTCTTACCAAAAAGGA<br>ACTTCTTAATCACCAGAGAAACAGAGGGAGAACTGAGATATGTTGCAGAAATTTATCTCTACT/C/J<br>AGAGACAATTCATAGTTCATAATCTTTCAGGGTGTGCTTTACTTGGGGGGC    |
| WI-20934a | 72 T G ---   | --- |  |  | CCACATGCAACATAGTCTTCATTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA<br>GAGAA/TJCTAAGACAAATGGTCAATATTTCAATGGCCTGGCACTAGTGGTAATTCAGCAGAG<br>AAACAGCATGAGAAAAGGCCGGGAGACAGTAATAATACGTGCCATTTGCAATGAGTTACCCAATC<br>AAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCNTTCCCCAGGAGA     |
| WI-21561  | 55 T T G --- | --- |  |  | TTTCCATTTTATCAGCCGGGCCATCAGAAACATAGCATCTATACCTTCGAACCTT/GJCCTCTTAAC<br>CTCTCCAGGCAAGAAAGGAAAGTATGAAATCTCAGAAATGGTGGGATCTCAAGACTT<br>TTTAGAAAGTGCTTATTAGATATAGAGGCTTGAATATATATGATGATAAATGGTAGCCCTTTCTGGA<br>AATAATTTTGTGTAATCTGTTTAAAAAGATTTTGGATGCATTGTCCCCA            |

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| WI-21961c | 200 T G --- | --- | AGCTTTGCTTGAAAATTTGGTACTACTACCTTTGCAATCTCTTTATTATTATTATTACTTTTATTTTCCGTAAGTTATTGGGTACAGGAGTATTTGGTTATAAAGTCTTTAGTGGGATTTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACCTGGTCTTTTATCCCTCGCCCCCT/GJC   |
| WI-21961b | 73 G A ---  | --- | TCCACTTTTCCCCTCAAGTCCCAAAGTCCATTGTATCATTCTTATGCG<br>AGCTTTGCTTGAAAATTTGGTACTACTACCTTTGCAATCTCTTTATTATTATTATTACTTTTATTTTCC[G/A]TAAAGTTATTGGGTACAGGAGTATTTGGTTATAAAGTCTTTAGTGGGATTTGTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACCTGGTCTTTTATCCCTCGCCCCCTC   |
| WI-21956  | 26 T G ---  | --- | TCCACTTTTCCCCTCAAGTCCCAAAGTCCATTGTATCATTCTTATGCG<br>CCACTTGGGTCTCTTTCAAGTGAAT[G/J]TCCCTTCGTTCTTAAAGCCCTTTTAAATGAACCTTCATTCCCTGTTCTGAACTTGCCCTAGTCTGTTTCTGCTTCATCCCTCAGTCGAATCTTTCTTCTGAGCGGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGTTGACGCGCGGTAACCTCAGGGTAACCTCTATCTTCCACCCGGTAACAGAGGGTTACATTATGGGGTCCAGGTT   |
| WI-21966  | 148 G A --- | --- | CAACATACATTATGGTGCCTTTATTTAAGAAATGTTTACTGAGAATCTGTACTGTAAACAATATTTTTGTAGAAGCATGAGTGAGAGTGTTGTGTGTGCGCGCGCGGCAAGGATGGCACTGAGGCGGATTGCAATGGG[G/A]AACAGGATAAAAGGTATAAAACTTGGTCCGAAATCTTTGCTTATTAACTTGGCCCTGCTCCTCACAAATGTTTCTACACTTAATTCATAAAGAGAGGTAGA   |
| WI-21930c | 146 G C --- | --- | TATACTGGTTTTGGTTACATGGATGAATGTCTAATGGTGAAGTCTGAGATTTAGTGTACCCATCACTGAGTAGTGATGATGTACCCAACTTGAGGCTTTTATCCCTTACCCTACCTCCACCCCTCCCATTTTGAGTCT[G/C]CATAGTCCATTATATCACTCTGTATGCCCTTTCATACCCATAGCTTAACTCCC   |
| WI-21139a | 165 T C --- | --- | GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTTCTGCCACTTAACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCCTCTCTGTGAAATGGGTACAA   |
| WI-20317b | 217 G T --- | --- | TGTGGGTCAGCAGTAAAGGAACTAATACAT[G/C]GTACAGCACTTCAGCACAAAGCCCTGGGCAACACAGCACTGCATGGAATACACAGGTAAACATTTTAAACAGTGGGGACAAAATTTAAGTACGTGGCCAGCTGTTGGTTGCTTGTGGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGGTTACA   |
| WI-22082e | 179 G A --- | --- | AATTTGTTCTCTTCAGTTTTTTCATTAAAGTAAATCTAATAGATGATATACATAATTACTGCAGATAAAACCATCATCAGAAA[G/T]TATTAATTAATTCATATTTTGAGGCTACTCT<br>CAGGACTTGGTTTGTCTGCCAACTGCACATAAATGTCCCTTTTGTGAGTTATGGTTGTGTGCGTTTTTCCTTTTGCATAAGAAATATGTCCATTATAGTCCAGAGGCTCTTGCTTTATCCGGATGACGGAGGTACACGGGGCGTCCGCTCAGTCCCGCGGAAAGGAGGTAT[G/A]CTGAACTGGGACGAGTCTACTCTCCCCCACAGGAGCCACGATTTCAAATCCTCTTTGTGCAACCTCT |

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| WI-22082b | 67 C T ---  | --- | CAGGACTTGGTTGCTGTCCTCCAACTGCACATAAATGTCCTTTTGTGTTGAGTTATGTTGTTGTTGTC<br>/TGTTCCTTTTGCATAAGAAATATGTCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG<br>AGGTACACGGGGCTCGCTAGTCCCGCCGAAGGACGTATTCGCTGAAGTGGGACGAGTCTACTC<br>CTCCCCACAGGAGGCCACGATTCAAATCCTCTTTGTGCAACCTCT           |
| WI-20993  | 139 A G --- | --- | AACACAACTCCATGCTTTCAAGATTCCACACCCAGATACTAAGACATATTAATAATTACAGCAAT<br>TAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAACCCCTGG<br>GCTTCTA/G]TAACAAGTGAGTATACATTAAAGACAGTATTGCAGAATGGCTTCAGGATTAAATTTGA<br>TTAATTTAGAGAGAGGCTATTTCAGGCTCTCCTAGCTCATCCACACATCACC   |
| WI-21723b | 125 A G --- | --- | AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAAATAATATTTCTGAAGATAACAATT<br>TGGACTTTAAGCTCGACATAAAATTAGTACTTCAAAAGGGTAGTCATATTTCCCAIA/G]CAACA<br>GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAATC<br>ATT   |
| WI-21723a | 82 G A ---  | --- | AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAAATAATATTTCTGAAGATAACAATT<br>TGGACTTTAAGCTC/G]ACATAAAATTAGTAGCTTCAAAAGGGTAGTCATATTTCCCAACAACA<br>GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAATC<br>ATT  |
| WI-22132  | 99 T G ---  | --- | CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAATTGAGAAATATCTTCATGTTTC<br>AACCTTTAATCTGACTTGCTTTTACTATCCTT/G]CCCCATTTCTCTAATCTCTTTTGCTTACAA<br>TATATTACCTTCTAGGTATCACCTCATCTATAGGAATGCCTCTAGTTTAAATGCTGCCCCAAACA<br>ATACTAACCCATTGAAGGATACTATGGAACCTTTAAATGGGACAGTGGG       |
| WI-21006a | 106 A G --- | --- | TGACAGATCACACCACATTTGTTTGTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA<br>GATTCTTTAAAGAACACATACACACATGTGCACACAC/G]AGAGGGCAAGTACAAAATGTAAACC<br>CCACCAAGTGCTATGTGAATGAAAGTGCAAAAAGGCTTCATTTGCAAACTCTGAGGATCATCTCT<br>CTGCTTCAGGAAATTAACAGAAAGGCTCCTAACTGCCCTAGGCCT          |
| WI-21761b | 138 C G --- | --- | CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGCTTGGAAATAACTGAAAAGATTCTAT<br>TTCTCTTTGTGTACAAAGGATTCAAAATATTTACATCTCTCTGCCAGTTAAACGTGCCGTGG<br>CTC/G]CAATACACACCAAGCCAAAGCGTAACTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG<br>ATGGTA   |
| WI-21079c | 166 G A --- | --- | AATGAAAATGCCACCCAGAGTTAACAGCTTGCCATGCATGCACTGTGTGCGCAAAATCAAGTTGT<br>TTTAATACCAAGTGTGCAGCTTTGATTCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACATAA<br>CTCAGGCGACCCCTGAAATATCTGCTAGTGGG/G]A/AAATTTACAACCCACTGACCATCTCAGCTCAAA<br>GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGCAAT |

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| WI-21079a | 50 G A ---  | --- | AATGAAATGCCACCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG/AJCGCAAAATCAAGT<br>TGTTTAAATACCAGTGTGCAGCTTTGATTOCTCATGAAATTAAGCTGTGTGCTCAGCTTGTITACA<br>TAACTCAGGCCACCCTGAAATATCTGCTAGTGGGGAATTTACAACCCACTGACCATCTCAGCTCAAA<br>GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT  |
| WI-22129a | 45 T G ---  | --- | TCGTAGATTTAGCCATGCCATATATTTAACTTTTAAAGGAAAAGT/GJTTATATAACAGTCATTGCT<br>TGGTAGAATCCAGTCTGTCATAAGTTAGCTTAACAGTTAACATTGAAGTCTTATACCTTATATTTA<br>AATGTTTAGCAATCTCTACTACATTTTCAAATATAAATAATTTGGTTGCAAAATCCAGNAAAGGGCA<br>TTAACCAACATGGGACTGATCTGGGGGCTTCCACCTGACTAAGGTTTTA |
| WI-21941  | 79 A G ---  | --- | TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAGGACTCGGAAGATGTTGATCCAGGGCAGAGT<br>GAGGGCAGACI/GJGGATGAGGCTCTTCTGTAAGTCCAACAGACGCTCAGAGATGCTGGGAGGCT<br>GGGACTGCCAGTTGGGAGCCTCACCCAGAGAGCCTCACTGCAATTGACCCACACCCACCACCTCAOC<br>CAGCACACAGGCACACGCGAGGGCACACGACACAGNTGCACCTCACACGGC |
| WI-18916b | 42 C T ---  | --- | AATGGCATCCTGTGATACCAAAACATCTTCAGCAGCTCAGC/CJTGJGCTTCCCACCTCTTGGTACCC<br>GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCAOC<br>AATGCCACCTTCATA   |
| WI-18916a | 35 G C ---  | --- | AATGGCATCCTGTGATACCAAAACATCTTCAGCAGCTCAGC/CJTGJGCTTCCCACCTCTTGGTACCC<br>GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCAOC<br>AATGCCACCTTCATA   |
| WI-19828c | 200 A G --- | --- | TTCCCTTCTCCCCAAGAAGTGGGCAGAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA<br>GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCAGGNGCTCTGGCCCCAATCTGGGTTCTCCCCAAG<br>CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCTGACCTCACCACCCACCCAAAAT/A/G<br>JCCTTTAATCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT       |
| WI-21863b | 47 C T ---  | --- | CACAAGTCTGTACAACCTTAGGCACACAGCCCTGGCCCTGCCCCTC/JAGCTGCATGCCACCTC<br>ATATCCACCCCATCCCCAGCCTCTGCCCCGACACCCAGGCTCCCTGCTCTGTTGAAGTATTTT<br>CTCCAAGGCAGGAATGAGTCTTGATCCAACCCACAGCATCT  |
| WI-19860  | 51 C G ---  | --- | TTGACCTAAAGCCTAGCATAAAATAGCTAAGTAGAATGTTTCCAAAGATG/CJGJCTGCATCAGTAT<br>CTCCCATCCACATAATTTCTGTTGATTTTGCCATTACCCCATAAATGGTGGGATCTACCTCCCCT<br>CCTTGCAAAATTTGAGCTGGNCTCTGATCCTGCTAAGGATCTGAAGC.  |
| WI-19889b | 80 C T ---  | --- | ACCAAGCTCCTTTACCTCTGGCTTTAGTAGGCTTTGGCTAATGGCCANTGAACCTGCAGGGCAAG<br>AGGAGTGAGGGG/CJTTACAGCATTTATTTCCCTCTTCACTCCCTGTAGCTTTGGTAGTGGCTGTAT<br>TTCTCTACTGATAGTTCCTTGGCCACAGTCGTAACCTATTCG  |

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| WI-19891c | 172 | C | G | --- |  |  | TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAATTGCTTGGTGGCCCCCTCCCCCCCCG<br>ACTCCTCTGTCTCTGGGAAACGTGGCTTTGNCCTCCAGACACGTGTGCAGATGCCAGCTCTCCTCAGCGG<br>AGTCCCGATCCCTCAATTTGCCATCTGTCTGACTC/C/GJGCTCTCCCGGGCGTGGGGCGTCTGTGT<br>CAGGCAGCGGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG |
| WI-20155a | 81  | C | T | --- |  |  | GCACCTGTAGGGGTGTAGCTTCCATGGTTCTCCAGCACGGGTGTACATTACCTTAGGCTGACCAT<br>TCCCTTGGGGGGG/C/JGCAAACTGCTTTGAGGAAATNTCCAGGAGGAATAAACTAGAAGACGC<br>ACCTGCTATTTACCATACTATGGAGAAATACAGCTAATGAAGTGGTGGCAGAGCTTGGCCGTGTGA<br>GTGCCCGAGGGTAAAGTCTCTCTCTGTCCAGTCCAGAGCAGAGACTTCTC     |
| WI-20270b | 91  | T | G | --- |  |  | AGCCATACAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGGCTCAGTGTACAAT<br>ACATTTCATGTCAGGATAAGGAGCAIT/GJACACCAGGATTTATACACGGTGGCAGCGGTATAGGCA<br>CGATGATACAAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT<br>GGGTGATCTTGTTCCTCCGAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA   |
| WI-20270a | 53  | G | A | --- |  |  | AGCCATACAATGCATTGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGG/C/JTCAGTGTAC<br>AATACATTTCATGTCAGGATAAGGAGCATACACAGGATTTATACACGGTGGCAGCGGTATAGGCA<br>CGATGATACAAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT<br>GGGTGATCTTGTTCCTCCGAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA     |
| WI-20622  | 130 | T | C | --- |  |  | CCACTTCAATATTTACAAATGCTCAGCAGCAATATGAAAAGCTTCAACACTTTCCTTTGTGTA<br>ACTTGTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAAT/C/J<br>TACTAATTTTATGATGTTACTCATATTTTATTCATATACCTTTAATGACATCATTGCCAAATACATA<br>CATTATTTCTNTAATTTATTTTACAAATAGCCAAACATCTGTGCATGAG      |
| WI-20768b | 190 | C | T | --- |  |  | TCCACTCAAAACTCCACCCCACTTCCCTGGAGGCGAGGCTAACAGGACCTCCTGCCTGCCTGC<br>TCACGACTGATTACTTCAATCCAGCTGCAATGCAACTGAAACTGAACTCATCTGTATATCACCACCTA<br>CAGGAGAGGTCATTTCTGGGCAACCCAGAGNTCAGCACACATCTGCTGGG/C/JTCAGGGACTC<br>GTAATTCGCCTTGGTCCAACTCCTCTATGGGGTTTAGCTGCCCTCATTC      |
| WI-20768a | 71  | C | T | --- |  |  | TCCACTCAAAACTCCACCCCACTTCCCTGGAGGCGAGGCTAACAGGACCTCCTGCCTGCCTGC<br>TCA/C/JTACTGATTACTTCAATCCAGCTGCAATGCAAACTGAAACTGAACTCATCTGTATATCACCACCT<br>CTACAGGAGAGGCTATTTCTGGGCAACCCAGAGNTCAGCACACATCTGCTGGGACACAGGACTC<br>GTAATTCGCCTTGGTCCAACTCCTCTATGGGGTTTAGCTGCCCTCATTC   |
| WI-21909  | 153 | A | T | --- |  |  | TGTTTGGTTTGTGCCAGGTACTCTACTGCTTTACATAAAATATCTCATCTGTACATCTAACGGCAA<br>CTAAGTATACGCTTACATCTGCTAGTGGCACCTTAAATAGGATATTTGGTCACTCTTTAAAGAAA<br>TGCTTAACATACCAAAG/JTJAGTGGGAATCAATAGATAAAATATTTAAGCTTACAAAGCGGTAC<br>GACACTAAAGTAATATAGGATACCCTAAATTTATTTCTATGTATGGAAAG    |

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| WI-22202  | 128 | A G --- |  |  | TGTTGCTTTGGTTGTTGCTTCTGTGGAACATATTGGAACACTGTTTTTCATAAGCTGTCTCCTGACAGT<br>GGCACAATCCCATCCATCTCAGGCCTTTTAATAAGGTCAATTATGAATCTGAATTTCTTGA/GJTAAAT<br>ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCAACCACTCTTGGCGGTGCAGCTCTCGG<br>AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACCTCTCCAGCTCAC      |
| WI-22189  | 70  | C T --- |  |  | CCAAGGATGAATTTCCACATTTATTNCTTTTATGTGAATAGAAAATGGCAGTGAAGTGTCTATG<br>AA/C/TJGAGGCGAGGAATGGCATGGCGTGGCTGCGGTACCAAGCTTGACGTTGTCTTCCAAAGTACAC<br>TATGTGTGGTGAGACAAAGGT   |
| WI-22283  | 109 | T C --- |  |  | GGGGAGGCATCATAGAAAAAACCCCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCCACTAACGA<br>GCTGTATGACCTTGGTCACTAGGCCTCTGCAGGCTCTGGTTG/CJTTCATTTGCAAAATAAACCCCA<br>GACCGGTCATCTTTCAGTTCCCTTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA<br>TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAAG |
| WI-22290a | 136 | C T --- |  |  | GACGTATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTTATGGGCCCTCTAAGCAOCCG<br>GCCAGTAGTGGGAATGCCACATGCAATGGGTGAGTGGGATCTGGGGGGGTGAGGACCTTGCCTTT<br>C/TJTTCCAACTCTCCTCTTAGCCAGAACTTTGCGAGAGCCCCCTTNAATTTCTCTTCCCTCTATTCC<br>CCTCCTTCCCAATGTGTAAAGTCCCAATTCGAGAGCCCCCTCCAG      |
| WI-22292  | 53  | A G --- |  |  | CCAGTGAAGGGTTACAGCCATAGTGAGGTTCCCCATTTGCTCAGTACCAGA/A/GJGTTTTGAGTAC<br>GGTCGTTTAAAAAATACTTATCTGACCACAGTGGAAA   |
| WI-22387  | 186 | C T --- |  |  | ACCTTGACACCTGCCATCCGGTGCCATCTCCTGGCTGGCACATCTATACCCACTCTGGCTCTGAAAG<br>GCTTGTCAACCAAAATGGCAGCTGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTT<br>TCACTGGGTCTAGCATCCAGCCTCTCTCTCAGCAAGGAGGATTGGGTG/CJTCTTGTGTTTTCTG<br>AACAGGGCCAGGGCAGCCAGGCATGCCATCACTGCAGCACTCAACCCT         |
| WI-22395b | 127 | A G --- |  |  | GCCGTTCCAGTATTGATAATAATTTGTGTTTTAATTTCTATACAGAAATGGTCTTTCTTGAATATTTT<br>GTAGGGATGGATGAATTGAAGTGAATTAAGTCAAGATAAAGGGGGCAACTCTTTAATTA/GJAAG<br>GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCCAGG<br>CTCCT  |
| WI-22405  | 90  | A C --- |  |  | TTTATGGCTCCTGAGTGCCTTACCCAGCTACACTTTACCTTGTATCTATAAAAGTGAATTTAGAGT<br>AAATACATTTGGCTGTAAAGTCG/A/CJGATCAGGTGCTCTCCACCAAAAGCAAAACAAAACCTGCTGA<br>AATGTGGCAAGGTTTCTCAGTG  |
| WI-22419b | 67  | T C --- |  |  | CCCTCTGGACAGTTTGTCTTATGTGTTTCAGACATCAAGGNTCCCTTCCAGGCACAGCCAGTGCCT<br>/CJCTGGATGGCATCAGCACAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTGCACGAT   |
| WI-21342d | 59  | T C --- |  |  | ATTTCCCTTTCTGTGTTTCGTATTTCCTTTTGTGAGTAAATNAGCAATACACTGA/T/CJTGGAA<br>ATCTGCATGATTAAATAACATTAAACAGTTCTAAACACACCCCATATCAGAGTATAAAGCAAGAG<br>GTTGAAAAATATCCCTAACCGAATGCAAAATTAGGTATCCCTCAAAATTCACATTTCTCTCCTCTAGTT<br>T   |



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| WI-21763b    | 154 | A G --- | --- | CATACCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTAGTCCCTTTAGGCTTCAAGA<br>TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT<br>GCTCTCCACAGCTGATTJAGJ/CAGACATTGCCTGTGCTTCTACCCACGAGCTGTCTAGTGCACCTT<br>GA   |
| WI-21763a    | 135 | T C --- | --- | CATACCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTAGTCCCTTTAGGCTTCAAGA<br>TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT<br>T/CJGCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCACGAGCTGTCTAGTGCACCTT<br>GA   |
| WI-22440     | 64  | A C --- | --- | CAGTCCATTGAGTCCCAGTCGAGGGTGCAATCTTCCCTTATCTTGTCTTAAGCCACTTGGGTAA/CJ<br>TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTCAAGTCCCTGGAGGGAGGCTTTCTGG<br>AAAT  |
| WI-22449     | 74  | T C --- | --- | CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAG<br>TTCCTTT/CJGAAAAAATACACAATGGGAACGTGACA   |
| WI-21965a    | 112 | A G --- | --- | CAGGTTCCACCAGAGGCTTTATTTACGCCACTCAGGACCCCTGGCTTTCTGCTCCAAAGGCACTGAACA<br>CAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCCACAGCCJAGJCCCCACAGGTTCTCTGTT<br>TCCAAAGTCTGATGGATTACAGCAAGACCTTACACATTACCCCACTACCTGCTGGAGAGGAGGTC<br>ATGAGGCAGCCTGTGGTCCAGCTCAGTGTGACACACTGCCAATGTGC |
| WI-21687c    | 115 | C G --- | --- | CACCTGGCAGTTGAGTCAGATTGTAGGAAAAATTAAOCAGATGGGTCTACATTTTNTTCAAGTTCA<br>AACCACATGGTTTCTAGTCAGAAAGTCTCATGGACTTCTTCTTAAGJ/GJTGTTCTATGATCAGAC<br>CACCTCTAAATGTGGCTTTTACCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG<br>AG   |
| WI-22374a    | 149 | T C --- | --- | AGCTTTTACAACAAAGCGAGGTTTAAAGAGCCTGAGAAGAAATTTCACAACTATTGACTATACAGAG<br>TCTTCAATCCAAAACAGTTAATAGTAACCTGGTGACACATAACAATGCATTGAATACTCTGTAT<br>TATTCAGTAACTAAAT/CJAGGNTCCTGCATCATCTCTTCACA  |
| WI-22250b    | 132 | C T --- | --- | ACTTGTCTTCAGGCAGGCAATTTCTGGGATCTAAACTAGAAATCCTTGAAAAACAAATAGTACCAGCCA<br>CTTTGAGGAATGTGCATTCAGTGTAGTGGTTTATTATGGGTCTCTGCTCCTGGCTGTGTTATG[C/J]<br>GGANCCAGGAGTGGAGGAGCCGTGGAAATAGACAGGGGAG   |
| WI-22250a    | 89  | G A --- | --- | ACTTGTCTTCAGGCAGGCAATTTCTGGGATCTAAACTAGAAATCCTTGAAAAACAAATAGTACCAGCCA<br>CTTTGAGGAATGTGCATTCAGTGTAGTGGTTTATTATGGGTCTCTGCTCCTGGCTGTGTTATG<br>GGANCCAGGAGTGGAGGAGCCGTGGAAATAGACAGGGGAG  |
| UTR-04932-2b | 192 | G C --- | --- | GCAGCCATCTCTCTCAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCCACGAGCAG<br>CTACGTGGCCCGAGTACGGACCCGCTGGCCAGGTTCTCGGCTCTCAGGACGTCOCAGCAAGTGA<br>GCCAGAGGTTTGTCTGGGACTCCAGCCAGGGGATAGGCCACGCCAGAACCTG[C/J]AGTGCTTC<br>TTTGACGGGGCCCGCTGCTCAGCTGCTCTGCTGGAGGTGAGGAAGGAGGT   |

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| UTR-<br>04932-2a | 149 C T --- | --- | GCAGCCATCTCTCTCAACACCTCCAGGCCACCCCTGGGGCCAGAGACCTCATGCCAGGACAC<br>CTACGTGGCCCGAGTACGAGCCCGCTGGCCCGAGTTCTGGCTCTAGGACGTCCAGGACGTCCAGGAAGTGA<br>GCCAGAGGTTGTC/TGGGACTCCAGAGGGGATGAGGCCAGCCAGCCAGAACCTGGAGTGTCTC<br>TTTGACGGGGCCGCGTCTCAGCTGCTCTGGGAGGTGAGGAAGGAGGT     |
| stFIBBb          | 412 G C --- | --- | GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTCGCTGAGCAGCTGTGATTGTGCCA<br>CGGAGCATGAGCCCTTTCCACCGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG<br>TTTGACCCAGCTCGAGTCTCCCATGTTGTAGTACATTCTCAAGATGCAGCCAGGAGCCTCTCTGA<br>AGGACCATGCTGGTTACGATGGTCTGAGCTTCCTTAGAACCTTCCATGGTT |
| stFIBBa          | 341 T C --- | --- | GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTCGCTGAGCAGCTGTGATTGTGCCA<br>CGGAGCATGAGCCCTTTCCACCGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG<br>TTTGACCCAGCTCGAGTCTCCCATGTTGTAGTACATTCTCAAGATGCAGCCAGGAGCCTCTCTGA<br>AGGACCATGCTGGTTACGATGGTCTGAGCTTCCTTAGAACCTTCCATGGTT |
| stGLV2           | 61 T C ---  | --- | GTCAAGAGGACGCGCTCTCGGAGCTCTCCACCATGGCTCTGCTGCTCCTCACTAC/TCTC<br>CTCACTCAGGACACAGGTGACGCCCTCAGGGAAGGGTCTTTGGGAACTCTGGGCTGATCCTTGGTC<br>TCTGCTCTCAGGCTCAGCGGGGCCAGCACTGACTCACTGGCATGT   |
| stSG1001<br>7c   | 70 T C ---  | --- | GTTACGGCTCATCTTGAACCTCTGGGTCAAGCGATCTCCACCTCGACCTCCAGGGTCTGGGAT<br>TA/TCTAGGCATGAGCCCGCACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT<br>TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC   |
| stSG1001<br>7a   | 33 G A ---  | --- | GTTACGGCTCATCTTGAACCTCTGGGTCAAGCGATCTCCACCTCGACCTCCAGGGTCTGGG<br>GATTATAGGCATGAGCCCGCACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT<br>TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC   |
| stSG1002<br>3    | 63 A T ---  | --- | TAATGATAATTAGGGCATCTTCCACACGAAGATGACACAATTGACCCCAATATCATTTGAGGC/T<br>AACAGTTTGGGCTGTTTTCCAGTAGTATGACAGTGA   |
| stSG1009<br>6    | 36 G C ---  | --- | GTGAGAAAGATGCTCTTCTCCCTCCCATGACG/CCTGGCTTCCCGGGGACCTGTGCGTTTCC<br>ACCCGAGACGGCCTTTGTAGGACCCACTGCCACTCCGCTGTGCGCTGGGTCCGCTCTCTAG<br>GGCTCGAGTGTTTAAG   |
| stSG1011<br>8    | 107 C A --- | --- | TAGGCTTAAACCTGGAACTCTACAAGCCAAAAGTCCCTCCCTGCTGAGGGCAGTACCTCCATTGGGC<br>ACAGTCCAGACCCCAAGTCAAGATGCCCATTCCTTGGG/C/ACTCAGCCCTCAGTTCTCTCATTTCC<br>ACCAAGCGGTGCTTGTGTTGAGTTTTCTCCCAAGTGA   |
| stSG1012<br>0    | 89 T C ---  | --- | TAGTAGGTAAGAAAGCAAGGAGGATGCTTATGCGATGACTGTTTACAGTGGTGTGACACTATGC<br>CGTGTTCACGAACACTTAAAT/TCTGTTGTGTAATCTGATTTTATCCCTGCTTACAAATG  |
| stSG1017<br>8    | 42 C T ---  | --- | TTGAAGCAATATTGTCTAGCACTCTGCTGGACATTAAAGTCCG/C/TGGAGGAGGAAGTGAACAGGAA<br>TCGATTCTTTGCTTTTAACTGCCCTTAGTTAGGAGATGTTAAATACTTTGGC  |

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| stSG1019<br>3  | 136 GA --- | --- | --- | GGACAATACTACCTAAGGACAAAATACTATTATTAATAAAAAAGTCTCTAGTGATATTGTGTAA<br>CACATTTCTGGAGCTGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAAACCTTTTAC<br>T[G/A]TTTGAAACCTGAGATTTAAGTTGCAAACT  |
| stSG1020<br>2c | 143 GT --- | --- | --- | AAGCTAACTTAGGTGAATGGTCCCACTCAAAGGCTTTCCGAGGGAAGCTCAGTCTGGCTGGCGAG<br>AGTCAGCCTTGGTCACCTCATACGGGGCTCCAAGCTAAGGCGTCAAGGAAGCAGTCCCAGCTCTCT<br>CGCTGTCA[G/T]CAAGACCACAAAGGAGATGCCACTGCTGCTCTTTCTTGTCTACTTTCT  |
| stSG1020<br>9b | 75 A G --- | --- | --- | TCTTTTCTCTTTTCACTCTCAGTCACCATGATTCATAATAAACTAATTCCTCTTAAGATCCCACCTTAT<br>TTTTA[G/G]CTCCAATAAATGTAATTATCAGCTGCTGAATT   |
| stSG1020<br>9a | 34 CT ---  | --- | --- | TCTTTTCTCTTTTCACTCTCAGTCACCATGATT[C/T]AAATAAACTAATTCCTCTTAAGATCCCACCT<br>TTATTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT  |
| stSG1021<br>8  | 29 TC ---  | --- | --- | TACTAGACATGCAAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAGTTATATTTGTTTGACAT<br>AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA  |
| stSG1025<br>2  | 108 AC --- | --- | --- | ATAGGTTTCAGGAACAAAATCATTAATGGAAAAATGAGAAGAAATTCCTTTATTTTGGACCAATTTT<br>AGGCACCTAAGAGTTTCTTTTCTCTCTTCCCTTTCCCTTGATCA[G/C]AGTGAAGATATGATAGGGAATTC<br>AGAAATTTCTCTCTTG   |
| EST10915<br>0  | 123 AC --- | --- | --- | CTGTATTAATTAGAAGGCACATTAATGAGGGACGGAAAAATCTACCTGTACACAAAAATCTGTAC<br>TTTAACAGCATCTTCAAAATAAACCTTTAAAGGATAATGGTTACGATCATTTTAAAG[G/C]ATTTTAA<br>GAACTGAGTTATTGGAC   |
| EST11023<br>1  | 166 TA --- | --- | --- | TTTTTTGTTAAACCAACCCTGAAAGTTCCACATGTGAATATAGATACAAACAGTGAACAAAAT<br>ATGGGCTCCCATGTACATTGGTTACCTATGTACAAAGTATCTATACACCAAGTAAACAGCAGGGC<br>AATTAGTCAATTAAAAAAATAGTACATGTTA[T/A]GTGTAATAAAATTTAAATTTACAAAGGCTTT<br>TCCACTCGTGGATTGATTCTTTTGGAGGGAGTAATCCTGG |
| EST14096<br>8  | 71 GC ---  | --- | --- | GGGATGTATATTACAGATAACACAACCTCACAATAATACCATCAGACATTGAAAACTAAGGCCATTCT<br>GTGA[G/C]TTATTTTAAACCTTGGTGTTCACATAATGATCTTAAAAAAAATGAATACCAAA<br>ACCAAGATTCTCTTCTAAATGAAAAATTAATGCAGGTACAGGATAAATTTAGGGCTATATCTAATC<br>TGAAG                                   |
| EST22113<br>6c | 125 CA --- | --- | --- | TGCAAAATTGTGAGAAGGCAGCGGGGCCAACCCCTGGGACCTCATCTCTGTAGATGTGAGGTG<br>CAGGGATGCTTAAGTCTTCTCTGGCAGAGACCCGAGGTGCAGAGATGATTCTTCTCA[G/C]CCCTTC<br>TCTCAGGGTCTGGAG  |
| EST22555<br>7  | 60 GA ---  | --- | --- | TCAAGCATGTGTAAAGGCACCTGCCCCCGCCAGACCCCTTTTAACTTCTGCACACTGGAAGGT[G/A]AAA<br>CCTGGGAGAGAGAAGACACTCCCTCCCTAGCTTCTACCTGGGCACCCCTCCAAGATGAGCATTCATC<br>TTGGAGACCAAAATAAAAAAGGACAAAAGACCAAGCCAGGGCTCAGAG  |

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|-----------------|-------------|-----|--|
| EST22917<br>6   | 74 C T ---  | --- | GTAAACCTTGCAACGCCATGCTAAATGGAAGCCTGACTACCAGGGGGCTCTTGGGCTCTCAATGCA<br>ATAGAAA[C/TT]GACATGGGGCCAAAGACTTCCAGACAAAGCACGGAAGGGTAGAGGATATAG<br>GTTAGCATCATCTGGTTGTGA  |
| EST36458<br>6   | 65 A G ---  | --- | CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCCCTCAGGCTGTCCTACTCA[A/<br>G]TGTGGTTTCTAGCCTCAGCTGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAAGTCACCTCCCA  |
| EST36745<br>3   | 56 A G ---  | --- | GAGGGGGAACCTTCAAAGAGGATTCCAACAGTGAAGCAGAATCATGGGGCAAAAGTCA[G/C]TATGG<br>GGCCAGACTGAGGTTGGACACACAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC<br>ACAGCACGGAGTAGCCAT   |
| STS-<br>R37410c | 201 A T --- | --- | TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCACCTTAAAAAACAACAAAA<br>AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA<br>ATTTATGGTTTGAATAAATAACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGTATG<br>T[A/TT]ATTGTGAGTGGTCTCTAGTGGCCAAAT |
| STS-<br>R37410b | 139 G T --- | --- | TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCACCTTAAAAAACAACAAAA<br>AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA<br>ATTTAT[G/T]GTTTGAATAAATAACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGT<br>ATGTATATTGTGAGTGGTCTCTAGTGGCCAAAT |
| STS-<br>R37410a | 48 C T ---  | --- | TGTGACCATACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCA[C/TT]TAAAAAACAACAA<br>AAAAACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTT<br>GGAAATTTATGGTTTGAATAAATAACAAAATGTGTATCTCCTGAGACACATTTATAAACATTTCTGGT<br>ATGTATATTGTGAGTGGTCTCTAGTGGCCAAAT |
| STS-<br>R42778  | 74 C T ---  | --- | TATCGTGGGAAGTTCCAACTCATACTTATGCTGCTTTTCTACTTGCTAATATTGGATGCTTCTTGCCA<br>GGCTC[C/TT]TAAATTGTGCTGTAACTGGGAAGAAACCTTCTCTCCACAAACCCCTGAA   |
| UTR-<br>04350   | 125 C G --- | --- | CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGGAGGTGGGACTGAGGAGCG<br>ACTGCTAATCAGTATGGGTTTCCCTCCGGGATGGTGAAATGTTCCGGACCTAGATA[C/G]TGACGA<br>AGGTAGCACGACACTGTGAGTGCACTAA   |
| stSG1026<br>6   | 55 T C ---  | --- | GAAATAAACTAAACTGCAAAAGCAAAATCACGTGTTAATAAGAAATTGTTCTTCTGT[TT/C]GACAGTTG<br>AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCTCAGAAATGCGGGCAAA<br>CTCCTCTGTGAAATGTAT   |
| stSG1028<br>2   | 70 T G ---  | --- | GTATAATCAGCATAAGCCAAAGCCCTTTTAAAAATAACCAATACTATCATTTTATGAAATCTTTACA<br>AGAT[G/A]AGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC  |
| stSG1031<br>0   | 128 C A --- | --- | CACTTTAGATATGAGGAAAATGGTTTTAATGGACACAAAAGGAGTCAGCACGTTGGAACCAACATAG<br>TTTCATACCACGTTGAAACCATGTGTTTGTATGCAATAACAGCAAAATAATTTTTCACCT[C/A]TTG<br>TCAATGCCAATGCATTGAAAGGCCACAGAAAATGAGAAAAGGATAACAAACCTTTTGATAAAAAAGGTA<br>AGAAATTTCTGTGTG                |

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| stSG1033 | 116 | T C --- | --- | TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTTCCGG<br>GCTCCAACCTGTCTAGGAAGCCTAGACCTCAACACCAACACCTCCAT/C/GCAATTCCCTCTTTGG<br>CTACTATGCTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTCAATCTGA<br>CTTAGGACCCCTCC  |
| stSG1033 | 107 | A T --- | --- | TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTTCCGG<br>GCTCCAACCTGTCTAGGAAGCCTAGACCTCAACACCAA/CACCTCCATGCAITTCCTCTTTGG<br>CTACTATGCTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTCAATCTGA<br>CTTAGGACCCCTCC   |
| stSG1243 | 225 | G A --- | --- | ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAATCCCTCCTCTTG<br>AAATTATGTCAGGGCCAGCATGGTAGCTTATGCCTGCAATCCAGCACTTCGGGAGGCCAAAGGAGA<br>AGGATCGCTTGAGCCAGGAGTTCGACACCCAGCCTGGGCAACATAGTAAGACCCCATCTCTGTTTTTT<br>TTTAAAAAAGAAATTCGTTC/G/A/AAAGTATTTTCAGACCACAAAAGGAGGT<br>AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACCTAGTTTGCTTCTTAC/G/ACGCT<br>TCACATTTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCATAAATGCGGCA<br>AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACCTAGTTTGCTTCTTACGCGCT<br>TCACATTTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCATAAATGCGGCA<br>TTAATGTCATCCAGGGAGGGGCCAGGGATGGAGGGAGGGTTGAGGAGCGAGAGCGAGTTATTT<br>TGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTG/T/G/TCAATCATTAAAGAA<br>GACAAAGGGTTGTTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAACATGGGC<br>CCAGCAGCTTCAGTCCCTTCTCGTCG |
| stSG1385 | 117 | T G --- | --- | TCGTCTCTTCCAGTGTCTGCCAGAACATCCCATGATGTTGTGACCGCACAGCACTTTGTGTCT<br>T/C/GCTTTGAGCACTTGCCACTCTGGCTGGTGTGCTGCCACTGATTGTGTACTGCTGCTGCC<br>GATCTGTTCCAGACAAGGCTGATTTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT<br>TGGCTCCTCCACTTCAGTTTGGCTTCTGCTCAT/CJAGTCTCTCTCCATGTGGCAACAAGATGGC<br>TACTGTGTCCAGGTTCACTGCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGTCTCACTCCCA<br>AAGTCCATAACTCAATCCTTGGGAAG  |
| stSG1427 | 103 | T C --- | --- | CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTGTAGGTCC/C/GJCTCCCTTGCATGA<br>AATGTGGGAGAGGGAAATAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC<br>GCA   |
| stSG1471 | 50  | A G --- | --- | CAAAACCAAAATCCTCCACGATATATTACTATTTAGTCTAAGT/C/JTTAATTCAAAGGTTGAGA<br>ATGACGAATTCAGGAATTTCTTCATACATAAAATGCTTTCCTTAGTTCTGCAGATGGTA  |
| stSG1483 | 44  | T C --- | --- | CACACCCACAAGTTTCATGTAAATGCCAAGTATCAACTTTGAGGACAAAGGCAAAACCAAGTGTGA<br>C/G/JAATGTGGAGGATGTCTGTTGCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAGAGAA<br>AATGCCTGA   |
| stSG1696 | 67  | C G --- | --- |   |

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| siSG1847<br>b | 95 GA ---  | --- | TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAAATTT<br>AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTGGTTTATAGACATTTGAA<br>TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATCACTGTGCT<br>TCAAACACAACCTG               |
| siSG1847<br>a | 49 CA ---  | --- | TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAATGAAAGA<br>ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTCCGTTTATAGACATTTGA<br>ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATCACTGTGCT<br>TTCAAACACAACCTG             |
| siSG1897<br>a | 83 AG ---  | --- | CTTAATGCCCTTCTCTCTCTGACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG<br>AGGAGGACACAGGACTT[G/G]GCCACCACTTCTCTCCCGTCTCCCAAGATGACT   |
| siSG2022<br>a | 86 TC ---  | --- | TGCTTTGAGGTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTTGATCAAGGTACAA<br>TTTTAACATTAAATATACAT[C/A]ATCCATAATCTCATCTATTTAACATTAAACACAGGCCCTTTGTTGT<br>TGTTATTTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCCTCAGTTGGGGGGTTGAC<br>T                     |
| siSG2076      | 104 CG --- | --- | AAACGTTGTCCCAAAATTGTTTCAGTTTCAACAAGTATAAATAAGACTTCTGAAAAAAGTTTACA<br>ATTAGTTATAAAACACTTAAGAATAATTTTGACATT[C/G]ACATCACAGTGGGCAATTT   |
| siSG2108<br>c | 71 AG ---  | --- | TTGAGCAACAATGATTGCGAATTGGCAGCTCCAACCAAAAAATGATT[C/G]AGGGGCTCCACAG<br>GAGC[G/T]AAGGGGAAGACTTTTATAGGACAACCTGTAAGTAAGTAAAGCAAAGCAGACGTTTGATTG<br>GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG<br>TTTGTGGGCTGTGTCTGA      |
| siSG2108<br>a | 49 TC ---  | --- | TTGAGCAACAATGATTGCGAATTGGCAGCTCCAACCAAAAAATGATT[C/G]AGGGGCTCCACAG<br>AGAGAGCATAAGGGGAAGACTTTTATAGGACAACCTGTAAGTAAGTAAAGCAAAGCAGACGTTTGATTG<br>GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG<br>TTTGTGGGCTGTGTCTGA      |
| siSG2141<br>b | 173 AG --- | --- | TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGGTGTAC<br>TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCCTGGCATGGCGATGGTGAGGTGGGT<br>GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAAG[G/A]AGTTCCCTATTATTATTTAAGGC<br>AGTTTCAGAGCACTGGCATCTTGTGCTCTG |
| siSG2141<br>a | 113 CT --- | --- | TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGGTGTAC<br>TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCCTGG[C/T]ATGGCGATGGTGACAGGTG<br>GGTGACGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAAGTCCCTATTATTATTAAAGGC<br>AGTTTCAGAGCACTGGCATCTTGTGCTCTG   |

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| stSG2148 | 50 A G ---  | --- | TGGGAACAACCGGCTATAGTCTAGTCAATATTTTATAGACCGTGATTC[AG]AAAGAAACAATAA<br>ATGTGGATTAGAAAGGAAACATCCATTACTGTATTTTCGATACCTTGTGATGTTCCACAGACGAGCTC<br>ATCAC                             |
| stSG2175 | 68 C T ---  | --- | CTCAATGAGGACTCCATCAGCCAGCGGTTTATATGGCAGATGAGCTGTACAAATCTGTGTGTGCT<br>[C]TGCCGCGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT<br>ACCTGGCAGAGGGAAGGAGTGAAGGACCA       |
| stSG2189 | 41 C T ---  | --- | CAAGTGTGAAAGCTGGGATTTGAGCCTGATATTCACACTA[C]TCTACATTCCTCCAGTATAATA<br>GGAACATCATCGCTAACTTTGAGCACCTAGTGTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC<br>CAGCTTTGCGAAC                     |
| stSG2200 | 49 T C ---  | --- | TGTTGATGACCATAGAGGATGCAAGCTCCGGCTGGTTCTGTATGATG[T/C]TTTATATTTATGTAT<br>AATGCTTACCTGATGATACCCAAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG<br>GTCAAT                          |
| stSG2243 | 85 G T ---  | --- | CATTTCTGCCTCTGCTTCCAGTACTACCCGTCAGCAACTGCCTCTGTATATAAATAAGTATCAA<br>GATGGTCAGTAGAAAAG[G/T]AGAGCATCTCTCAGCCCTGGAGACAGTGTGGGAGCTTCAGCT   |
| stSG2257 | 65 A C ---  | --- | TCAGTGATTGTAGGAGCTGGCTAAGTCATGCTAAACTCTGTGAGGCAGGCTATCAGAAGGGCAG[A/<br>C]GTGCAGGAACCTCGCCAAGCACTGGGCTGCTCTCAGGCAGAAATTCCTCCT   |
| stSG2306 | 67 A G ---  | --- | GTCATCAGCGTAGAGGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGGAACATTTTACA<br>[A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACACCATGAGGTGAACACTTTCACTGTTTCACAG<br>TTCTCCAGAGA                       |
| stSG2334 | 70 T G ---  | --- | GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCCGCAAAAAACA<br>AAAAAT[G/T]GCAGTGGAGGGGCTGTGGGAGGGTGAATG   |
| stSG2339 | 63 T C ---  | --- | AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGTCTTGAAGTGCAGAAAGTAACTGCTGTCAC[T/C]<br>GTTCTCAGAGTCACCATTAAGGTGACTGTCTATTTCTGGCTGTGCTTCTTCTATTCATCA  |
| stSG2465 | 76 C T ---  | --- | CAAGACTAAGAAGCGCCACCCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTTACCTCAAATG<br>CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC<br>ATCTTCAAAGTGTGGGTATGCA                |
| stSG2549 | 140 T C --- | --- | TTGCAGGCTTGTATCCACAATAACAAAGTCATGTATAGAGAATGTGAAATGATACTTGAAAAACCAA<br>GATATATAAATATTGAAGTCATTTATGCCCTTTTGTGACTGGTTAAATATGCAAGCAGCTAAAG<br>GAATAT[T/C]TACACCAACCCACCCCTTTTAACT |
| stSG2577 | 123 T G --- | --- | AATTGCCAAATGGAAAATTCACAGAGGATTTTAGACCAACTTTGCCCTGTGTGATTCCCAGTTTGGT<br>CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCCGAACCTGTGAAAGCA[T/G]GAACAATC<br>CCGGCCCAAGATTAATTATT         |

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| siSG2577<br>a | 121 | C T | --- |  | AATTGCCAAATGGAATAATCCAGAGGATTTTAGACCAACATTTGCCCCTGTTGCATTCGCCAGTTTGGT<br>CCCAATATAGGCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGC/TTATGAACAATC<br>CCGGCCAGATTAAATTAT                                 |
| siSG2700      | 58  | G A | --- |  | ATCTCTCGACTGCTTATAGTGGGAAAGGAATCAATTATTAAGAACTGTCCGGCCCGC/GA/AGTCAC<br>TCAGCGTTTGGCGGAAATAAACCACTGTCCAGAGCAGAGGAAGGCTACTTGAGCCGGACACCA   |
| siSG2724<br>b | 101 | T G | --- |  | AAACAAGCTTTGTCATTTCCACTACATTTTGTGTGCTTTATATTAATAATTGCAAAATGCTATAAT<br>TTAATCTTATATCCAAATGCTTGCATAATCAIT/GITTTTTTAACTCCTGGGGTGTGAAAGAAC   |
| siSG2776<br>a | 65  | G A | --- |  | GTGGCCGATCTTTACTTTCCAGAAAAGGGGTAAATAAAAAACCTGTAGAAAAGTCTCGAATATGC/G/<br>ATATTGGCCCTTTTGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAACCAAAAA<br>ATATCCACTAAITCCCGAATATAGTAACCCCTGTCTGTCCGAATG            |
| siSG2791<br>b | 109 | G T | --- |  | AAGGAAAGGTGGAGGGAAGGGAAGAAATACAATGGTTAGAAAAGAGCAACTAAAGATTATTC<br>TATTATACCTCTGAACGGTAACTAGCAATTTTAAATAATTTG/TGGGTCCACTTAAATCTATTA<br>AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG |
| siSG2791<br>a | 100 | A G | --- |  | AAGGAAAGGTGGAGGGAAGGGAAGAAATACAATGGTTAGAAAAGAGCAACTAAAGATTATTC<br>TATTATACCTCTGAACGGTAACTAGCAATTTTAAATAATTTG/TGGGTCCACTTAAATCTATTA<br>AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG |
| siSG2826      | 85  | C T | --- |  | CCGCAATTTCAACACACATTTCTATGAAAACCTAAGGGTGGATCATGTACAAAACACAAAAAAGC<br>TCCCTCCCTCCAAAAACAA/C/TTGAACAAAAATAAAGAAAGAAAAACCCATGAAATGCCAGGTTTA<br>ATTTTTTTCC   |
| siSG2850      | 88  | G A | --- |  | ATGGTGCATTGTAAAGGCAAAATTAATACTTTTTCAGGCGGGGCTGGCAAAATTTAATGAGCTGA<br>TGTGTCCCAAGGGAGACGGCC/GA/GGCTCACACATCCCATCAAAATACTCTCCCAT   |
| siSG3031      | 71  | T C | --- |  | ATACTCACGGGGCTGAAGGGCAATGTGAAGAGTGAAGTCAAGTCTCTGGCATTTTCTGTGGTGCAGC<br>AAAT/C/GCCCTTTATTTTAAATGATTCAGACATCTGGGCGAGCATAGCT  |
| siSG3058      | 81  | G A | --- |  | GTCCCAACTCCTCTCCTCTTAGAGAAAAAAGTGTGATTACCTCAACTTGAATATGAAACTGTGATTG<br>AAAAAAGTCAAAAC/GA/ITGAAGAAGCATCAAGGCCAAAAAGGCAAAACTGGCTGAGGC  |
| siSG3092      | 94  | T G | --- |  | CAGCATCTCCAGAACATTCCTAGAACTGAACCATTTCTGTCATAATTGAAAAACAAAGCCAAAGTTC<br>CAATCCAAATAATAATGAACGTGC/T/G/GATAAACATTCCTTATGTTCCAGCCCCCTACTTT<br>AGTT   |
| siSG3230      | 95  | A G | --- |  | AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTGAGATACGAGCACCTG<br>CATCTTTTAGTCAATTGTGAGTGGAGT/C/G/GTGGGGTGTGAAGTGTCTGAAGTGAAGTAG  |
| siSG3245      | 160 | G C | --- |  | ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCC<br>CAGGTATGTAGAGGCCAGTGGGGTGGCCACTTGGTGTCTTACCAACCCCTGCCATCCAGTCTG<br>GCCCCAGTACCTACCTGGGAGGTG/C/TGTACTTGGCTTAAGTACTTCATGCTTAT  |



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| stSG3265      | 42  | T C --- |  |  | AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAATTCGCAATTGTGAATAGTTTCTCAG<br>TTTTCAATTATGAAAGATGATGATTTTCAAGCCACATTCAGTGTATGTTTCTTAATAACACAATCGAC<br>AGGACTGTCTGTTTCACTACATGAGGACAGCTTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA<br>ATCTGTCTTGTGAGCTGAATTTCTGGGCTTATGTGGCAGTGTGGTAAAA   |
| stSG3269<br>b | 141 | C T --- |  |  | TGTACTACTGTGTCATCCTATCCATTCCTTCCCTGAGCCTGGAGTGTCTTCCAAAGGGAGACTAGG<br>AGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGAATAATTAGCTCCATAGCCATGCTAAA<br>GCATGA[CT]TGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT   |
| stSG3269<br>a | 24  | A G --- |  |  | TGTACTACTGTGTCATCCTATCC[AG]TTCCTTCCCTGAGCCTGGAGTGTCTTCCAAAGGGAGACT<br>AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGAATAATTAGCTCCATAGCCATGCT<br>AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT   |
| stSG3284      | 130 | C T --- |  |  | TTAACCTCAAGAACTTTTCAGTTACAGGAAGATTTATCTAATATTAATGACTAAATTACAAAAAGC<br>ATAAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA[CT]<br>TCCCTAACCTTTTGTAAATGCTGTAAATGGGACATTTGTTTGTGATCTACCC  |
| stSG3292      | 99  | A T --- |  |  | GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA<br>CACATCATTTGGACAAGTGACTTAAATATCTAA[AT]TACAAATCAAAATAGCATTTTCTTAACITCAA<br>TAAATGTCATATCTTTAGCTCTCACT[CA]CCAGTGTATCCATTTTCCCCAGCGGTAGAGCTTTCTG<br>TTTCTGTAGATTGCCTGTCCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTCCGACTTCTCTC<br>ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTGTCTTCAATCCCTTTAA<br>GATCCCGCAGTATTATTTCTAAATGAACTTGTTTGTGGAAATAAAAAATCTGAGGACCACCTCAGAG<br>GG[CT]ATAAGGGGAACCTCTTTGTCTTAGTTCATAGGACTTTCT |
| stSG3323      | 26  | C A --- |  |  | CAAGACTGTAAAGACGTAGGCTTGTGAGAGTGAAGGAGGATGCTGAACTTGCCCAGGACTCAGG<br>CTTCAGCTTCACATCCCGAGGAAGGAATGACATTTCCAACTGTCACTTTGTAGC[GT]CTGGGT<br>CAAAGTCTAAGAGGACAAATAAATAGAGACT   |
| stSG3369      | 69  | C T --- |  |  | TCTTACTGTTAACCTAGTCTGGAGTAAAGGATGCAATCAG[AG]CTCACTGTAGCCTGGACCTCC<br>TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA<br>CCTAAGTTTTGTAGAGACAG   |
| stSG3416<br>a | 43  | A G --- |  |  | GTAAGACAAAGTTTTGCTATGTTGACCAGGCTGGTCTTGAACCTCTTGGCTTCAAGCGACCGTACCA<br>CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTAGCCACTGCCCGCCGACTTTTAACTGAAT<br>GTTGAAATCATTTCTGCTCTTTGCTGGGTAACTGAT[AT]CAAGTTGCTTAACTTTGTGAAACCCAC<br>TTTCCCTATCTGTACAAATGGACAAACAGAACTTTTCCCTTCTCTC   |
| stSG3424      | 173 | T A --- |  |  | GTTTATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTGAGGTGATGTGATGGAGGCGCTCACAGA<br>ATGAGTGGCAGAGAGGGCCCC[TA]GAAATAGCTTACTCTGTCTTCTCTATC  |
| stSG3436      | 88  | T A --- |  |  |   |

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| stSG3463 | 103 | C T | --- |  |  | GATACAGAAGATAGTGGTATGGATGGATAGTATGAAGGACAAAATAATACAAAATATATTTATTG<br>AAATAAACAAAAATGCATACACAGCTCAATGGGTCA[C/T]TGGAAACAACTTGCTTGACTATATTA<br>CTGA   |
| stSG3491 | 71  | G A | --- |  |  | CAAGATACCTCATTGTCTCTAAGTAGTGCAGTGTGGCAAATATTTCTCACGAACAAGGACGATTTG<br>AAGA[G/A]GTGGAAATCTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA<br>ACAACTCTCTAATCTTTTACTGGCACCTGTGGATTCTATTAACTCAATTTATACTATTTTCTGTGATG<br>ACAGAAAATAAGTTAAC                                   |
| stSG3523 | 33  | C T | --- |  |  | TAGCCATCTTACTAGTCTTTTGGGTTT[A/C]TGCATATATGTGTGTACAAACACACACACACC<br>CCTAATCTCTCAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC  |
| stSG3536 | 213 | A G | --- |  |  | AGTACAAACACAGATTTAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT<br>ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAACCAAAATACAGAATGGCTTC<br>TGTGATACTGGCTTGTCTGAAACGCATCTCAGCTGCTATTCTATTGTTTATTTGTTAAATGAGCTTG<br>TGCACCAATTAG[G/T]CTCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG |
| stSG3583 | 112 | G A | --- |  |  | GAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACTCTGGCATGATCCA<br>CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT<br>CTAGTTATCAACACCTAC  |
| stSG3586 | 60  | G C | --- |  |  | CCTAGTAACATAGTGAGACCTGCTCTCTACTAAAAATTTAAAAATCAGGTGTGGTGGT[G/C]ACG<br>CCTGTAGTCCCTACTTGGGAGGTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT<br>GAGTTATGATGGGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAA   |
| stSG3589 | 101 | T C | --- |  |  | ATATAGTGTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAGT<br>GTATATACCCCTGGCACAAAAACCCCAATGA[T/C]CCTATTTCCAAGAAATGTATCCAGATGAAA<br>GTATCCAACAACAACAAAAAGCTATATACAC  |
| stSG3590 | 70  | A T | --- |  |  | GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTTCTAAAAAAA<br>AAA[A/T]TTTCTGTGATGCTCTTGACCCCTGTAGGAAACACATTCAGTTTCTACACT  |
| stSG3619 | 78  | A C | --- |  |  | CAGTGAGACTTCTCATTTTATAGCAAATACATTTTTCAGCTTAAATTTTCTGAATTCATACGCT<br>TCTGTCAATTT[A/C]AACAACTCCAGAGAAAACCTGGGCTCTATATATTTAAG   |
| stSG3644 | 40  | T C | --- |  |  | ACATATGTAACCTGCCATTAGTAGCCATATTAGGATGAGAT[G/C]GGATTGAGAGGCATGAACCAAGG<br>ATGCGTAATAATCATTATGAAATAATAAGTTATCTGGGGAACGGCCATTTGTCCAACATTTACTAA<br>GTGCCTACTA  |
| stSG3646 | 70  | G A | --- |  |  | CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAATATATGATGAACAATAATATGCTTACT<br>GGT[G/A]ATATACTTGTACTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCAAT<br>CTTCTCTTTGTA  |

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| stSG3646<br>b | 55 A G ---  | --- | CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATA[A/G]TATGTCCTT<br>ACTGGTGATATTAACTTTGATACTTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT<br>CTTCTCTTTGTA                                   |
| stSG3646<br>a | 43 A T ---  | --- | CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG[A/T]TGATAACAATAATATGTCCTT<br>ACTGGTGATATTAACTTTGATACTTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT<br>CTTCTCTTTGTA                                   |
| stSG3693<br>b | 85 A C ---  | --- | ATTGTTTCCCTGAACATTCOCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCCTGGACTCACCT<br>GAAATATCCTACGAGGC[A/C]TGGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG   |
| stSG3693<br>a | 30 C T ---  | --- | ATTGTTTCCCTGAACATTCOCGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAACCCCTGGACTCA<br>CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG   |
| stSG3698<br>b | 145 G A --- | --- | TCITGGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTTGCTCTCTGACTTCCACCAT<br>TCACTGACTTTTATTGCCAGAGGAGCTCCCAGGAATCCACAGTTCTTGGAAAGAGAGGGGCTCTAAGTCT<br>TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA |
| stSG3698<br>a | 51 C G ---  | --- | TCITGGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTTG[C/G]TCTGACTTCCA<br>CCATTCACTGACTTTTATGCCAGAGGAGCTCCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA<br>AGTCTTATTGGGGAGATACCCACCCACCTTCCCTCACTGCAGA        |
| stSG3724      | 107 C T --- | --- | ACCAGCCTCATGTCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGCCATCCCTGGGCCTAGACTTCT<br>GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA<br>GTGGCTATGCTGGTGCT                                |
| stSG3725      | 104 G A --- | --- | GCCAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA<br>ATCAATATATTATTACAGCAACAGCAACAGCC[C/G]A]GACAGGAATCGGCACATAGTCATAA<br>ATAACATCAGGGTAAATAACGGCACATTTA                          |
| stSG3751      | 128 G A --- | --- | CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTTATACCTTTTAGAAAGATGATTTTG<br>AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC[G/A]TT<br>GCTGACTCCATGTTGCAAGAG                               |
| stSG3787      | 49 T A ---  | --- | TTCTGTGCAAAAGAAATCCACATCATTGTTGGTAGCAGAGGATCTTTATTA]AAAGTTCCCTAAGA<br>CACTGAGGGCATAAAACCAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT   |
| stSG3880<br>b | 115 G C --- | --- | GACAAAGGGGAAGAGATGCGCCAGAGACCAGGGCTGGGGCAGCTGGGGTCCCTGAGTCCAGGCCG<br>CACCACACGTCCTGTGGTGCAAGGCCCTCCTCTGGGGAGCAGGTCTA[G/C]GGCACGGAGGATGCAG<br>GGCTGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCT    |

|               |     |         |     |   |
|---------------|-----|---------|-----|---|
| stSG3880<br>a | 36  | G C --- | --- | GACAAGAGGGAAGAGATGGCCAGAGACCAGGGCTG[C]GCGAGCTGGGGTCCCTGAGTGCCAGG<br>CGCCACCACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGGAGCAGGTCTAGGGCACGGAGGATGCAG<br>GGCTGGGAGGGGACCCACCTCGGGGACCCCAAAGGAGTCCATTCTGCOCT |
| stSG3895      | 44  | A G --- | --- | AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTG[C]GJTITTTTTTCCATTAACTAA<br>TACATGCCCTCATAGATATATCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCTCAACTG<br>AAAAAT  |
| stSG3902      | 104 | T C --- | --- | TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCAGCTCTGTGGGAACCTGGCTTCCTGATAACA<br>TCATCTATTTACACCTAAATGTGAACCTGCTTTCTTTTC[C]TCAGCTCAATAGCTTAACATCTAATTC<br>ATGTTGCTCCCTTTGCTGGACAAT                       |
| stSG3935      | 50  | G A --- | --- | GGGTGCTGACGGACAGGCACACCCAGAGTTTCAACAAGCAATTTGTCC[C]G/C]CTAGTGTGCAGGC<br>TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACCTTCTCTGGACGT   |
| stSG40        | 25  | A G --- | --- | GAGGAAGAGGTTGAAGAAGTGTG[C]G/JAATATATTTAAGATTTCTTTGGGGAGAAATCTCGTGC<br>CCAAACCTGGTGATGGATCCCTTACTATTAGAATAAGGAACAATAAACCCCTTGTGTATGTATCA<br>CCCA   |
| stSG4009      | 32  | A G --- | --- | GTGTGGGCTGCTGATGATGAATGGCGCGCT[C]G/JTACTCTTTACGGTCTTACACITTTATGCTCCT<br>ATGAATTCCTGATGGCTTTAAGGGCTGAACCATATCTGAAGTTTCCCACACACTGCTTACA   |
| stSG4033      | 123 | T C --- | --- | AGAAGCCTTGGGGACAATGGCAGTGCCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT<br>TGAACCTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTTT[C]JTGGAAC<br>AGGTGGGCAACAC                                    |
| stSG4038<br>a | 29  | G A --- | --- | GCTGAGAGCACGTGTACAGCCACGCCTGT[C]G/C]GAGGCCACCTCTGTGCAATAAACATGTTCTGOC<br>CATGTTCTCAGTCAAGAGGTTCAAGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT  |
| stSG406       | 53  | T C --- | --- | ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAA[C]G/JGTTTTAGTT<br>TTGCTGAAGACTGGCCTTATTATGGACAGCTTTCCTAACAGAGATTATTAACTTTTATCAGGTGTT<br>AACATCTGTTTCAGGAACATGGCA                         |
| stSG4095<br>b | 55  | G T --- | --- | ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTATTAG[C]TATAAAAA<br>GTTTGCTTCTGTAATACTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG<br>CCTTTGGACTAACCCAGGCATTGCCCTTCATCCTGG              |
| stSG4095<br>a | 27  | A C --- | --- | ATCTGGGCTGAATTAGTCAAGCAGGTC[C]G/JGATACTATTGTCTGCTAGATGTATTAGGATAAAAA<br>GTTTGCTTCTGTAATACTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG<br>CCTTTGGACTAACCCAGGCATTGCCCTTCATCCTGG            |
| stSG4120      | 65  | G A --- | --- | TGCATGTTTCCACATCTTTCAATAACAGCAAAATGTATAATAAATACGTACTTATGGATAATCAC[G/<br>A]CTTTTCCCTCAGAGAGCCCCACAGTTAAACACGTTCCAGCACACCATTAATCCACCGAGCT   |

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| stSG4128      | 54 A G ---  | --- | CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCTTATATATTT<br>TACTTCTTCTGAAAATGCCACATAATTTGCAATAAATGATTCACCTCTTAGCTCCAAAAGCAAGTCC<br>TTTATCAAAATGCAAAATGTTCCAGAGGG                               |
| stSG4209<br>b | 128 G A --- | --- | CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAAAGC<br>AGGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTC[G/A]GC<br>AGGGGGACACGAGGCGACAGGTGCTTTGATGCTCGAAGAGCTGAGCTCCATTCCA |
| stSG4209<br>a | 65 G A ---  | --- | CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAA[G<br>/A]CAGGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCGGC<br>AGGGGACACGAGGCGACAGGTGCTTTGATGCTCGAAGAGCTGAGCTCCATTCCA   |
| stSG4254<br>b | 31 G A ---  | --- | CATTACCCAGAACGCCATGGAGGACCAGAGC[G/A]CCACGGCCGGGACTCCCGCGATGGCTGGGGGG<br>GCTATGGCTCTGACAAGAGGATGAGCGAGGGCCGGGGGCTGCCTCCTCCCCCAGGGGCGACAGGTGAC<br>TGGGGGACCATGGCCGAAGAGAGGATGACCGGTGATG                 |
| stSG4301      | 81 T G ---  | --- | TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTTCCAT<br>TTAAGCAATAAATTT/GIAGCTTCTGAGTAGTTGTTCCAGTTTCAACCAACATTTTG   |
| stSG4331<br>b | 71 T G ---  | --- | CTCACAAGGCCAACACAGAAAAGATACAAATACATTATCCAGCTAAATATTTAGTTTATGACAC<br>AGAGT/GITTTCAAACAAGTTTAAAGTGCACCTGAAGAGCATGTTAAAAAGTTTAAAGTTATCACTT<br>GGAGAGCAGATTTCTTGGCCTCGCCTTGATTTCTGTTTGAAGGGTGTGC          |
| stSG4340      | 76 G A ---  | --- | TTTGGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC<br>ACATGTTCTC[G/A]TAAGTGGGAGATAAACAAATGTGTACACCTGGACGTGGAGAGCAGAA   |
| stSG4361<br>b | 109 A C --- | --- | TCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC<br>AAGTTCITGGAAATTTCCATAAGGGATAACTGCATCTTTTGC[C/C]CCTTCACAACTAGAAAACGACTC<br>AGCGACTTTTCTGTGAGCAAAATGTCGAGG                       |
| stSG4361<br>a | 24 T C ---  | --- | TCCCAACCATTTGAGTGACAGAGCT[C/C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG<br>CACAAGTTCITGGAAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACTAGAAAACGACTC<br>AGCGACTTTTCTGTGAGCAAAATGTCGAGG                      |
| stSG4376      | 73 A G ---  | --- | TTTCACTGCTACTGGTTTCGGTGTCTGAGTCCCTCAAACCTGCTTTGCAAGTGTCTCTCCAAAGGGAG<br>AACAG[G]CTGGAACTGGGGCTCTGCAAGAGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC  |
| stSG4381      | 50 T C ---  | --- | GAAGGCCACAAACACTCCATAGCCAGAGAAATGACAACATACGATTTCTTT[C/C]TCAGTCTTGTAGT<br>ATCCACAGTAGTGTCTGTCCATGTACAAGTGTGTCCAGAACACCCATTAAATTCATGCC  |
| stSG4410      | 79 A G ---  | --- | ACCAATGGTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAATCTGCAAGGGCTTAACCAT<br>TCAAACACCGC[G]GTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT<br>CAGCTGGGT  |

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|----------|-----|----|-----|--|--|---|
| stSG443  | 65  | CT | --- |  |  | AGCAGATCAGTCAGCCACTGTCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/      |
| stSG4430 | 54  | AG | --- |  |  | TJGTATGCAATGAGAAATAACCAACTGGTAGGATGGGGAGGGAGGCAGGGAATAGGCAC           |
| a        |     |    |     |  |  | AAATGGAAATCTATCTCTGGCTGTCTCTCAGGTC                                    |
| stSG4448 | 99  | GA | --- |  |  | ATGCACATTAAATGAATGGCCTAACTACTGGAACTTTAGTAGTTCTATAAGGTJAGJATTAAACATA   |
|          |     |    |     |  |  | GGTAGGATCCAGTTCTCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCCATTTT    |
|          |     |    |     |  |  | CCCTCCCTCCCTCTCTCTCCCTCCAGTCTTTCCATCTGTTCCCTCCCTCCCTCCCTCCCTCCCTCCCT  |
|          |     |    |     |  |  | CGCCTAGCCCTGCCCTCTGGGGTCACTGCG/ATJGGGTTAGGCCCCCAAAAAA                 |
| stSG4449 | 92  | TC | --- |  |  | ATTAGCCATTCTGTCGCAACAATTGCTTTACTGTAACAAAGTACTGTACTGATGATGTTTACAAT     |
|          |     |    |     |  |  | TAACTTTGGACAACCTTAAACTTA/TJCTAGTGACATTTGCTGTCTAATAATCAAACTACTTCATCATA |
|          |     |    |     |  |  | GGCTGAACATAATTATTAAAGAGCAAAAGTTACCCCTCCC                              |
|          |     |    |     |  |  | CAGACATGAGGGATGGCCCTGTCTCTCTGGGACAGAGCCCTCA/CJAGATGATGTCCATGTTTGTGT   |
| stSG4467 | 42  | CA | --- |  |  | GAAATGAAACTCAAACTCTCTCAGTTTATAGAGTCAATTTCTGTATCGAGCGACACACCGAGGAG     |
|          |     |    |     |  |  | CACACCTGCTTCCAAAGGCTGCTGCTCTGACACAGT                                  |
| stSG4475 | 21  | AC | --- |  |  | ACATGTCAATTCCTGACCAGG/CJATTAAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGGA    |
|          |     |    |     |  |  | TTAAGAGACACAACTGGACTTTTGTTTCTTTTCTTACTGTAGCACCCAGGTTTTCATG            |
|          |     |    |     |  |  | GTAACATTCTGGGGTGGGGTGAGACAACA/CJATGAACCAATAATTAAATACAATTATACATT       |
| stSG4477 | 32  | AG | --- |  |  | TCAAAGGAGACTTTTAACTAGTTAATGTGAACCGCAGCCATCAATGGTTGTGAGGAAAGGGAGA      |
|          |     |    |     |  |  | TGAAGTCTGCTCTGGGCAACGTTTGGCTCATTGCACTGACACTTGGC                       |
|          |     |    |     |  |  | TGAACCTCAGAGCTGGTGGGAGCTGCAGGCGAGGGAGGCTGGGGGCGCAGATGAGCCGGCGGGGA     |
| stSG4531 | 79  | CT | --- |  |  | CAGCAGGCTGCTGCTGCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCCTTGGACTCGATCT   |
| stSG4550 | 86  | GA | --- |  |  | GATTCTCATTGACAGGGGAGACGCTGTTGTCATCA                                   |
|          |     |    |     |  |  | TGCATTAGGAATGATACGGCATAATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT    |
| stSG4550 | 85  | CG | --- |  |  | AAAAGAGACAGTGGGCAC/CJCAATTTGGAGGGGAAGCGGGCGCAGGTTTATAGAGAAC           |
| a        |     |    |     |  |  | TGCATTAGGAATGATACGGCATAATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT    |
|          |     |    |     |  |  | AAAAGAGACAGTGGGCAC/CJGCAATTTGGAGGGGAAGCGGGCGGAGGTTTATAGAGAAC          |
| stSG4590 | 47  | AG | --- |  |  | AATCAGGCACAAGCTCGGGAGAGAGCCCAACAAAAGCTCTTCTGCAC/CJATGGGAGGGAGACAC     |
|          |     |    |     |  |  | CATTGAAAAGGCACTGCTCTCTCTCATGCAAGGAGGCTGGCTCCACAGGCATGGTCTCTTG         |
|          |     |    |     |  |  | AACTGTATCACCCAGCGTGGT/CJCAATGTACTAGTAGCTTTCCACAGGGAATTTTATACTATTC     |
| stSG4623 | 22  | TC | --- |  |  | CTATAAGGTTTATCATGAATAAAAAGCTCACAACTCTTTTCAGCCATTGCAGATTCACATTTATCT    |
|          |     |    |     |  |  | TAATATTCCTGTTCAAGATGCTCTGGAG  |
| stSG4843 | 102 | AC | --- |  |  | TAAAAAAAACAACCCCCCAAAAAACACCCAGAGTTTTTGTAGTTTTTATGTTTTTTCAGATTTAAAG   |
|          |     |    |     |  |  | GTATTTCTTTCTTAGCTTCTAAATTTTGAGTCA/CJATCAGAAAAGTCTCCCTACTCCTCAAGGTGA   |
|          |     |    |     |  |  | GAAAGGA   |

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|---------------|-----|-----|-----|--|--|---|
| stSG4850<br>a | 38  | CT  | --- |  |  | GGAACTAACTGGGAATGGCCGAGGAGGAAGGGGCTC/TGTGCACCTGCAGGCCACGTCAGGAG<br>AGCCAGCGGTGCCTGTCGGGAGGTTTCCAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC<br>TTGGTGGATTCTTGGGTCCC  |
| stSG4879      | 86  | A G | --- |  |  | AACCTTCC  |
| stSG4885      | 104 | GA  | --- |  |  | AACTCTGAAGGGGTGACCTCAACCCAGCCCTGTTTCTGTGAGGTCTGCTTTTCAGAAATGGCCTG<br>CCCCCTGGGACTGGAGCAG/GTCTTGGGTGAGCTCTAGGTGGAGGGTGGTGGAGGGGCATAGAAAT<br>AAACCTTCC  |
| stSG4896      | 112 | CT  | --- |  |  | ACTGGACTGGCTGCTTGCTGAGCCGGCTGAGCGCGTGGGACTGCGGCTGACACCTCGCTCTTCAG<br>AGACTGCCCGCGCGGTACACGACTACGCTCTGCC/GA/GTGGGAAAGCAGAACGAGGACC   |
| stSG4932      | 22  | GA  | --- |  |  | AAACAAATCAAAACCAATCCCCAGCAGTCTATGTACAGGGCCACTCCCTGCTCTCTGCCATAGAGA<br>GGTGGGGGCGAGCTGAGGAGTGGTGGGGCTGGGCACCTTTCTC/TACGCCACAGGCCCTTGAGG  |
| stSG4950      | 24  | A G | --- |  |  | AATTAATTGACTG   |
| stSG4957      | 136 | GA  | --- |  |  | ACAGTCCCGATGGTTACACAA/TG/TTGTAAATGATTTAATCCCACTACGAATGATTAATAATGA<br>TAACTTATGTTTATTTTCATCACTACCAAGGCTGTGGTGCAGGGGTGCTGTTCTGGTCT  |
| stSG4961      | 91  | CT  | --- |  |  | TCATGACTCCAGGAAAGGTCTG/TGTTCTTAGCTTCTCTCCCTACTTCTCTACATGGTCAGC<br>ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG  |
| stSG4967      | 72  | A G | --- |  |  | AGATACGGGCAAAACACTGGGATGGCTTCTGACAACTTAAGAGGTCTCCGAGTTATATTCTGGGT<br>GGGAAACACTGACCCAGCCCTTATTCCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTTCATGAGCC<br>CC/GA/GTGACACAGATGGGGCCCTGCTCTATATTCAAC  |
| stSG4967      | 91  | CT  | --- |  |  | GAAGGTGCTCTGAGGAGGTGACTCTCCCTGGCTGACAGGGGGAAGGCTTAGCAGAGCTTTGTCTTAG<br>AGGAGTAGATGAAAGGAAAGTA/C/TJAGAGAGGGCATTGAGGCCAAGTCAGCAACACAGACAA   |
| stSG4967      | 72  | A G | --- |  |  | ACTGGTCCCTCTCAGCAGATTCAGGGGTGTCAGGGGTGGTTACCACAACTCAGTAGGAGTGCAA<br>GGGCTJ/GT/ACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCCCTTTCTTCTGTGC<br>AACCTTG  |
| stSG4997      | 22  | T C | --- |  |  | CAAAGGAGAGTAGGAGCCCAA/T/CJT/TTTAAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAA<br>CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGAGGAGGCAAGAA<br>GGGATAGGAGAAATGGTGATCCAAAT  |
| stSG6312      | 37  | CT  | --- |  |  | ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAAAC/C/TJ/TATGCCATGCGGGAATAAAATGCTT<br>ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACCTCAAGCAGAAGAC  |
| stSG6345<br>a | 107 | GA  | --- |  |  | GCCTGGTCAAGCAAATTTCTCCAGGACAGCAAGCAAGGACAGTAACACACATGTATGACCCCTTA<br>CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTTGTCCAC/G/ATAGTTCAGGCAATTAAGAATAT<br>GCAACCCAGAGAAATTTCTGTGAAAAACATTTGCTCTTTGGCCTGGTGTGGACAGAAAGGGTGGCCAA<br>ATGGATTGAGTGATGAGACATG |

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|----------|-------------|-----|---|
| stSG6362 | 88 G C ---  | --- | TGTGAAATGTACACTCAGGTCTAACAAATACCTATTATTCTCTGGTTAAGAAAGGTTTAGCAGGAGC<br>CTCCAATGAGCACTGTATGTAG/CAG/AGAAAAAGGGAAGGAGCAGGAGGAGAACAGATCTGCACAGA<br>AT   |
| stSG8010 | 62 G T ---  | --- | CACATCTGTGTTCTGGAGCAAGGAAACACAGAAAGCCAGGAGTTTGGGTGTGCACTGG[G/T]<br>GTCTTTCAACTGGGTGGAACCAAACTGAGTCCTTGAAGTCTCGCTCTGAGGCTGCAGAAGAATAGA<br>TGGCTT   |
| stSG8022 | 53 G A ---  | --- | AGCTCCTGACTCCCTGTTACGTGACGTGTCATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTAT<br>TTACACCATGGAAACTGGAAACTCTACAAATCAATGCGTTATTCTTTATTTTCAGAGGGCAGGTT<br>TATCAGCACACGCTGTATCTCC                                |
| stSG8032 | 67 G C ---  | --- | TGATTGTTAGGGATAAGTGGGCATTGTGTTACAAATTACTTCCAAAGAAATTCAGAAAAATTTGTGTGTT<br>G/CJTGGAGGCGAGGTAGCAAGATAAAAAAGGGAGGACAGCTGGGGTTGGTAAAA   |
| stSG8064 | 46 C A ---  | --- | AGCTGGCTCTTCTCTGTGCGTGTTCGGGAGGCTTACGTCCTCG[C/A]CCGTGGTCCCTGGGTGGCC<br>TGCAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAACAGGGAACA   |
| stSG8064 | 23 G C ---  | --- | AGCTGGCTCTTCTCTGTGCGTGTTCGGGAGGCTTACGTCCTCGCCGCTGGTCCCTGGGTGGCC<br>TGCAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAACAGGGAACA   |
| stSG8072 | 59 A G ---  | --- | CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGGGTCTTGTCTTAGGG[A/G]TGGC<br>AGAGGAGAGGAAAGTCCGAGTATTAGTGGCCGCATGCAAGCTTCAAGCCTGTGCTGTTCAAAA  |
| stSG8100 | 40 A G ---  | --- | ATACACCCACACACCCCACTCAACCTTGATCAAAATTC[A/G]AAGTGTAACATAAGATAAAGAAT<br>ATCATGACTAGTTAAAAGATAGCAATACCATAAGGTACAAGTTCAAGTATTAGTATAACAAAGTAT<br>CTGAGTAACAAATGTCCTTGGAAATGGG                              |
| stSG8102 | 138 T C --- | --- | AAGGCTCCTTTGAAAGCATGGTTATTGTTCCATTAACTTGTCTCAGCTATACCTGAAGTATGATT<br>GACAAATAAACTTGCATATATTGAGATGTACAGTGTGATGATACATGTATGTATACAAATGTGAAA<br>TGAT/CJTGTCATAATCATAATCAATAATTGGTATATTGGTTTAGGAAATGTGATGGT |
| stSG8105 | 110 A G --- | --- | CAGTGGTTCTCAAACTCCAGCGTACACGAGGATGGTCTTGTGCTTGTAAACACAGATGACTAGGCC<br>CACCTGCGGAGTTCCTGTTGGAGTCTAGGCTGAGAAATTC[A/G]TTCTAACAAAGTCCCAGGTGA<br>CCCTGAGGCTCTTGGACTGGGGAACATGCTTTGAG                       |
| stSG8130 | 96 T C ---  | --- | GTGTGTACATCATTTGGGAATGGAGGGAATAAAATGACTGGTGGCTGCTTTTAAAGTTTCAAAAT<br>GACATTCAGACAAGCGGTGCGCTGAGCCT/CJTGCCCTGTCTTCAGATCTTCACAGCACAGTTCC  |
| stSG8130 | 36 C G ---  | --- | GTGTGTACATCATTTGGGAATGGAGGGAATAAAATGA[C/G]TGGATGGTGGCTGCTTTTAAAGTTTCA<br>AATTGACATTCAGACAAGCGGTGCGCTGAGCCTGTGCTTCAGATCTTCACAGCACAGTTCC  |
| stSG8145 | 124 T A --- | --- | TTGTGGACTTCAAAATCTTCTTCAGATTTTAAATGACATTTATGATGTACATATTTTAAATTT<br>AGACACATTTTAGAGAACACAAATGTGAACACAAATCTAAGAAATGAATGAGATGTT[A/C]TGAAA<br>TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCTCTGCTGCTGTGAAAGG   |



[illegible]

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|-----------------|----|----|----|-----|-----|-----|---|
| ESTD-<br>AT3a   | -- | -- | -- | --- | --- | --- | AGACCTCAGTTTCTCTGTAAAGGAAAGTTTGTCTTGGATCTCCATGGGCCAGCCAGCACTG<br>GTGCCCTGTGAGTGTATCAGGTAGAGGAGATGGACCAGGTGGAGGAATTTGAAAGGGCATTG<br>GAATTCAGAGCAAGAGACAGATATTAGAGCTGGGGAATGTGG   |
| ESTD-<br>B3AR   | -- | -- | -- | --- | --- | --- | GGCTGCCAGGGTTCCGTGGAGCGGCCCTAGCCGGGGCCCTGCTGGGCTGGGGTCTGGCCACC<br>GTGGAGGCAACCTGCTGGTCATCGTGCCATCGCCCGGACTCCGAGACTCCAGACCATGAACCAACGT<br>GTTCTGACTTCGCTGGCCGAGCCGACCTGGTGATGGGACTCTGTGGTGGCCCGGGGGCCACCTTT<br>GGCGC   |
| ESTD-<br>BA511  | -- | -- | -- | --- | --- | --- | GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGGTAGCAAGTGC<br>CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGCTGCAG<br>TGAGCCAAGATGGTGCCACTGCA  |
| ESTD-<br>BCL2   | -- | -- | -- | --- | --- | --- | AGCTGGATTATACTCTCTTCTCTGGGGGCGTGGGTGGGAGCTGGGGCGAGAGGTGCCGTT<br>GGCCCCGTTGCTTTCTCTGGGAGGATGGCGCACGCTGGGAGAACAGGTACGACAACCCGGGAG<br>ATAGTATGAAGTACATCCATTATAAGCTGTGCGAGAGGGCTACGAGTGGGATCGGGGAGATGTGG<br>GGCGCGCGCCCGGGGGCGCCCGCCGACCCGGGCATCTTCTCTCCCA            |
| ESTD-BCR        | -- | -- | -- | --- | --- | --- | CAGTGGCTAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCTGCGCAAGA<br>GACCAAGAGGTGAGCTTCTGTTGTCGGGAAAGGGAGGAGGTGACAAGCTAACTCTGCTTCAAA<br>ATCAACATCCGTGGACACTGTGTGGCTGCCATCTGCTCTGGCACA   |
| ESTD-<br>BRCA1a | -- | -- | -- | --- | --- | --- | AAGAAGAGAACTAGAAACAGTTAAGTGTCTAATAATGCTGAAGCCCCAAAGATCTCATGTTAA<br>GTGGAGAAAGGGTTTGCAACTGAAAGATCTGTAGAGATGAGAGTATTTCACTGGTACCTGGTAC<br>TGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA<br>CCAAATAAAT  |
| ESTD-<br>BRCA1b | -- | -- | -- | --- | --- | --- | ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTAGGAACATTCAATGTCACCTGAAAGAGAA<br>ATGGAAATGAGAAATCCAAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT<br>TTTAAAGAACCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA<br>TTAATGAAA                                       |
| ESTD-<br>BRCA1c | -- | -- | -- | --- | --- | --- | ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTGTAGATGATGGTGAATAAAGGAAGATAC<br>TAGTTTGTCTGAAAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG<br>CTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGA<br>AATTAGAGTCTCAGAAGAGAACTTATCTAGTAGGATGAAGAGCTTCCC |
| ESTD-C1R        | -- | -- | -- | --- | --- | --- | ACACAGGTGCTGGCACTGGGGCTGGGGATCCCTCTCCCTAATTTGCTCCGGGAAGCACATTCAACAA<br>CCCAGTCAGTTTGGGGGACAGCCATGCACCTGAGCCTCTGGTAGCCTTTCAACCATGCATTCATCTAA<br>GCTCTGCAAAAT   |
| ESTD-C6         | -- | -- | -- | --- | --- | --- |   |

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| ESTD-C7      | -- | -- | -- | -- | --- | --- | --- | --- | ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA  |
| ESTD-CB22    | -- | -- | -- | -- | --- | --- | --- | --- | GGCAAGTTTTATTGATAGAGAGAAATCAAATATATGGCAATGAGGAGACATCACCTGGAATGTTAG<br>GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCCAAACCCTAGGGCGGATACAAAAGAC<br>AGGCAAGGAAGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCTCAAGCAAGGAGGACCTAG<br>TAACATAATTGCTTCATTATGGTCTTTCCCGGCTTCTCTCACACAC |
| ESTD-CB23    | -- | -- | -- | -- | --- | --- | --- | --- | TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC<br>TTCATTATGGTCTTTCCCGGCTTCTCTCACACATACAGAGCCCCCTACAGGACGACAGCT<br>CTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAACGTGTCCCAACCCGA<br>GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAA      |
| ESTD-CB24    | -- | -- | -- | -- | --- | --- | --- | --- | ACAGGACAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA<br>AAACGTGTCCACCCGAGTCTGTGTTTGAAGCATCAGAAGCAGAGATCTCCACACCCAAAAG<br>GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACACGTGGAGCTGAGCTGGTGGTGAATGG<br>GAAGGAGTGCACAGTGGGTGACAGACAGACCCGAGCCCTCAAGGAG       |
| ESTD-CB25    | -- | -- | -- | -- | --- | --- | --- | --- | GTTCCTTTCAGACTGTGGCTTCACTCCGTAAGTGAGTCTCTCTTTCTCTCTATCTTCGCCGTC<br>TCTGCTCTCGAACCCAGGGCATGGAGAACTCCAGGACACAGGGCGTGAGGGAGCCAGAGCCACCTG<br>TGACAGGTACCTACATGCTCTGTTCTTGTCACAGAGTCTTACCAGCAAGGGTCTCTGCTGCCACC<br>ATCCTCTATGAGATCTTGTAGGGAAGGCCACCTTGATGCCGTG    |
| ESTD-CB27    | -- | -- | -- | -- | --- | --- | --- | --- | TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT<br>TGTGTGTTGGGCTGGTGCATTTGAGGAGTGTCTGTGGAGTTCTGCTCATCTGACCTATCTCTGA<br>TTAGGGAAGCAGCATTCCTTGGACATCTGAAGTACAGCCCTCTTCTCTCCACCAATGCTGCT<br>TTCTCTGTTTCATCTGATGGAAGTCTCAACACCATTTCCATACC     |
| ESTD-COL2A1c | -- | -- | -- | -- | --- | --- | --- | --- | AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA<br>GTGGTGACATACGTTGCTATTTATGCTCTCTTTCTGTCACCTTCAGGGTGTCAAGGTGGAAGAGGT<br>GAACAGGGTCCCGTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCGCTTG<br>GTCAGCCTATTGAGCTGTAATCAACCATACCGTACCT      |
| ESTD-COL2A1d | -- | -- | -- | -- | --- | --- | --- | --- | TGAGAGAACACCTAGTCTCCATCTTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC<br>AATAGACTGAGTTTGTGGACCTGGAACACTGGACTCTTCTACTGCAGCAGACAAGACTTACCC<br>AAGAGAGATTAAATGGCAAAGATATACAATAATTTATTTGACCAACACTATCATGGAACAGC<br>ATT  |
| ESTD-CPT2    | -- | -- | -- | -- | --- | --- | --- | --- | GCCGCAATGCCGGGAGTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGATGCTTAGAA<br>GGCAATCCCATCAAAAGTTAACTCTGGGCAGATGAAAAGCTACCATCCTTCCCTCATCATGAAAC<br>TGGGAGGCCGGGCATAGTGTCTATGCCTGTAATCCAGCATTTTGAGAGGCTGAGGCGGGTGGATCAC<br>TTGAGGTGAGGAGTTTGAGACCAACCTGGCCAACT         |

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| ESTD-<br>D7S399 | -- | --- | --- | --- | --- | TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT<br>AACTGCTAGAGAGCCAGTCTCCTACATCATCTTTTCAAAACATTTTCATCCATGGACTCCATAGTAG<br>AATATTTGAAGAAACAACATGACAAACATTTTC   |
| ESTD-DM         | -- | --- | --- | --- | --- | GTGGGACACCCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCCCTCCACT<br>TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGAGGGAGACA<br>GAATGCTGATTATCTGTGTGAGAACCAAGAACTTCTGGCTGTGGGTAGGGCAGCTGCTTCCAAAGACC<br>TCTGATTTGAGGAAGGGAGCAGAGAGCGAAGAGAACAGAGT           |
| ESTD-<br>DRD1   | -- | --- | --- | --- | --- | TCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTTGGAGAAGATCCAAACCCATCAC<br>ACAAAACGGTCAGCACCCAACTGAACCTGCAGATGAATCTGCCACACATGCTCATCCCCAAAAGCT<br>AGAGGAGATTGCTCTGGGGCTCGCTATTAGAACTAAGGTAC  |
| ESTD-<br>DRD2   | -- | --- | --- | --- | --- | TCTGCCTTTGTGAGGAGGCTGCCGGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA<br>GCCAACCAGAGAGGACCCGTACAGCCCCATCCACCCAGCCACACAGCTGACTCTCCCGACCCG<br>TCCCACACGCTCTCCACAGCACTCCGACAGCCGACAGCCGACAGAGAAATGGGCATGCCAAAG<br>ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCAATG           |
| ESTD-<br>DRD3   | -- | --- | --- | --- | --- | AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCTGGCTGG<br>CACTGTGGAGTTCTGTCCCCACAGGTGTAGTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA<br>GCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTGTGAGGAGA  |
| ESTD-<br>ER882  | -- | --- | --- | --- | --- | TCTTTCAGGATCCGCATCTGGGCTGTTGGGCATCGCTCCGCTAGGTGTACGCGCTCCACAGCTGG<br>GGTGAGGGGTGGTGGTCACTGCCGGGGCCGGTGCAGACCCACCGGGCTGGGAGGACTTCACCC<br>CGCCTCACCTCCGTTCTCGCAGCAGTCTCCGCATCGTGACT  |
| ESTD-<br>ETS2   | -- | --- | --- | --- | --- | ACTCACAGTGTCTTTAAGTGAATGGTCGAGAAAGAGGACCCAGGAAGCCGCTCCTGGCGCTGGCA<br>GTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTCTGTGGACACAC<br>AGACTATTTTAGATTTTCTTTTGGCTTTTGAACCCAGGAACAGAAATGCAAAAACCTCTTTGAGAGG<br>GTAGGAGGTGGGAAGGAACAACCATGTCTATTTTCAAGATTAGTTTG |
| ESTD-F2         | -- | --- | --- | --- | --- | GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT<br>GCACCAAATGGCTCCAAAGGCCGTAGGGGAACCTAGGGGATCTAGGGGATGGTGAGGAATGGCCC<br>AGCCAGTCCCGCGCGTGCCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGGAGATGGGC<br>TGGATGAG   |
| ESTD-F9         | -- | --- | --- | --- | --- | AGATCCTGATGATTTTTTCTATTTTTTCTAAATGTTTTACAGTTTGAAGTTTTAGATTTATGCCCA<br>TGCTCCATTTTGAGTTAATTTTGTAAAGTATGATGTTAAGTCAAACTTCATTTTTTTTTTCCATA<br>GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC  |

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| ESTD-GDH    | -- | -- | --- | ---- | --- | CGCAGAACGGTGAGTGGGGTGGGAGTGGAGGAAAGGAGGAGGAACCTGGGGTTTAGGGACTTCCGGGGTACTTCCCGTTCTGTGCTTGACAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGAAGGGACCTCTGTGTGCGACCGGTGTGTCTGCTGCCCCCTGTTACGTGTCTGTCTGCGCGCAGTCGACTCTGTCCCGGAAATTCGAGAGCT                            |
| ESTD-GCK    | -- | -- | --- | ---- | --- | GTTTATGCATGGCAGCTTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGACAACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGCTGGAGCAGGAATGCCAGCGCGCCTGAGCCACAGGAAGCAGGCTAGGATGTGAGAGACACAGTCAACCTGTCAGCCTAATTACTCAAAGCTGTCCCCAGGTCACAG               |
| ESTD-GNAT2  | -- | -- | --- | ---- | --- | GACCCCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACACAGGCATCATTGAAACCAAGTTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCTCCTAGG  |
| ESTD-GPPK2L | -- | -- | --- | ---- | --- | AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC  |
| ESTD-HRAS   | -- | -- | --- | ---- | --- | CTGGGCTGCCCCGACGAGCTGCTGGCACCTGGACGGCGCGCCAGGCTCACTCTATAGTGGGTGCTATTCTGCCACAAATGCATCTGGATCAGCT  |
| ESTD-HSD3B1 | -- | -- | --- | ---- | --- | TTGGAAGTTCTCCACTGTTAACCGAGTCTATGTTGGCAATGTGGCCTGGGCCCAACATCTGGCCCTTGAGGCCCTGCAGGACCCCAAGAGCCCCCAAGCTCCGAGGACAGTTCTACTATATCTCAGATGACACGCTCACCAAAGCTATGATAACCTTAATTACACCCCTGAGCAAAGAGTTCGGCCTCCGGCTTGATTCCAGATGGAGCTTCCCTTATCCCTGATGTATTGGATTGGCTTCCTGCTG |
| ESTD-HT2    | -- | -- | --- | ---- | --- | GGGCTAAATTTCCGAGCACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGGCAGGGAGAGGAAGATGTGTACAGTTTGTACAGAGAAATAAAAGGATAACCTGGGGTTTCTGTGCTTTGTCTTCCACATCCCTGGGAGTTAATAGCTGCAATTTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTTCAAACAAGACACACCTT               |
| ESTD-HT4    | -- | -- | --- | ---- | --- | ACCAACGAGCCGGATACAGACACTCTTAAGTTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTTCTGATAAACTAGGTTCTTGGTGCTTCTATCGCAAGAAATCGTACTTATTTGAATAGTAGAGGTAA ACCACAGCCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCGAAGACATGCAGATGTC              |
| ESTD-HT5    | -- | -- | --- | ---- | --- | AACACAAAGCCCCAGCGAGAAATTGAACTCGCGACCCCTGGTTTACAAGACCAAGTGCCTCTAACCCCTGAGCTATGGAGCCCTCGTCTGCTGTGGTTTTTCTCCCTTTCATCTATAGATTGATGTTATGCTCCTAGCATTCGCGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCTCCTACAAAATGAAACATTTTCGTGCTCTGTAATCCCTCGAAAAGGTTCT            |
| ESTD-GERP1  | -- | -- | --- | ---- | --- | ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAAGGAAGATGTTCCAGGGCACACATAGCTTAGTGGAGACTC   |

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| ESTD-<br>IGHV4-6 | -- | -- | -- | --- | --- | --- | TTTACTATTTCAATGGATACAGAAATTGTGGGAGTCACTATATCTCTATGAACAAAAATTCAGATTT<br>CAGTGTAAAGTAATGTGCTACATGTGTGAGTGACGGGAGTGGTGGATCCGAGAGTGTGGTGGG<br>TGACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT<br>ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA |
| ESTD-IL1A        | -- | -- | -- | --- | --- | --- | CAAAGTAAGCACCCAAATAATGTTAGCTATTACTATCATTAATTAATTAATTTATTTATTTT<br>AGATGGAGTCTGGCTGTCAACCGGCTGAGTGGAGTGCAGTGCACAATCTCGGCTCACTGCAAGCTCTG<br>CCTCTGGTTCATGCCATCTCTGCTCAGCTCAGCTCCGAGTAGCTGGAAATACAGGCACCCGCCACT<br>GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCAACCGT  |
| ESTD-IL1B        | -- | -- | -- | --- | --- | --- | CCACTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT<br>GGGTCTCTACCTTGGGTGCTGTTCTGCTCAGGAGCTCTCTGCAATTGCAGG  |
| ESTD-<br>KRT10   | -- | -- | -- | --- | --- | --- | CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAAGTTACCTTTTGGCAATATT<br>AAAGGAAGAAATGCAATTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG<br>AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC<br>TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA    |
| ESTD-<br>KRT18   | -- | -- | -- | --- | --- | --- | ACCTCACCCCTCCCTAGCCGTGGGAGCAGGAATCTCTCCAAATCCATGAATACACATCGG<br>ATTGGACACCTTGAGAGTCTTAACAGAGGGCTGACATGAGACCTCAGACAGAACTTCTAGAGTT<br>TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG<br>GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCAACATTGACACA       |
| ESTD-<br>LF79    | -- | -- | -- | --- | --- | --- | GGGTGATTTTGAGGCTCAGTTAATATTCAAAAATGTAACCGTAGCAAAACTGCATTGGTATTTAGA<br>AAAATAAAATTTCCAATATGTAGTGTGTTATACCTGCCTCTGCCATGCAGCATATAGCCTGT<br>GGGAACAGGAGGGCTTCCCTTACCACCCAGA  |
| ESTD-<br>LMP2    | -- | -- | -- | --- | --- | --- | TACACACTTCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA<br>CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG  |
| ESTD-LPL         | -- | -- | -- | --- | --- | --- | TGTCAGTGTCCCTAGGGGCACCTCAACCTCCAGCTCTTCAAGCTCTGCGCTGCTGCTGCTGCA<br>AGGTTTTGCTTAATCTCAATCAATGTCTCTTCACTCTTTAGCAGCTGTGGGTTTTGTTGTTTC<br>TTCGTTTTTGTAGTATCTGACTACTTTTAAATATAAAGAGAGATGTATCTAAACAAAATAGAG<br>ATTGTTATCAGAAAGTTCACAACATTTATTAATAATTTTTCACCTG        |
| ESTD-MCC         | -- | -- | -- | --- | --- | --- | TTGTGAGGAGTGTGCTGATGTGCTGCCCTCCAGCTCTGCTCCCTAGCCGAACCTCAGGACAACGTGCAG<br>CATCCATGTAGGAGAGCCCTAGTCAAGTGAATGCTGAGGAAGCAGTAACACAGCATGCATCCCCGAA<br>TCTCAGGAAGTCTCTGCTTCCAAAGGGTTTGGTCTAAGTTGCTGATTACCCGGATTTTCTGACGATC<br>TTTCAACTGCTAGAGCATGTGTTCCCTGTTTACCATGG  |
| ESTD-NF1         | -- | -- | -- | --- | --- | --- | ATTATCCAGATGAATTTACAAAACATAACAGATCCACAGACTGATATGGCTGGT   |

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| ESTD-NFKB1   | -- | -- | -- | --- | --- | --- | --- | --- | AACATGGACTTGATATTTGTACAAAAAAGTTTTATTTTCTAAAAAAGAAAAAGAA<br>AAATTTAAGGGTGACTTATATCCACACTGCACACTGCTAGCCCAAAACGCTTATTGTGGTAGG<br>ATCAGCCCTCATTTGTGCTTTGTGAACCTTTGTAGGGACGAGAAAGATCATTTGAAATTTCTGAG<br>AAAATCTTTTAAACCTCACCTTTGTGGGTTTTTGAGAAGGTTATCA           |
| ESTD-NPPA    | -- | -- | -- | --- | --- | --- | --- | --- | TGTCCTAGGCCAGCCCTGCTTGTCTCCCTGGCTGTATCTTCTAGTACTGCAAGAGAACACAGAC<br>AT  |
| ESTD-NRAMP   | -- | -- | -- | --- | --- | --- | --- | --- | GGAGGAGGAGGTGGGAGGGGCTGTCTGCTCCAGGTCACAGACCAGAGAGGGGCTCAGTG<br>TATCCACACCCCAATGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT   |
| ESTD-NRAS    | -- | -- | -- | --- | --- | --- | --- | --- | GTGTTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT<br>GGGTTTTCTTTATGTAGGGTGATATGGATACITTTTGTGATTATATAGCAATTTGAGGG<br>ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTC<br>ATCCCTGTGTTTTTAATAAAAT                           |
| ESTD-OTC     | -- | -- | -- | --- | --- | --- | --- | --- | GTGACCTTCTACITTTAAAACTTTACGGAGAGAAATTAATATATGCTATGGCTATCAGCAGA<br>TCTGAAATTTAGGATAAACAGAAAGGAGGTATGTAACA  |
| ESTD-PAI1    | -- | -- | -- | --- | --- | --- | --- | --- | GCCACCACCCACCCACAGCACACCTCCAAACCTCAGCCAGACAGGTTGTTACACAAGAGAGCCC<br>TCAGGGCACAGAGAGAGTCTGGACACGTGGGAGTCAGCGTGTATCATCGGAGGCGCGGGCAC<br>ATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTTAGACAGACAAAAACCTAG<br>ACAATCACGTGGCTGGCT                              |
| ESTD-PAR     | -- | -- | -- | --- | --- | --- | --- | --- | CTCTCAGGAACCCAGCTCTTACCACACGACTATTGCTGCCGAGAGGTACAACCCGTAGA<br>ACTTCTTCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT<br>AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTCTACITTTCTGTGTTCTAGAACGTTTCTAG<br>GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCCATGCCC |
| ESTD-PBDA    | -- | -- | -- | --- | --- | --- | --- | --- | CCTTCTCATGCCAGATGGAATTCAGTCCCTTCAAGATCTGCCTAACCTGTGACAGTCTAAAGAGT<br>CTGAGCCGTGGCTGGGAGGGGAGGACTAATCCAAATCTTACCCGAGCTTGCTCGCATACAGACG<br>GACAGTGTGTGGCAACATTGAAAGCCTCGTACC  |
| ESTD-PS-1    | -- | -- | -- | --- | --- | --- | --- | --- | GGGAGTAAACITTTGGATTGGGAGATTTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA<br>GCCAGTGGAGACTGGAACACACACCATAGCCTATTTCGTAGCCATATTAAATGGTTTGTGCCCTACATT<br>ATTACTCCTTGCCATTTCAAGAAAGCATTGCCAGCTCTTCCATCTCCATCACCTTTGGGCTTGT<br>CTACTTTGCCACAGATTATCTGTA                |
| ESTD-PXIPI   | -- | -- | -- | --- | --- | --- | --- | --- | ATGAAACATGGTCTTTTAAATTTATGATATGTTTATAGCTATCTTAAAGGGCTCTTTTTTTTA<br>ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGTGACAGGTTTCTTCTCAAGGCTCATACAGA<br>TTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTATATCTT   |
| ESTD-Per/RDS | -- | -- | -- | --- | --- | --- | --- | --- | ACCTACAGACGTGGCTGGATGTGTGTCCAAACCCAGGAATCTGAGAGGAGAGCAGGGCTGGCTG<br>CTGGAGAAAGAGCGTGGCGGAGACCTTGAAGGCT  |



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| ESTD-RDS      | -- | -- | -- | -- | --- | --- | CCCGAGGAATCTGAGCGAGCGAGGGCTGGCTGCTGGAGAAGAGCGTGCCGGAGACCTGGAAGG<br>CCTTTCTGGAGAGTGTGAAGAGCTGGCAAGGGCAACAGGTGAAGCGAGGGCGAGACGCGAGG<br>CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC<br>CCAAGAAAGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA            |
| ESTD-<br>RYR1 | -- | -- | -- | -- | --- | --- | CTTCGTGACGGGAGGTACGTCCTCCGCTCTTTATGGACATATGGATGAGTGTCTGACCATTTCCC<br>CTGCTGACAGTGTATGACAGCGCAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCCGC<br>TCCCTCTGAGGCTGGAGCCACTGAGATCAGCTGGAGTGGAGGCCAOCCTGCGCTGGGGCCAGCCACT<br>CCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCAGG |
| ESTD-<br>SPTB | -- | -- | -- | -- | --- | --- | TGAACACCTGTGTCCGGAGCCAGGTGTGTCTCTCCGGAGCCTGAGGAGTTTGTGTGTGTG<br>CAGTCCCCCGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCCTTTGGCCCGGAGAAGAC<br>ATTTACCCACTGGCCATGTCCCTGGCTGTGTGACACCCCTCTGTGAAGACCCCAACCCCTGCTCC<br>CCACCCAAAGCCAGTTTCTAGCAAGGGCAGGAC                      |
| ESTD-<br>SSA1 | -- | -- | -- | -- | --- | --- | TTCACTTTGTGGATTGTTCTTTGCTGTGCAGCACCTTTCAACATGATGTATCCCATTTGTCCAAG<br>TTTGCTTTGGCTGCTGTGTGGGATATTTGAAGAGATCTTTGCCAGTCCCATGTCTCTAGAGAG<br>TTTCCCAATGTTTCTGTAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTTAATCCATTTTG<br>ATTGATTCTGTA  |
| ESTD-TAT      | -- | -- | -- | -- | --- | --- | AAATGGTCAGGACCCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCATCAGTTTCATTCAGCTC<br>CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAATGACTTGTGGGACAGGATCA<br>ATTTCTCTCAGCTAGAACGTTTGTACAACCTTTCTTCCAGTATGGATGGGATTATGATGGGGGG<br>GAGAAGCAATTTTAAATAGGACCCATGAGACACATCA           |
| ESTD-<br>THRB | -- | -- | -- | -- | --- | --- | TGCGCCTTCTCCGGCAGGTAGACTTCTTACTGGCTGTGATTTCCAAAGAGAAAGAGTCCCAAG<br>CAGACGAAACAGAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATCACTTCATCCA<br>CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG   |
| ESTD-<br>TNFA | -- | -- | -- | -- | --- | --- | TTCTGCATCCTGTCTGGAAGTTAGAAGGAACAGACCACAGACCTGGTCCCCAAAGAAATGGAGG<br>CAATAGGTTTTGAGGGCATGAGGACGGGTTTCCGCTCCAGGTCCTACACACAAATCAGTCAGTG<br>GCCAGAGACCCCCCTCAGATCGGAGCAGGGAGGATGGGGGTATCCTTGATGCTT<br>GTGTGTCCTCACTTCCAAATCCCGCCCCCGGATGG                             |
| ESTD-TYR      | -- | -- | -- | -- | --- | --- | TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTTGTTCCACCCGCAACAAGAGTCTATGC<br>CAAGGCAGAAAGCTGGTGTCTATGGCAAAATCAATGTCTCTCCAGATTCAGATCCCCCAAGCA<br>GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATTTGATGTCGTAAACAT<br>GGGTGTGATCCATTTTCATTTGGCCATAGGTCCTATGGGGATGACA         |

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| ESTD-<br>TYRP1  | -- | -- | --- | --- | --- | AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCATGATCAATGCTATGCTGAAGAATATGAA<br>AAATCCAGAAATCCTAAATCAGTCTGTGCTGAACAAATGCCCTACTCTCTTATGCAATAGTATCACAA<br>AACCACTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACTTTATTAACCTCTCTTCT<br>AATACAAGCATATGTTAGAAATTAAGTTCTAGGCATACCTT   |
| ESTD-<br>VB12   | -- | -- | --- | --- | --- | TTCCCAAGGCCTCAATACAAGCTTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA<br>GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTACAGAGACAGGAACACCCAGTG<br>ACTCTGAGATGTCACCAGACTGAGAACCCCGTTATATGTAAGTCTGGTATCGACAAGACCCCGGGGCATG<br>GGCTGAGGCTGATCCATTACTCATAT   |
| ESTD-VWF        | -- | -- | --- | --- | --- | AGTAGGAAAGCAAGAGATTGATTAGTGAAGGAGAGAATGGACCTACCTCCACACTGTCCTTTGG<br>TCCCCTAGAGTCTG   |
| ESTD-WT1        | -- | -- | --- | --- | --- | AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTGCTGCAGGATGCTG<br>CGACGTGTGCTGGAGTAGCCCCGACTCTTGACGGTGGCATCTGAGACCAGTGAGAAACGCCCTT<br>CATGTGTGCTTACCCAGGCTGCAAT  |
| ESTD-<br>s14544 | -- | -- | --- | --- | --- | TTGGGAAGTTAGAGCCTATATTAATACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA<br>TATCCCAAGATTGAAATGTCTCAGTTCGCTGTGTGGGTAGATGCAGGATTATATGATCCCGTTAACC<br>TCT  |
| EST71770<br>6   | -- | -- | --- | --- | --- | AGCACCACTCTCAGCTCAAGCCTCAGCACCAGATGCTGTTCTATAGGATGACGTGCTGTTTACAA<br>CATCTCCTCCATGAAGAGCACAGAGAGTTATTTTATCCTGAAGTCCGGATCTATGACTCAGGACAT<br>ATAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAGCTGTTGGTGGAAAGG<br>AGTGCCAGTCCCAGGGTGACACTGGACAAAGAGGCCATCCAAGG   |
| EST52418<br>6   | -- | -- | --- | --- | --- | CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCCAGTCACCCCTTTGGTGGCTACAAGATGTCG<br>GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAAACTGTGAGTGTGG<br>CCCCTCTATTTGCCAGCCCCCAGGGACAGAGCTGATCCTTGAAGTCTTAAGTTCACATTGCCAGGA<br>CCAGTGAGCAGCAACAGGCCAGGGCTGGCTTATCAGCTCCAGCCAGACCTGGCTGCAGACAT<br>AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCTGCTGCTGCCCCG<br>GTCACCTG |
| EST13586<br>3   | -- | -- | --- | --- | --- | AGGCAGAAACTGGCCCCCATGCGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA<br>GGGACAAGGTCAACTCCTCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT<br>CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGGAGCAGGAGGTCAGATGCTGGCC<br>CCTTTGGAGAGCTGAGCTGCCCTGGTGC   |
| EST51976<br>7   | -- | -- | --- | --- | --- |  |

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|---------------|--|--|--|--|--|--|
| EST11458<br>6 |  |  |  |  |  | CCACITTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTTCTCGAGITTT<br>CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCAGATGATTTACCATTTTCCACAGTGGT<br>CCCATTAAACACATTCTATGAGCCAGGAGAGATACGTATTCCTCGCAAGCCGGCTATGTGTCC<br>CGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC  |
| EST39852<br>8 |  |  |  |  |  | CGGCTTCTCTCCAGGTATTGTCAGAAAGCCGAGATGACCTCTATGTCTCAGATGCATTCACATAAG<br>GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTACGGTACAGAAAGGAGATGCATGAACAGCA<br>GGAACACGTGGAAAGGCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT<br>ACAGCCCT                                      |
| EST62448<br>0 |  |  |  |  |  | ACCTGGTGTGCTGGGTGAACCTGGTCTCTTGGCATTGCCGCCCTCTCTGGGGCCCGTGG<br>TCTCTGGTGTGCTGGGTAGTCTCGAGTCAACGGTCTCTCTAGTGAAGCTGGTCTGATGCAACC<br>CTGGGAACGATGTTCCCGAGGTGCGATGGTCAACCCGACACAAGGAGAGCGCGGTTACCTGG<br>CAATAT   |
| EST36027<br>2 |  |  |  |  |  | AGTGACTTCCAGGAAATGGCTACCCAACTTGCCTTCATCGCGCTGCTGGCCAACTATGCCCTCTCAGA<br>ACATCACCTACCCTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAAACCTGAAAAAGG<br>CTGTCACTTACAGGGCTCTAATGATGTTGAACCTTGTCTGAGGGCAACAGCAGGTTCACTTACACT<br>GTTCTGTAGATGGCTGCTTAAAGACAAATGAATGGGAAAGACAA  |
| EST12274<br>0 |  |  |  |  |  | CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCCAAATAGAGCCCTTACCAAAGTGTAT<br>TACATAAAGAAGTCAAGTGGTTTACTCCTCATGACCAATATCTTTCCCTCTTAGGATGAGGTGA<br>TAGTAAATGACCGATGGGTGAGAACTGTTCTGTCAACCATGGAGGATACTATAACTGTGAAGATAA<br>ATTCAAGCCACAGAGCTTGCCAGATC                         |
| EST76807<br>7 |  |  |  |  |  | ATGCTAAGGGGATCGGACATGAAAGGACCTGTGAGCCGATTGCTCTATCTCCAGGGCCCTGTCTATC<br>CAGCTCACTCATCAATGGGCCAGTCAGGCCAGGCACTGGGCTCCGAGGACTCACCACTGCCCCCT<br>GCTGCCATGTGGACTGGTCAAGTTGAGGACTTCTTG   |
| EST44438<br>3 |  |  |  |  |  | GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCT<br>GCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCCGAGGTGGG   |
| EST12839<br>3 |  |  |  |  |  | TGCAAAACACACAAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTTGCT<br>CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG<br>CCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGAAACTTGAATGTTATTCAACTGG<br>ATTTCCAGTAGGTTTCACTTATGAATATATGATACTTAGCTTAG |
| EST54419<br>8 |  |  |  |  |  | CTTCTGCCAATTTGAATGATATTGTTGCTGTGGGACCTGAGCACCTTTATGGCACAATGATCACTA<br>TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTGTGTTGTTGTTACTA<br>TAGTCCAAAGTGAA   |

|               |    |    |     |     |     |   |
|---------------|----|----|-----|-----|-----|---|
| EST10398<br>2 | -- | -- | --- | --- | --- | TGCTGGGGTGGCAAGCTGCAACAAGGAGGCAACCCAGGAGGCTTTATGAAGCGGGCCATGGTA<br>AGATGCTGCCACCTCTATCTACTTGTATGATGATGTTACATTTGGGCTTGACTTTCCAACACGGAAG<br>CATTGTTTCTTCGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTG   |
| EST36751<br>7 | -- | -- | --- | --- | --- | CCAAAGTCGTTCAATTTAGCTTTCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA<br>TTGAATATGAACCTAGTTTCTGATCTATGTTTCAAGTTAAACAG   |
| EST40562      | -- | -- | --- | --- | --- | CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGATCTGTCCCAAACCTTGTGGCTGAC<br>TTTATGGCTAAGAAGTTTCACTGGATGCATTATAAGAAATATTTACCTTTGAAAAAATAATG<br>AAGGATTGACCTGCTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTGAACAATACAGAT<br>GGCTTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCCCTA                   |
| EST18288<br>3 | -- | -- | --- | --- | --- | GCTCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA<br>GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG<br>ACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAAGCAACCTCTCTGCTGGCTCTGGC<br>CCTAGGACTTAGTATCC                          |
| EST70523<br>3 | -- | -- | --- | --- | --- | TTCCGGCCAGCCCCCATCTTGGACCCCTGGTCCCCCTCAGGGGCCACCCCGGGCCTCACCCGCTCT<br>CGCTCTCGGTAAATCCGGCCGGCGCGCTCTTGGACATAGCTGGACCGTTCCGTATAGGAGG<br>ACCGTGTAGGCTTCTGTCGGGGCTTGGCAGGGGCCAGCCCTGCAGAGAGAGGGGTCCCTGTGGT<br>TGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG                    |
| EST58707<br>7 | -- | -- | --- | --- | --- | CAGTGATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGCTTT<br>AAGTTGAGCATCTTGGCTCACATGAAGGCCAAATTCGAGAGACCTAGAAGATACACGAGACCGA<br>ATGATCAATGGACATTCAGCAGGAACCTTCAACGATACCTGTCTGTGGTAGGCCAGGTTTATAGCA<br>CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGTGCTAAGAACCTT   |
| EST74167<br>6 | -- | -- | --- | --- | --- | AGACCATGAAGGAGTTGAAGGCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG<br>AGACGGGGCACGGCTGTCCAAGGAGCTGCAGGCGCGCAGCCCGGGCTGGCGCGGACATGGAGGA<br>CGTCGGCGCGCGCTGGTGCAGTACCGCGGCGAGTGCAGGCCATGCTCGGCCAGAGCACCCGAGGAGC<br>TGCGGGTGCGCCTCGCTCCACCTGGCAAGCTGGTAAAGCGGCTCCTC |
| EST43211<br>8 | -- | -- | --- | --- | --- | CGCCTGGTGCAGTACCGCGGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCG<br>CCTCGCCTCCACCTCGCAAGCTGCGTAAGCGGCTCTCCCGCATGCCGATGACCTGCAGAAAGCGCC<br>TGGCAGTGTACAGGCGGGCGCGGAGGGCCCGAGCGGCTCAGCGCCATCCGCGAGCGCGCTG<br>GGGCCCCGTGTGGAACAGGGCGCGGTGCGGGGCCGCCACTGTGGGCTC     |
| EST36770<br>4 | -- | -- | --- | --- | --- | TGTAGCCAAAGTCACTGCATCATCTTTGGCTGTGGCAGGCTTGGCCAGTTTGGCAGCTATAATCC<br>ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTCTTCCATTATGAGTCCCAAAAT<br>TCAACCCCTCCGATAGGCTGGGCTGACCAAAATATACTGGGTTCTGTTTCTTCTTCTGATCAT<br>TCTTACAAGTTATCTCTATTGGAAAGGCCCTAAAGAAGGCTTATG        |



|  |     |     |     |     |     |   |
|--|-----|-----|-----|-----|-----|---|
| EST65258<br>8  | --  | --- | --- | --- | --- | TGCCCCATCAGCGGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAAGAAAT<br>CCAGTTATTTTCCACCCTCAAATGACAGCCATGGCCGCGGGTGCTTCTGGGGCTCGTCGGGGGG<br>ACAGCTCCACTCTGACTGGCAGACTCTTTCATGGAGACTTGAGGAGGAGGGCTTGAGGTTGGTGAG<br>GTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA |
| EST38216<br>3  | --  | --- | --- | --- | --- | ATGCAGGATGAAGGTGGACAGGGAGGAGAGGGCCAACTGTATCCAGGGCCTGCAGATGTCGCTG<br>GACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG   |
| EST62782<br>--   | --- | --- | --- | --- | --- | ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTAATAGCAATTTGTTTAGCATTACCTAA<br>TTTTTTCTGCTCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATTTAAATGACAGTGGAAAG<br>TTTTTTTCTCGAAGTGCCAGTATCCAGAGTTTTGGTTTTTGAACCTAGCAATGCCTGTGAAAAA<br>GAACTGAATACCTAAGATTCTGTCTTGGGGTTTTTGGTGCATGCA   |
| EST35879<br>9  | --  | --- | --- | --- | --- | GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCCTCCAACTCTTGTCGTTCCACCGATG<br>GAACTGCCGGCAAATCCTGACACGTGTGCCACAGGCTGTACCAATAGGTGAACATGGCTTCGAG<br>AGAGTTGAACAGATTCTCGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGAA  |
| EST68308<br>5  | --  | --- | --- | --- | --- | GGAAGAGATTTAAGAAGCTTGATTGGACAATCTGGTCTTTGAGTGTGGAAGAGTTTCATGTCTCT<br>GCTGAGTTACACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA<br>GAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTTA   |
| EST54045<br>6  | --  | --- | --- | --- | --- | GGAATATTAATAATTTTTAAATACCTCCATTTTGCTTATCCTTTAGTGAAGATGATACCTGCAA<br>AAGACATGGCTAAAGTTATGATTGTCTATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAATCT<br>GTTAAGTAAGTACTGTTTGCCCTTGGAAATGGATTTTAAATGTTGACTTTATCAT   |
| EST52908<br>0  | --  | --- | --- | --- | --- | ATCACAGGTCTCTGGTCTCTGCCCATCTTCTCTGGGAGAGATGGATGGTGGTCTGCAAGCCCTTTGG<br>CAATGTGAGATTGATG   |
| EST19590<br>--   | --- | --- | --- | --- | --- | AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGATGACATTGATGAGTGAAGATGTCGGCTCAGGAT<br>GCCGGAAAATGAC  |
| EST76136<br>--   | --- | --- | --- | --- | --- | TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACCCCGCTCATACCTTTATCTATAGCCTTCCCC<br>TAGGTCIT  |
| EST58607<br>0  | --  | --- | --- | --- | --- | CTCTGGATGGTTCACAGGTGGCAGGCACCAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC<br>CAAGTTGCTCTCCTCACTGGAGAACCAAGGACAGCCACATGGCGGGATGGCCGGGAGTTCTGGT<br>TGCGGCCACGGCTGTGCCCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGTTCT<br>TGCCCAAGGAGGGCGGGTGCATGCCTGAGATGTAGATGCGGCC |
| Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer<br>6=SNP Reverse Primer 7=Sequence |     |     |     |     |     |   |

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## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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## CLAIMS

## WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a  
20 segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.



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12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
- 15 10 15. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining  
comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.
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